

RNAlib-2.5.1

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# Chapter 1

## RNAlib-2.5.1

### 1.1 A Library for predicting and comparing RNA secondary structures

The core of the ViennaRNA Package ([14], [12]) is formed by a collection of routines for the prediction and comparison of RNA secondary structures. These routines can be accessed through stand-alone programs, such as `RNAfold`, `RNAdistance` etc., which should be sufficient for most users. For those who wish to develop their own programs we provide a library which can be linked to your own code.

This document describes the library and will be primarily useful to programmers. However, it also contains details about the implementation that may be of interest to advanced users. The stand-alone programs are described in separate man pages. The latest version of the package including source code and html versions of the documentation can be found at

<http://www.tbi.univie.ac.at/RNA>

#### Date

1994-2020

#### Authors

Ivo Hofacker, Peter Stadler, Ronny Lorenz, and so many more

### 1.2 License

#### Disclaimer and Copyright

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## 1.3 Contributors

Over the past decades since the `ViennaRNA Package` first sprang to life as part of Ivo Hofackers PhD project, several different authors contributed more and more algorithm implementations. In 2008, Ronny Lorenz took over the extensive task to harmonize and simplify the already existing implementations for the sake of easier feature addition. This eventually lead to version 2.0 of the `ViennaRNA Package`. Since then, he (re-)implemented a large portion of the currently existing library features, such as the new, generalized constraints framework, RNA folding grammar domain extensions, and the major part of the scripting language interface. Below is a list of most people who contributed larger parts of the implementations:

- Daniel Wiegreffe (RNAturtle and RNApuzzler secondary structure layouts)
- Andreas Gruber (first approach on RNALfold Z-score filtering)
- Juraj Michalik (non-redundant Boltzmann sampling)
- Gregor Entzian (neighbor, walk)
- Mario Koestl (worked on SWIG interface and related unit testing)
- Dominik Luntzer (perturbation fold)
- Stefan Badelt (cofold evaluation, RNAdesign.pl, cofold findpath extensions)
- Stefan Hammer (parts of SWIG interface and corresponding unit tests)
- Ronny Lorenz (circfold, version 2.0, generic constraints, grammar extensions, and much more)
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- Ivo Hofacker, Peter Stadler, and Christoph Flamm (almost every implementation up to version 1.8.5)

We also want to thank the following people:

- Sebastian Bonhoeffer's implementation of partition function folding served as a precursor to our `part_func.c`
- Manfred Tacker hacked constrained folding into `fold.c` for the first time
- Martin Fekete made the first attempts at "alignment folding"
- Andrea Tanzer and Martin Raden (Mann) for not stopping to report bugs found through comprehensive usage of our applications and RNAlib
- Thanks also to everyone else who helped testing and finding bugs, especially Christoph Flamm, Martijn Huynen, Baerbel Krakhofer, and many more

If you want to get involved in the development of the `ViennaRNA Package` yourself, please read the [Contributing page](#).

## Chapter 2

# Getting Started

- [Installation and Configuration](#) describes how to install and configure `RNAlib` for your requirements
- [HelloWorld](#) presents some small example programs to get a first impression on how to use this library
- [HelloWorld \(Perl/Python\)](#) contains small examples that show how to use `RNAlib` even without C/C++ programming skills from within your favorite scripting language

## 2.1 Installation and Configuration

A documentation on how to configure the different features of `RNAlib`, how to install the ViennaRNA Package, and finally, how to link you own programs against `RNAlib`.

### 2.1.1 Installing the ViennaRNA Package

For best portability the ViennaRNA package uses the GNU autoconf and automake tools. The instructions below are for installing the ViennaRNA package from source. However, pre-compiled binaries for various Linux distributions, as well as for Windows users are available from Download section of the [main ViennaRNA homepage](#).

#### 2.1.1.1 Quick-start

Usually you'll just unpack, configure and make. To do this type:

```
tar -zxvf ViennaRNA-2.5.1.tar.gz
cd ViennaRNA-2.5.1
./configure
make
sudo make install
```

#### 2.1.1.2 Installation without root privileges

If you do not have root privileges on your computer, you might want to install the ViennaRNA Package to a location where you actually have write access to. To do so, you can set the installation prefix of the `./configure` script like so:

```
./configure --prefix=/home/username/ViennaRNA
make install
```

This will install the entire ViennaRNA Package into a new directory `ViennaRNA` directly into the users `username` home directory.

### 2.1.1.3 Notes for MacOS X users

**2.1.1.3.1 Compilation** Although users will find `/usr/bin/gcc` and `/usr/bin/g++` executables in their directory tree, these programs are not at all what they pretend to be. Instead of including the GNU programs, Apple decided to install clang/llvm in disguise. Unfortunately, the default version of clang/llvm does not support OpenMP (yet), but only complains at a late stage of the build process when this support is required. Therefore, it seems necessary to deactivate OpenMP support by passing the option `--disable-openmp` to the `./configure` script.

**2.1.1.3.2 Missing EXTERN.h include file** Furthermore, as far as we are informed, users are discouraged to use the Perl 5 interpreter that is shipped with Mac OS X. Instead, one should install a more recent version from another source, e.g. `homebrew`. If, however, for any reason you do not want to install your own Perl 5 interpreter but use the one from Apple, you need to specify its include path to enable building the ViennaRNA Perl interface. Otherwise, the file `EXTERN.h` will be missing at compile time. To fix this problem, you first need to find out where `EXTERN.h` is located:

```
sudo find /Library -type f -name EXTERN.h
```

Then choose the one that corresponds to your default perl interpreter (find out the version number with `perl -v | grep version`), simply execute the following before running the `./configure` script, e.g.:

```
export CPATH=/Library/Developer/CommandLineTools/SDKs/MacOSX10.15.sdk/System/Library/Perl/5.18/darwin-thread-m
```

if your default perl is v5.18 running on MacOSX10.15. Change the paths according to your current setup. After that, running `./configure` and compilation should run fine.

See also <https://stackoverflow.com/questions/52682304/fatal-error-extern-h-file-not-found>

**2.1.1.3.3 Universal binaries** Additionally, if you intend to build the ViennaRNA such that it runs on both, x86\_64 and the armv8 (such as for the M1 processors in recent MacBooks), architectures, you need to build a so-called universal binary. Note, however, that to accomplish this task, you might need to deactivate any third-party library dependency as in most cases, only one architecture will be available at link time. This includes the Perl 5 and Python interfaces but also MPFR and GSL support, possibly even more. In order to compile and link the programs, library, and scripting language interfaces of the ViennaRNA Package for multiple architectures, we've added a new configure switch that sets up the required changes automatically:

```
./configure --enable-universal-binary
```

#### Note

Note, that with link time optimization turned on, MacOS X's default compiler (Illum/clang) generates an intermediary binary format that can not easily be combined into a multi-architecture library. Therefore, the `--enable-universal-binary` switch turns off link time optimization!

## 2.1.2 Configuring RNAlib features

The ViennaRNA Package includes additional executable programs such as RNAforester, Kinfold, and Kinwalker. Furthermore, we include several features in our C-library that may be activated by default, or have to be explicitly turned on at configure-time. Below we list a selection of the available configure options that affect the features included in all executable programs, the RNAlib C-library, and the corresponding scripting language interface(s).

### 2.1.2.1 Streaming SIMD Extension (SSE) support

Since version 2.3.5 our sources contain code that implements a faster multibranch loop decomposition in global MFE predictions, as used e.g. in RNAfold. This implementation makes use of modern processors capability to execute particular instructions on multiple data simultaneously (SIMD - single instruction multiple data, thanks to W. B. Langdon for providing the modified code). Consequently, the time required to assess the minimum of all multibranch loop decompositions is reduced up to about one half compared to the runtime of the original implementation. This feature is enabled by default since version 2.4.11 and a dispatcher ensures that the correct implementation will be selected at runtime. If for any reason you want to disable this feature at compile-time use the following configure flag:

```
./configure --disable-simd
```

### 2.1.2.2 Scripting Interfaces

The ViennaRNA Package comes with scripting language interfaces for Perl 5, Python 3.x, and Python 2.x (provided by swig), that allow one to use the implemented algorithms directly without the need of calling an executable program. The interfaces are build by default whenever the autoconf tool-chain detects the required build tools on your system. You may, however, explicitly turn off particular scripting language interface support at configure-time, for instance for Perl 5 and Python 2, before the actual installation.

Example:

```
./configure --without-perl --without-python2
```

Disabling the scripting language support all-together can be accomplished using the following switch:

```
./configure --without-swig
```

### 2.1.2.3 Cluster Analysis

The programs AnalyseSeqs and AnalyseDists offer some cluster analysis tools (split decomposition, statistical geometry, neighbor joining, Ward's method) for sequences and distance data. To also build these programs add

```
--with-cluster
```

to your configure options.

### 2.1.2.4 Kinfold

The Kinfold program can be used to simulate the folding dynamics of an RNA molecule, and is compiled by default. Use the

```
--without-kinfold
```

option to skip compilation and installation of Kinfold.

### 2.1.2.5 RNAforester

The RNAforester program is used for comparing secondary structures using tree alignment. Similar to Kinfold, use the

```
--without-forester
```

option to skip compilation and installation of RNAforester.

### 2.1.2.6 Kinwalker

The Kinwalker algorithm performs co-transcriptional folding of RNAs, starting at a user specified structure (default↵: open chain) and ending at the minimum free energy structure. Compilation and installation of this program is deactivated by default. Use the

```
--with-kinwalker
```

option to enable building and installation of Kinwalker.

### 2.1.2.7 Link Time Optimization (LTO)

To increase the performance of our implementations, the ViennaRNA Package tries to make use of the Link Time Optimization (LTO) feature of modern C-compilers. If you are experiencing any troubles at make-time or run-time, or the configure script for some reason detects that your compiler supports this feature although it doesn't, you can deactivate it using the flag

```
./configure --disable-lto
```

Note, that GCC before version 5 is known to produce unreliable LTO code, especially in combination with SIMD (see [Streaming SIMD Extension \(SSE\) support](#)). We therefore recommend using a more recent compiler (GCC 5 or above) or to turn off one of the two features, LTO or SIMD optimized code.

### 2.1.2.8 OpenMP support

To enable concurrent computation of our implementations and in some cases parallelization of the algorithms we make use of the OpenMP API. This interface is well understood by most modern compilers. However, in some cases it might be necessary to deactivate OpenMP support and therefore transform *RNAlib* into a C-library that is not entirely *thread-safe*. To do so, add the following configure option

```
./configure --disable-openmp
```

### 2.1.2.9 POSIX threads (pthread) support

To enable concurrent computation of multiple input data in RNAfold, and for our implementation of the concurrent unordered insert, ordered output flush data structure `vrna_ostream_t` we make use of POSIX threads. This should be supported on all modern platforms and usually does not pose any problems. Unfortunately, we use a threadpool implementation that is not compatible with Microsoft Windows yet. Thus, POSIX thread support can not be activated for Windows builds until we have fixed this problem. If you want to compile RNAfold and RNAlib without POSIX threads support for any other reasons, add the following configure option

```
./configure --disable-pthreads
```

### 2.1.2.10 SVM Z-score filter in RNALfold

By default, RNALfold that comes with the ViennaRNA Package allows for z-score filtering of its predicted results using a support vector machine (SVM). However, the library we use to implement this feature (libsvm) is statically linked to our own RNALib. If this introduces any problems for your own third-party programs that link against RNALib, you can safely switch off the z-scoring implementation using

```
./configure --without-svm
```

### 2.1.2.11 GNU Scientific Library

The new program RNApvm computes a pseudo-energy perturbation vector that aims to minimize the discrepancy of predicted, and observed pairing probabilities. For that purpose it implements several methods to solve the optimization problem. Many of them are provided by the GNU Scientific Library, which is why the RNApvm program, and the RNALib C-library are required to be linked against libgsl. If this introduces any problems in your own third-party programs that link against RNALib, you can turn off a larger portion of available minimizers in RNApvm and linking against libgsl all-together, using the switch

```
./configure --without-gsl
```

### 2.1.2.12 Disable C11/C++11 feature support

By default, we use C11/C++11 features in our implementations. This mainly accounts for unnamed unions/structs within *RNALib*. The configure script automatically detects whether or not your compiler understands these features. In case you are using an older compiler, these features will be deactivated by setting a specific pre-processor directive. If for some reason you want to deactivate C11/C++11 features despite the capabilities of your compiler, use the following configure option:

```
./configure --disable-c11
```

### 2.1.2.13 Enable warnings for use of deprecated symbols

Since version 2.2 we are in the process of transforming the API of our *RNALib*. Hence, several symbols are marked as *deprecated* whenever they have been replaced by the new API. By default, deprecation warnings at compile time are deactivated. If you want to get your terminal spammed by tons of deprecation warnings, enable them using:

```
./configure --enable-warn-deprecated
```

### 2.1.2.14 Single precision partition function

Calculation of partition functions (via RNAfold -p) uses double precision floats by default, to avoid overflow errors on longer sequences. If your machine has little memory and you don't plan to fold sequences over 1000 bases in length you can compile the package to do the computations in single precision by running

```
./configure --enable-floatpf
```

#### Note

Using this option is discouraged and not necessary on most modern computers.

### 2.1.2.15 Help

For a complete list of all `./configure` options and important environment variables, type

```
./configure --help
```

For more general information on the build process see the `INSTALL` file.

### 2.1.3 Linking against RNAlib

In order to use our implemented algorithms you simply need to link your program to our *RNAlib* C-library that usually comes along with the ViennaRNA Package installation. If you've installed the ViennaRNA Package as a pre-build binary package, you probably need the corresponding development package, e.g. *viennarna-devel*, or *viennarna-dev*. The only thing that is left is to include the ViennaRNA header files into your source code, e.g.:

```
#include <ViennaRNA/mfe.h>
```

and start using our fast and efficient algorithm implementations.

#### See also

In the [C Examples](#) and [Some Examples using RNAlib API v3.0](#) sections, we list a small set of example code that usually is a good starting point for your application.

#### 2.1.3.1 Compiler and Linker flags

Of course, simply adding the ViennaRNA header files into your source code is usually not enough. You probably need to tell your compiler where to find the header files, and sometimes add additional pre-processor directives. Whenever your installation of *RNAlib* was build with default settings and the header files were installed into their default location, a simple

```
-I/usr/include
```

pre-processor/compile flag should suffice. It can even be omitted in this case, since your compiler should search this directory by default anyway. You only need to change the path from `/usr/include` to the correct location whenever the header files have been installed into a non-standard directory.

On the other hand, if you've compiled *RNAlib* with some non-default settings then you probably need to define some additional pre-processor macros:

- `VRNA_DISABLE_C11_FEATURES` . . . Disable C11/C++11 features.

#### Warning

Add this directive to your pre-processor/compile flags only if *RNAlib* was build with the `--disable-c11` configure option.



See also

[Disable C11/C++11 feature support](#) and `vrna_C11_features()`

- `VRNA_WARN_DEPRECATED` . . . Enable warnings for using deprecated symbols.

Note

Adding this directive enables compiler warnings whenever you use symbols in *RNAlib* that are marked *deprecated*.

See also

[Enable warnings for use of deprecated symbols](#) and [Deprecated List](#)

- `USE_FLOAT_PF` . . . Use single precision floating point operations instead of double precision in partition function computations.

Warning

Define this macro only if *RNAlib* was build with the `--enable-floatpf` configure option!

See also

[Single precision partition function](#)

Simply add the corresponding definition(s) to your pre-processor/compile flags, for instance:

```
-DVRNA_DISABLE_C11_FEATURES
```

Finally, linking against *RNAlib* is achieved by adding the following linker flag

```
-L/usr/lib -lRNA -fopenmp
```

Again, the path to the library, `/usr/lib`, may be omitted if this path is searched for libraries by default. The second flag tells the linker to include *libRNA.a*, and the remaining two flags activate [Link Time Optimization \(LTO\)](#) and [OpenMP support](#) support, respectively.

Note

Depending on your linker, the last two flags may differ.

Depending on your configure time decisions, you can drop one or both of the last flags.

In case you've compiled *RNAlib* with LTO support (See [Link Time Optimization \(LTO\)](#)) and you are using the same compiler for your third-party project that links against our library, you may add the

```
-flto
```

flag to enable Link Time Optimization.

### 2.1.3.2 The pkg-config tool

Instead of hard-coding the required compiler and linker flags, you can also let the *pkg-config* tool automatically determine the required flags. This tool is usually packaged for any Linux distribution and should be available for MacOS X and MinGW as well. We ship a file *RNAlib2.pc* which is installed along with the static *libRNA.a* C-library and populated with all required compiler and linker flags that correspond to your configure time decisions.

The compiler flags required for properly building your code that uses *RNAlib* can be easily obtained via

```
pkg-config --cflags RNAlib2
```

You get the corresponding linker flags using

```
pkg-config --libs RNAlib2
```

With this widely accepted standard it is also very easy to integrate *RNAlib* in your *autotools* project, just have a look at the `PKG_CHECK_MODULES` macro.

## 2.2 HelloWorld

Below, you'll find some more or less simple C programs showing first steps into using *RNAlib*. A complete list of example C programs can be found in the [C Examples](#) section.

### Simple MFE prediction for a given sequence

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/fold.h>
#include <ViennaRNA/utils/basic.h>
int
main()
{
    /* The RNA sequence */
    char *seq = "GAGUAGUGGAACCCAGGCUAUGUUUGUGACUCGCAGACUAACA";
    /* allocate memory for MFE structure (length + 1) */
    char *structure = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* predict Minimum Free Energy and corresponding secondary structure */
    float mfe = vrna_fold(seq, structure);
    /* print sequence, structure and MFE */
    printf("%s\n%s [ %6.2f ]\n", seq, structure, mfe);
    /* cleanup memory */
    free(structure);
    return 0;
}
```

#### See also

examples/helloworld\_mfe.c in the source code tarball

### Simple MFE prediction for a multiple sequence alignment

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/alifold.h>
#include <ViennaRNA/utils/basic.h>
#include <ViennaRNA/utils/alignments.h>
int
main()
{
    /* The RNA sequence alignment */
    const char *sequences[] = {
        "CUGCCUCACAACGUUUGUGCCUCAGUUACCCGUAGAUAGUGAGGGU",
        "CUGCCUCACAACAUAUUUGUGCCUCAGUUACUCAUAGAUGUAGUGAGGGU",
        "---CUCGACACCACU---GCCUCGGUUAACCAUCGGUGCAGUGCGGGU",
        NULL /* indicates end of alignment */
    };
    /* compute the consensus sequence */
    char *cons = consensus(sequences);
    /* allocate memory for MFE consensus structure (length + 1) */
    char *structure = (char *)vrna_alloc(sizeof(char) * (strlen(sequences[0]) + 1));
    /* predict Minimum Free Energy and corresponding secondary structure */
    float mfe = vrna_alifold(sequences, structure);
    /* print consensus sequence, structure and MFE */
    printf("%s\n%s [ %6.2f ]\n", cons, structure, mfe);
    /* cleanup memory */
    free(cons);
    free(structure);
    return 0;
}
```

#### See also

examples/helloworld\_mfe\_comparative.c in the source code tarball

## Simple Base Pair Probability computation

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/fold.h>
#include <ViennaRNA/part_func.h>
#include <ViennaRNA/utills/basic.h>
int
main()
{
    /* The RNA sequence */
    char *seq = "GAGUAGUGGAACCAGGCUAUGUUUGUGACUCGACAGACUAACA";
    /* allocate memory for pairing propensity string (length + 1) */
    char *propensity = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* pointers for storing and navigating through base pair probabilities */
    vrna_ep_t *ptr, *pair_probabilities = NULL;
    float en = vrna_pf_fold(seq, propensity, &pair_probabilities);
    /* print sequence, pairing propensity string and ensemble free energy */
    printf("%s\n%s [ %.2f ]\n", seq, propensity, en);
    /* print all base pairs with probability above 50% */
    for (ptr = pair_probabilities; ptr->i != 0; ptr++)
        if (ptr->p > 0.5)
            printf("p(%d, %d) = %g\n", ptr->i, ptr->j, ptr->p);
    /* cleanup memory */
    free(pair_probabilities);
    free(propensity);
    return 0;
}
```

### See also

examples/helloworld\_probabilities.c in the source code tarball

## Deviating from the Default Model

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/model.h>
#include <ViennaRNA/fold_compound.h>
#include <ViennaRNA/utills/basic.h>
#include <ViennaRNA/utills/strings.h>
#include <ViennaRNA/mfe.h>
int
main()
{
    /* initialize random number generator */
    vrna_init_rand();
    /* Generate a random sequence of 50 nucleotides */
    char *seq = vrna_random_string(50, "ACGU");
    /* allocate memory for MFE structure (length + 1) */
    char *structure = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* create a new model details structure to store the Model Settings */
    vrna_md_t md;
    /* ALWAYS set default model settings first! */
    vrna_md_set_default(&md);
    /* change temperature and activate G-Quadruplex prediction */
    md.temperature = 25.0; /* 25 Deg Celcius */
    md.gquad = 1; /* Turn-on G-Quadruples support */
    /* create a fold compound */
    vrna_fold_compound_t *fc = vrna_fold_compound(seq, &md, VRNA_OPTION_DEFAULT);
    /* predict Minimum Free Energy and corresponding secondary structure */
    float mfe = vrna_mfe(fc, structure);
    /* print sequence, structure and MFE */
    printf("%s\n%s [ %.2f ]\n", seq, structure, mfe);
    /* cleanup memory */
    free(structure);
    vrna_fold_compound_free(fc);
    return 0;
}
```

### See also

examples/fold\_compound\_md.c in the source code tarball

## 2.3 HelloWorld (Perl/Python)

### 2.3.1 Perl5

#### Simple MFE prediction for a given sequence

```
use RNA;
# The RNA sequence
my $seq = "GAGUAGUGGAACCAGGCUAUGUUUGUGACUCGCAGACUAACA";
# compute minimum free energy (MFE) and corresponding structure
my ($ss, $mfe) = RNA::fold($seq);
# print output
printf "%s\n%s [ %6.2f ]\n", $seq, $ss, $mfe;
```

#### Simple MFE prediction for a multiple sequence alignment

```
use RNA;
# The RNA sequence alignment
my @sequences = (
    "CUGCCUCACAACGUUUGUGCCUCAGUUACCCGUAUGAUGUAGUGAGGGU",
    "CUGCCUCACAACAUUUUGUGCCUCAGUUACUACAUAGAUGUAGUGAGGGU",
    "---CUCGACACCACU---GCCUCGGUUACCAUCGGUGCAGUGCGGGU"
);
# compute the consensus sequence
my $cons = RNA::consensus(\@sequences);
# predict Minimum Free Energy and corresponding secondary structure
my ($ss, $mfe) = RNA::alifold(\@sequences);
# print output
printf "%s\n%s [ %6.2f ]\n", $cons, $ss, $mfe;
```

#### Deviating from the Default Model

```
use RNA;
# The RNA sequence
my $seq = "GAGUAGUGGAACCAGGCUAUGUUUGUGACUCGCAGACUAACA";
# create a new model details structure
my $md = new RNA::md();
# change temperature and dangle model
$md->{temperature} = 20.0; # 20 Deg Celcius
$md->{dangles} = 1; # Dangle Model 1
# create a fold compound
my $fc = new RNA::fold_compound($seq, $md);
# predict Minimum Free Energy and corresponding secondary structure
my ($ss, $mfe) = $fc->mfe();
# print sequence, structure and MFE
printf "%s\n%s [ %6.2f ]\n", $seq, $ss, $mfe;
```

### 2.3.2 Python

#### Simple MFE prediction for a given sequence

```
import RNA
# The RNA sequence
seq = "GAGUAGUGGAACCAGGCUAUGUUUGUGACUCGCAGACUAACA"
# compute minimum free energy (MFE) and corresponding structure
(ss, mfe) = RNA.fold(seq)
# print output
print("{}\n{} [ {:.6.2f} ]".format(seq, ss, mfe))
```

#### Simple MFE prediction for a multiple sequence alignment

```
import RNA
# The RNA sequence alignment
sequences = [
    "CUGCCUCACAACGUUUGUGCCUCAGUUACCCGUAUGAUGUAGUGAGGGU",
    "CUGCCUCACAACAUUUUGUGCCUCAGUUACUACAUAGAUGUAGUGAGGGU",
    "---CUCGACACCACU---GCCUCGGUUACCAUCGGUGCAGUGCGGGU"
]
# compute the consensus sequence
cons = RNA.consensus(sequences)
# predict Minimum Free Energy and corresponding secondary structure
(ss, mfe) = RNA.alifold(sequences);
# print output
print("{}\n{} [ {:.6.2f} ]".format(cons, ss, mfe))
```

## Deviating from the Default Model

```
import RNA
# The RNA sequence
seq = "GAGUAGUGGAACCCAGGCUAUGUUUGUGACUCGCAGACUAACA"
# create a new model details structure
md = RNA.md()
# change temperature and dangle model
md.temperature = 20.0 # 20 Deg Celcius
md.dangles     = 1     # Dangle Model 1
# create a fold compound
fc = RNA.fold_compound(seq, md)
# predict Minmum Free Energy and corresponding secondary structure
(ss, mfe) = fc.mfe()
# print sequence, structure and MFE
print("{}\n{} [ {:.2f} ]".format(seq, ss, mfe))
```



## Chapter 3

# Concepts and Algorithms

This is an overview of the concepts and algorithms for which implementations can be found in this library.

Almost all of them rely on the physics based Nearest Neighbor Model for RNA secondary structure prediction.

- [RNA Structure](#) gives an introduction into the different layers of abstraction for RNA structures
- [Distance Measures](#) introduces different metrics to allow for the comparison of secondary structures
- [Free Energy of Secondary Structures](#) shows how the stability of a secondary structure can be quantified in terms of free energy
- [Secondary Structure Folding Grammar](#) explains the basic recursive decomposition scheme that is applied in secondary structure prediction
- [RNA Secondary Structure Landscapes](#) describes how transition paths between secondary structures span a landscape like graph
- [Minimum Free Energy Algorithm\(s\)](#) compute the most stable conformation in thermodynamic equilibrium
- [Partition Function and Equilibrium Probability Algorithm\(s\)](#) enable one to apply statistical mechanics to derive equilibrium probabilities of structure features
- [Suboptimal and \(other\) Representative Structures](#) allow for alternative description and enumeration of the structure ensemble
- [RNA-RNA Interaction](#) introduces how to model the interaction between RNA molecules
- [Locally Stable Secondary Structures](#) offer insights into structuredness of long sequences and entire genomes
- [Comparative Structure Prediction](#) augment structure prediction with evolutionary conservation of homologous sequences
- [Classified DP variations](#) perform an *a priori* partitioning of the structure ensemble and compute various properties for the resulting classes.
- [RNA Sequence Design](#) constitutes the inverse problem of structure prediction
- [Experimental Structure Probing Data](#) can be used to guide structure prediction, for instance using SHAPE reactivity data
- [Ligand Binding](#) adds more complexity to structure prediction by modelling the interaction between small chemical compounds or proteins and the RNA
- [\(Tertiary\) Structure Motifs](#) extend the abstraction of secondary structure beyond canonical base pair formation

## 3.1 RNA Structure

### 3.1.1 RNA Structures

### 3.1.2 Levels of Structure Abstraction

#### 3.1.2.1 Primary Structure

#### 3.1.2.2 Secondary Structure

#### 3.1.2.3 Tertiary Structure

#### 3.1.2.4 Quarternary Structure

#### 3.1.2.5 Pseudo-Knots

## 3.2 Distance Measures

A simple measure of dissimilarity between secondary structures of equal length is the base pair distance, given by the number of pairs present in only one of the two structures being compared. I.e. the number of base pairs that have to be opened or closed to transform one structure into the other. It is therefore particularly useful for comparing structures on the same sequence. It is implemented by

```
int bp_distance(const char *str1,
               const char *str2)
```

Compute the "base pair" distance between two secondary structures s1 and s2.

For other cases a distance measure that allows for gaps is preferable. We can define distances between structures as edit distances between trees or their string representations. In the case of string distances this is the same as "sequence alignment". Given a set of edit operations and edit costs, the edit distance is given by the minimum sum of the costs along an edit path converting one object into the other. Edit distances like these always define a metric. The edit operations used by us are insertion, deletion and replacement of nodes. String editing does not pay attention to the matching of brackets, while in tree editing matching brackets represent a single node of the tree. [Tree](#) editing is therefore usually preferable, although somewhat slower. String edit distances are always smaller or equal to tree edit distances.

The different level of detail in the structure representations defined above naturally leads to different measures of distance. For full structures we use a cost of 1 for deletion or insertion of an unpaired base and 2 for a base pair. Replacing an unpaired base for a pair incurs a cost of 1.

Two cost matrices are provided for coarse grained structures:



```

/* Null, H, B, I, M, S, E */
{ 0, 2, 2, 2, 2, 1, 1}, /* Null replaced */
{ 2, 0, 2, 2, 2, INF, INF}, /* H replaced */
{ 2, 2, 2, 0, 1, 2, INF, INF}, /* B replaced */
{ 2, 2, 1, 0, 2, INF, INF}, /* I replaced */
{ 2, 2, 2, 2, 0, INF, INF}, /* M replaced */
{ 1, INF, INF, INF, INF, 0, INF}, /* S replaced */
{ 1, INF, INF, INF, INF, INF, 0}, /* E replaced */

/* Null, H, B, I, M, S, E */
{ 0, 100, 5, 5, 75, 5, 5}, /* Null replaced */
{ 100, 0, 8, 8, 8, INF, INF}, /* H replaced */
{ 5, 8, 0, 3, 8, INF, INF}, /* B replaced */
{ 5, 8, 3, 0, 8, INF, INF}, /* I replaced */
{ 75, 8, 8, 8, 0, INF, INF}, /* M replaced */
{ 5, INF, INF, INF, INF, 0, INF}, /* S replaced */
{ 5, INF, INF, INF, INF, INF, 0}, /* E replaced */

```

The lower matrix uses the costs given in [22]. All distance functions use the following global variables:

```
int cost_matrix;
```

Specify the cost matrix to be used for distance calculations.

```
int edit_backtrack;
```

Produce an alignment of the two structures being compared by tracing the editing path giving the minimum distance.

```
char *aligned_line[4];
```

Contains the two aligned structures after a call to one of the distance functions with [edit\\_backtrack](#) set to 1.

See also

[utils.h](#), [dist\\_vars.h](#) and [stringdist.h](#) for more details

### 3.2.1 Functions for Tree Edit Distances

```
Tree *make_tree (char *struc)
```

Constructs a [Tree](#) (essentially the postorder list) of the structure 'struc', for use in [tree\\_edit\\_distance\(\)](#).

```
float tree_edit_distance (Tree *T1,
                        Tree *T2)
```

Calculates the edit distance of the two trees.

```
void free_tree(Tree *t)
```

Free the memory allocated for [Tree](#) t.

See also

[dist\\_vars.h](#) and [treedist.h](#) for prototypes and more detailed descriptions

### 3.2.2 Functions for String Alignment

```
swString *Make_swString (char *string)
```

Convert a structure into a format suitable for [string\\_edit\\_distance\(\)](#).

```
float      string_edit_distance (swString *T1,  
                                swString *T2)
```

Calculate the string edit distance of T1 and T2.

See also

[dist\\_vars.h](#) and [stringdist.h](#) for prototypes and more detailed descriptions

### 3.2.3 Functions for Comparison of Base Pair Probabilities

For comparison of base pair probability matrices, the matrices are first condensed into probability profiles which are then compared by alignment.

```
float *Make_bp_profile_bppm ( double *bppm,  
                             int length)
```

condense pair probability matrix into a vector containing probabilities for unpaired, upstream paired and downstream paired.

```
float profile_edit_distance ( const float *T1,  
                             const float *T2)
```

Align the 2 probability profiles T1, T2

.

See also

ProfileDist.h for prototypes and more details of the above functions

## 3.3 Free Energy of Secondary Structures

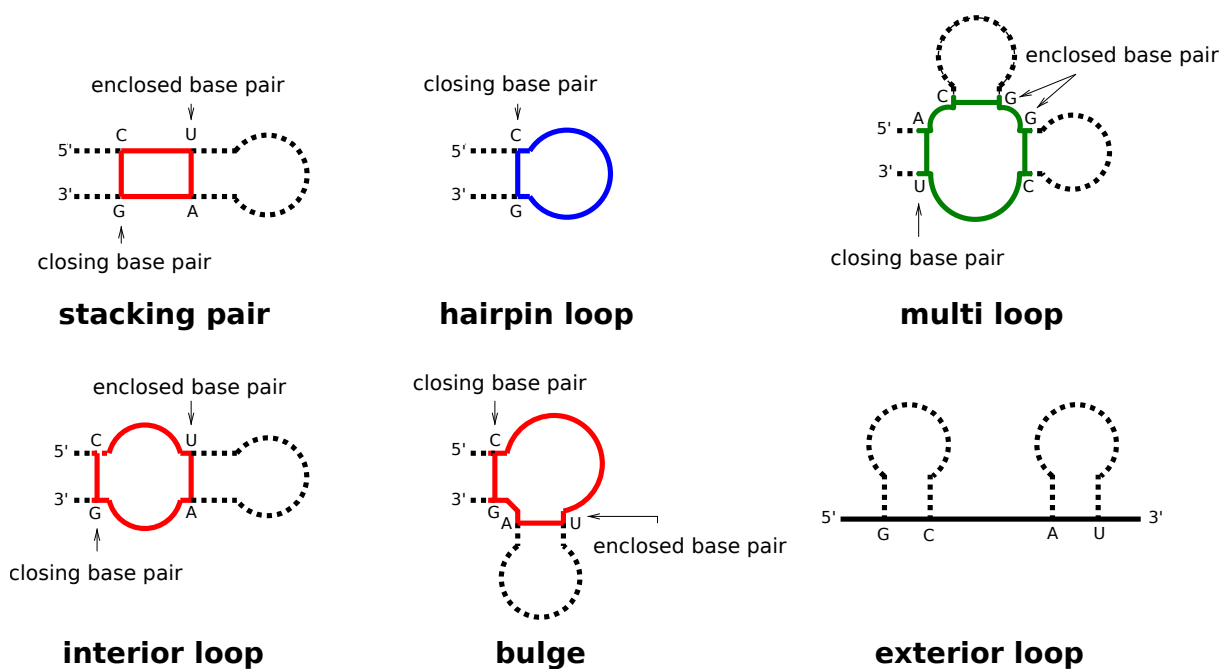
A description on how secondary structures are decomposed into individual loops to eventually evaluate their stability in terms of free energy.

### 3.3.1 Secondary Structure Loop Decomposition

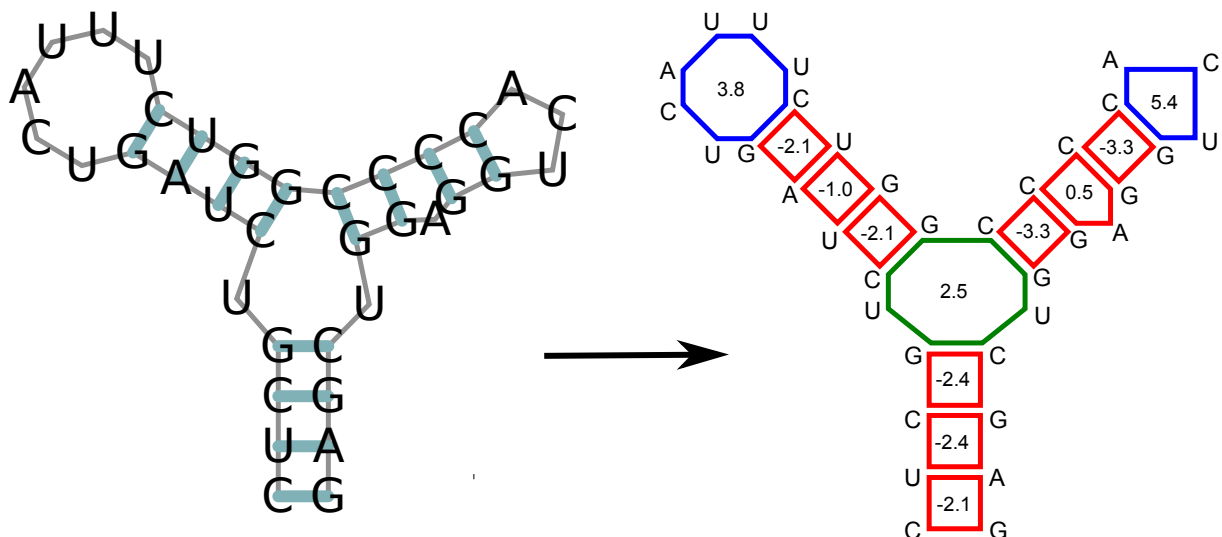
Each base pair in a secondary structure closes a loop, thereby directly enclosing unpaired nucleotides, and/or further base pairs. Our implementation distinguishes four basic types of loops:

- hairpin loops
- interior loops
- multibranch loops
- exterior loop

While the exterior loop is a special case without a closing pair, the other loops are determined by the number of base pairs involved in the loop formation, i.e. hairpin loops are 1-loops, since only a single base pair delimits the loop. interior loops are 2-loops due to their enclosing, and enclosed base pair. All loops where more than two base pairs are involved, are termed multibranch loops.



Any secondary structure can be decomposed into its loops. Each of the loops then can be scored in terms of free energy, and the free energy of an entire secondary structure is simply the sum of free energies of its loops.



### 3.3.1.1 Free Energy Evaluation API

While we implement some functions that decompose a secondary structure into its individual loops, the majority of methods provided in **RNAlib** are dedicated to free energy evaluation. The corresponding modules are:

See also

[Free Energy Evaluation](#), [Energy Evaluation for Individual Loops](#)

### 3.3.2 Free Energy Parameters

For secondary structure free energy evaluation we usually utilize the set of Nearest Neighbor Parameters also used in other software, such as *UNAFold* and *RNAstructure*. While the *RNAlib* already contains a compiled-in set of the latest *Turner 2004 Free Energy Parameters*, we defined a file format that allows to change these parameters at runtime. The *ViennaRNA Package* already comes with a set of parameter files containing

- Turner 1999 RNA parameters
- Mathews 1999 DNA parameters
- Andronescu 2007 RNA parameters
- Mathews 2004 DNA parameters

#### 3.3.2.1 Free Energy Parameters Modification API

See also

[Energy Parameters](#), [Reading/Writing Energy Parameter Sets from/to File](#)

### 3.3.3 Fine-tuning of the Energy Evaluation Model

See also

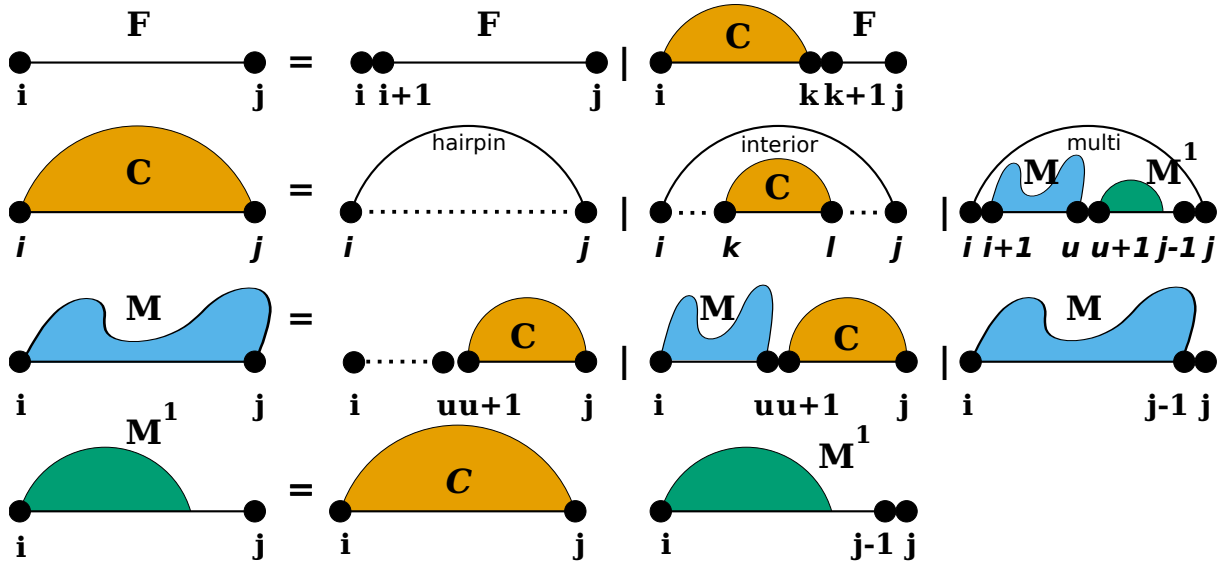
[Fine-tuning of the Implemented Models](#)

## 3.4 Secondary Structure Folding Grammar

A description of the basic grammar to generate secondary structures, used for almost all prediction algorithms in our library and how to modify it.

### 3.4.1 Secondary Structure Folding Recurrences

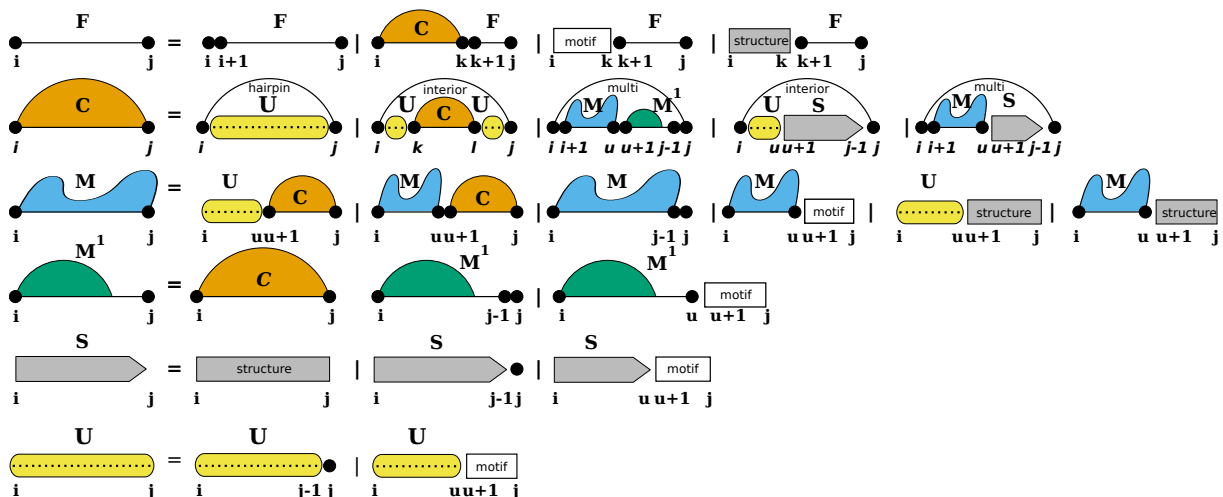
To predict secondary structures composed of the four distinguished loop types introduced before, all algorithms implemented in *RNAlib* follow a specific decomposition scheme, also known as the *RNA folding grammar*, or *Secondary Structure Folding Recurrences*.



However, compared to other RNA secondary structure prediction libraries, our implementation allows for a fine-grained control of the above recursions by constraining both, the individual derivations of the grammar as well as the evaluation of particular loop contributions. Furthermore, we provide a mechanism to extend the above grammar with additional derivation rules, so-called *Domains*.

### 3.4.2 Additional Structural Domains

Some applications of RNA secondary structure prediction require an extension of the *regular RNA folding grammar*. For instance one would like to include proteins and other ligands binding to unpaired loop regions while competing with conventional base pairing. Another application could be that one may want to include the formation of self-enclosed structural modules, such as *G-quadruplexes*. For such applications, we provide a pair of additional domains that extend the regular RNA folding grammar, [Structured Domains](#) and [Unstructured Domains](#).



While unstructured domains are usually determined by a more or less precise sequence motif, e.g. the binding site for a protein, structured domains are considered self-enclosed modules with a more or less complex pairing pattern. Our extension with these two domains introduces two production rules to fill additional dynamic processing matrices  $S$  and  $U$  where we store the pre-computed contributions of structured domains ( $S$ ), and unstructured domains ( $U$ ).

### 3.4.2.1 Structured Domains

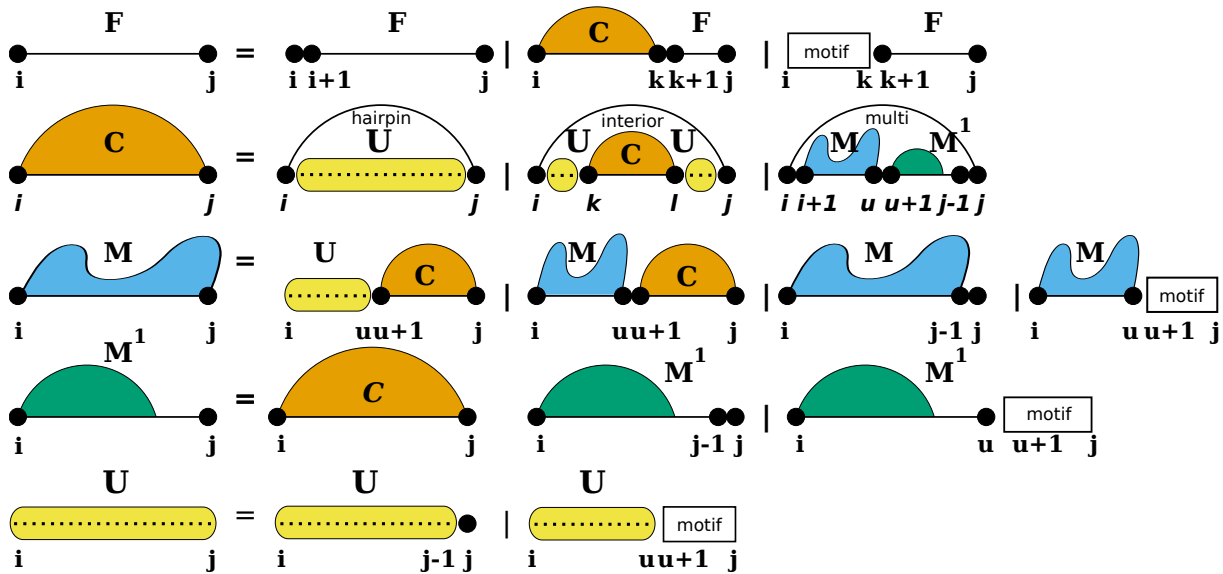
Usually, structured domains represent self-enclosed structural modules that exhibit a more or less complex base pairing pattern. This can be more or less well-defined 3D motifs, such as *G-Quadruplexes*, or loops with additional non-canonical base pair interactions, such as *kink-turns*.

#### Note

Currently, our implementation only provides the specialized case of *G-Quadruplexes*.

### 3.4.2.2 Unstructured Domains

Unstructured domains appear in the production rules of the RNA folding grammar wherever new unpaired nucleotides are attached to a growing substructure (see also [16]):



The white boxes represent the stretch of RNA bound to the ligand and represented by a more or less specific sequence motif. The motif itself is considered unable to form base pairs. The additional production rule  $U$  is used to precompute the contribution of unpaired stretches possibly bound by one or more ligands. The auxiliary DP matrix for this production rule is filled right before processing the other (regular) production rules of the RNA folding grammar.

### 3.4.2.3 Domain Extension API

For the sake of flexibility, each of the domains is associated with a specific data structure serving as an abstract interface to the extension. The interface uses callback functions to

- pre-compute arbitrary data, e.g. filling up additional dynamic programming matrices, and
- evaluate the contribution of a paired or unpaired structural feature of the RNA.

Implementations of these callbacks are separate for regular free energy evaluation, e.g. MFE prediction, and partition function applications. A data structure holding arbitrary data required for the callback functions can be associated to the domain as well. While *RNAlib* comes with a default implementation for structured and unstructured domains, the system is entirely user-customizable.

See also

[Unstructured Domains](#), [Structured Domains](#), [G-Quadruplexes](#), [Ligands Binding to Unstructured Domains](#)

### 3.4.3 Constraints on the Folding Grammar

Secondary Structure constraints can be subdivided into two groups:

- Hard Constraints
- Soft Constraints

While Hard-Constraints directly influence the production rules used in the folding recursions by allowing, disallowing, or enforcing certain decomposition steps, Soft-constraints on the other hand are used to change position specific contributions in the recursions by adding bonuses/penalties in form of pseudo free energies to certain loop configurations.

Note

Secondary structure constraints are always applied at decomposition level, i.e. in each step of the recursive structure decomposition, for instance during MFE prediction.

#### 3.4.3.1 Hard Constraints API

Hard constraints as implemented in our library can be specified for individual loop types, i.e. the atomic derivations of the RNA folding grammar rules. Hence, the pairing behavior of both, single nucleotides and pairs of bases, can be constrained in every loop context separately. Additionally, an abstract implementation using a callback mechanism allows for full control of more complex hard constraints.

See also

[Hard Constraints](#)

### 3.4.3.2 Soft Constraints API

For the sake of memory efficiency, we do not implement a loop context aware version of soft constraints. The *static* soft constraints as implemented only distinguish unpaired from paired nucleotides. This is usually sufficient for most use-case scenarios. However, similar to hard constraints, an abstract soft constraints implementation using a callback mechanism exists, that allows for any soft constraint that is compatible with the RNA folding grammar. Thus, loop contexts and even individual derivation rules can be addressed separately for maximum flexibility in soft-constraints application.

See also

[Soft Constraints, Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints, SHAPE Reactivity Data](#)

## 3.5 RNA Secondary Structure Landscapes

A description of the implicit landscape-like network of structures that appears upon modelling the transition of one structure into another.

### 3.5.1 The Neighborhood of a Secondary Structure

### 3.5.2 The Secondary Structure Landscape API

## 3.6 Minimum Free Energy Algorithm(s)

Computing the Minimum Free Energy (MFE), i.e. the most stable conformation in thermodynamic equilibrium.

### 3.6.1 Zuker's Algorithm

Our library provides fast dynamic programming Minimum Free Energy (MFE) folding algorithms derived from the decomposition scheme as described by "Zuker & Stiegler (1981)" [28].

### 3.6.2 MFE for circular RNAs

Folding of *circular* RNA sequences is handled as a post-processing step of the forward recursions. See [13] for further details.

### 3.6.3 MFE Algorithm API

We provide interfaces for the prediction of

- MFE and corresponding secondary structure for single sequences,
- consensus MFE structures of sequence alignments, and
- MFE structure for two hybridized RNA strands

See also

[Minimum Free Energy \(MFE\) Algorithms, RNA-RNA Interaction, Computing MFE representatives of a Distance Based Partition](#)



## 3.7 Partition Function and Equilibrium Probability Algorithm(s)

### 3.7.1 Equilibrium Ensemble Statistics

In contrast to methods that compute the property of a single structure in the ensemble, e.g. [Minimum Free Energy Algorithm\(s\)](#), the partition function algorithms always consider the entire equilibrium ensemble. For that purpose, the McCaskill algorithm [18] and its variants can be used to efficiently compute

- the partition function, and from that
- various equilibrium probabilities, for instance base pair probabilities, probabilities of individual structure motifs, and many more.

The principal idea behind this approach is that in equilibrium, statistical mechanics and polymer theory tells us that the frequency or probability  $p(s)$  of a particular state  $s$  depends on its energy  $E(s)$  and follows a Boltzmann distribution, i.e.

$$p(s) \propto e^{-\beta E(s)} \text{ with } \beta = \frac{1}{kT}$$

where  $k \approx 1.987 \cdot 10^{-3} \frac{\text{kcal}}{\text{mol K}}$  is the Boltzmann constant, and  $T$  the thermodynamic temperature. From that relation, the actual probability of state  $s$  can then be obtained using a proper scaling factor, the *canonical partition function*

$$Z = \sum_{s \in \Omega} e^{-\beta E(s)}$$

where  $\Omega$  is the finite set of all states. Finally, the equilibrium probability of state  $s$  can be computed as

$$p(s) = \frac{e^{-\beta E(s)}}{Z}$$

Instead of enumerating all states exhaustively to compute  $Z$  one can apply the [Secondary Structure Folding Recurrences](#) again for an efficient computation in cubic time. An *outside* variant of the same recursions is then used to compute probabilities for base pairs, stretches of consecutive unpaired nucleotides, or structural motifs.

See also

Further details of the Partition function and Base Pair Probability algorithm can be obtained from McCaskill 1990 [18]

### 3.7.2 Partition Function and Equilibrium Probability API

We implement a wide variety of variants of the partition function algorithm according to McCaskill 1990 [18]. See the corresponding submodules for specific implementation details.

See also

[Partition Function and Equilibrium Properties](#), [RNA-RNA Interaction](#), [Partition Function for two Hybridized Sequences as a Step](#), [Computing Partition Functions of a Distance Based Partitioning](#)

## 3.8 Suboptimal and (other) Representative Structures

### 3.8.1 Suboptimal Secondary Structures

### 3.8.2 Sampling Secondary Structures from the Ensemble

### 3.8.3 Structure Enumeration and Sampling API

See also

[Suboptimal Structures sensu Stiegler et al. 1984 / Zuker et al. 1989](#), [Suboptimal Structures within an Energy Band around the Minimum Free Energy Structure](#), [Random Structure Samples from the Ensemble](#), [Compute the Structure with Maximum Expected Accuracy \(MEA\)](#), [Compute the Centroid Structure](#)

## 3.9 RNA-RNA Interaction

### 3.9.1 `<br>`

The function of an RNA molecule often depends on its interaction with other RNAs. The following routines therefore allow one to predict structures formed by two RNA molecules upon hybridization.

### 3.9.2 Concatenating RNA sequences

One approach to co-folding two RNAs consists of concatenating the two sequences and keeping track of the concatenation point in all energy evaluations. Correspondingly, many of the `cofold()` and `co_pf_fold()` routines take one sequence string as argument and use the global variable `cut_point` to mark the concatenation point. Note that while the *RNAcofold* program uses the `'&'` character to mark the chain break in its input, you should not use an `'&'` when using the library routines (set `cut_point` instead).

### 3.9.3 RNA-RNA interaction as a Stepwise Process

In a second approach to co-folding two RNAs, cofolding is seen as a stepwise process. In the first step the probability of an unpaired region is calculated and in a second step this probability of an unpaired region is multiplied with the probability of an interaction between the two RNAs. This approach is implemented for the interaction between a long target sequence and a short ligand RNA. Function `pf_unstru()` calculates the partition function over all unpaired regions in the input sequence. Function `pf_interact()`, which calculates the partition function over all possible interactions between two sequences, needs both sequence as separate strings as input.

### 3.9.4 RNA-RNA Interaction API

## 3.10 Locally Stable Secondary Structures

### 3.10.1 local\_intro

### 3.10.2 local\_mfe

### 3.10.3 local\_pf

### 3.10.4 Locally Stable Secondary Structure API

## 3.11 Comparative Structure Prediction

### 3.11.1 Incorporate Evolutionary Information

Consensus structures can be predicted by a modified version of the [fold\(\)](#) algorithm that takes a set of aligned sequences instead of a single sequence. The energy function consists of the mean energy averaged over the sequences, plus a covariance term that favors pairs with consistent and compensatory mutations and penalizes pairs that cannot be formed by all structures. For details see [\[11\]](#) and [\[1\]](#).

### 3.11.2 Comparative Structure Prediction API

## 3.12 Classified DP variations

### 3.12.1 The Idea of Classified Dynamic Programming

Usually, thermodynamic properties using the basic recursions for [Minimum Free Energy Algorithm\(s\)](#), [Partition Function and Equilibrium](#) and so forth, are computed over the entire structure space. However, sometimes it is desired to partition the structure space *a priori* and compute the above properties for each of the resulting partitions. This approach directly leads to *Classified Dynamic Programming*.

### 3.12.2 Distance Class Partitioning

The secondary structure space is divided into partitions according to the base pair distance to two given reference structures and all relevant properties are calculated for each of the resulting partitions.

See also

For further details, we refer to Lorenz et al. 2009 [\[15\]](#)

### 3.12.3 Density of States (DOS)

### 3.12.4 Classified DP API

## 3.13 RNA Sequence Design

### 3.13.1 Generate Sequences that fold into particular Secondary Structures

### 3.13.2 RNA Sequence Design API

See also

[Inverse Folding \(Design\)](#)

## 3.14 Experimental Structure Probing Data

### 3.14.1 Guide the Structure Prediction using Experimental Data

#### 3.14.1.1 SHAPE reactivities

### 3.14.2 Structure Probing Data API

See also

[Experimental Structure Probing Data](#), [SHAPE Reactivity Data](#), [Generate Soft Constraints from Data](#)

## 3.15 Ligand Binding

### 3.15.1 Small Molecules and Proteins that bind to specific RNA Structures

### 3.15.2 `ligand_binding_api`

In our library, we provide two different ways to incorporate ligand binding to RNA structures:

- [Ligands Binding to Unstructured Domains](#), and
- [Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints](#)

The first approach is implemented as an actual extension of the folding grammar. It adds auxiliary derivation rules for each case when consecutive unpaired nucleotides are evaluated. Therefore, this model is applicable to ligand binding to any loop context.

The second approach, on the other hand, uses the soft-constraints feature to change the energy evaluation of hairpin- or interior-loops. Hence, it can only be applied when a ligand binds to a hairpin-like, or interior-loop like motif.

See also

[Ligands Binding to Unstructured Domains](#), [Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints](#)

## **3.16 (Tertiary) Structure Motifs**

### **3.16.1 Incorporating Higher-Order (Tertiary) Structure Motifs**

### **3.16.2 RNA G-Quadruplexes**

### **3.16.3 (Tertiary) Structure Motif API**



## Chapter 4

# I/O Formats

Below, you'll find a listing of different sections that introduce the most common notations of sequence and structure data, specifications of bioinformatics sequence and structure file formats, and various output file formats produced by our library.

- [RNA Structure Notations](#) describes the different notations and representations of RNA secondary structures
- [File Formats](#) gives an overview of the file formats compatible with our library
- [Plotting](#) shows the different (PostScript) plotting functions for RNA secondary structures, feature probabilities, and multiple sequence alignments

## 4.1 RNA Structure Notations

### 4.1.1 Representations of Secondary Structures

The standard representation of a secondary structure in our library is the [Dot-Bracket Notation](#) (a.k.a. [Dot-Parenthesis Notation](#)), where matching brackets symbolize base pairs and unpaired bases are shown as dots. Based on that notation, more elaborate representations have been developed to include additional information, such as the loop context a nucleotide belongs to and to annotated pseudo-knots.

#### 4.1.1.1 Dot-Bracket Notation (a.k.a. Dot-Parenthesis Notation)

The Dot-Bracket notation as introduced already in the early times of the ViennaRNA Package denotes base pairs by matching pairs of parenthesis ( ) and unpaired nucleotides by dots . .

As a simple example, consider a helix of size 4 enclosing a hairpin of size 4. In dot-bracket notation, this is annotated as

```
(( (( . . . . ) ) ) )
```

#### Extended Dot-Bracket Notation

A more generalized version of the original Dot-Bracket notation may use additional pairs of brackets, such as <>, {}, and [], and matching pairs of uppercase/lowercase letters. This allows for annotating pseudo-knots, since different pairs of brackets are not required to be nested.

The following annotations of a simple structure with two crossing helices of size 4 are equivalent:

```
<<<<[ [ [ [ . . . . >>>> ] ] ] ]  
( ( ( ( A A A A . . . . ) ) ) ) a a a a  
A A A A { { { { . . . . a a a a } } } }
```

See also

[vrna\\_db\\_pack\(\)](#), [vrna\\_db\\_unpack\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#), [vrna\\_db\\_from\\_ptable\(\)](#),  
[vrna\\_db\\_from\\_plist\(\)](#), [vrna\\_db\\_to\\_element\\_string\(\)](#), [vrna\\_db\\_pk\\_remove\(\)](#)

#### 4.1.1.2 Washington University Secondary Structure (WUSS) notation

The WUSS notation, as frequently used for consensus secondary structures in [Stockholm 1.0 format](#).

This notation allows for a fine-grained annotation of base pairs and unpaired nucleotides, including pseudo-knots. Below, you'll find a list of secondary structure elements and their corresponding WUSS annotation (See also the infernal user guide at <http://eddylab.org/infernal/Userguide.pdf>)

- **Base pairs**

Nested base pairs are annotated by matching pairs of the symbols `<>`, `()`, `{}`, and `[]`. Each of the matching pairs of parenthesis have their special meaning, however, when used as input in our programs, e.g. structure constraint, these details are usually ignored. Furthermore, base pairs that constitute as pseudo-knot are denoted by letters from the latin alphabet and are, if not denoted otherwise, ignored entirely in our programs.

- **Hairpin loops**

Unpaired nucleotides that constitute the hairpin loop are indicated by underscores, `_`.

Example: `<<<<_____>>>>`

- **Bulges and interior loops**

Residues that constitute a bulge or interior loop are denoted by dashes, `-`.

Example: `(( (--<_____>- ) ) )`

- **Multibranch loops**

Unpaired nucleotides in multibranch loops are indicated by commas, `,`.

Example: `(( („<_____> , <_____> ) ) )`

- **External residues**

Single stranded nucleotides in the exterior loop, i.e. not enclosed by any other pair are denoted by colons, `:`.

Example: `<<<_____>>>:::`

- **Insertions**

In cases where an alignment represents the consensus with a known structure, insertions relative to the known structure are denoted by periods, `.`. Regions where local structural alignment was invoked, leaving regions of both target and query sequence unaligned, are indicated by tildes, `~`.

**Note**

These symbols only appear in alignments of a known (query) structure annotation to a target sequence of unknown structure.

- **Pseudo-knots**

The WUSS notation allows for annotation of pseudo-knots using pairs of upper-case/lower-case letters.

**Note**

Our programs and library functions usually ignore pseudo-knots entirely treating them as unpaired nucleotides, if not stated otherwise.

Example: `<<<_AAA____>>>aaa`

See also

[vrna\\_db\\_from\\_WUSS\(\)](#)



#### 4.1.1.3 Abstract Shapes

Abstract Shapes, introduced by Giegerich et al. in (2004) [10], collapse the secondary structure while retaining the nestedness of helices and hairpin loops.

The abstract shapes representation abstracts the structure from individual base pairs and their corresponding location in the sequence, while retaining the inherent nestedness of helices and hairpin loops.

Below is a description of what is included in the abstract shapes abstraction for each respective level together with an example structure:

```
CGUCUUAAACUCAUCACCGUGUGGAGCUGCGACCCUCCCUAGAUUCGAAGACGAG
(((((((...(((...))))))...(((...))...))))))... .
```

Shape Level	Description	Result
1	Most accurate - all loops and all unpaired	[ _ [ _ ] ] _ [ _ [ ] _ ↔ ] ] _
2	Nesting pattern for all loop types and unpaired regions in external loop and multiloop	[ [ _ [ ] ] [ _ [ ] _ ] ]
3	Nesting pattern for all loop types but no unpaired regions	[ [ [ ] ] [ [ ] ] ]
4	Helix nesting pattern in external loop and multiloop	[ [ ] [ [ ] ] ]
5	Most abstract - helix nesting pattern and no unpaired regions	[ [ ] [ ] ]

#### Note

Our implementations also provide the special Shape Level 0, which does not collapse any structural features but simply convert base pairs and unpaired nucleotides into their corresponding set of symbols for abstract shapes.

#### See also

[vrna\\_abstract\\_shapes\(\)](#), [vrna\\_abstract\\_shapes\\_pt\(\)](#)

#### 4.1.1.4 Tree Representations of Secondary Structures

Secondary structures can be readily represented as trees, where internal nodes represent base pairs, and leaves represent unpaired nucleotides. The dot-bracket structure string already is a tree represented by a string of parenthesis (base pairs) and dots for the leaf nodes (unpaired nucleotides).

Alternatively, one may find representations with two types of node labels,  $P$  for paired and  $U$  for unpaired; a dot is then replaced by  $(U)$ , and each closed bracket is assigned an additional identifier  $P$ . We call this the expanded notation. In [8] a condensed representation of the secondary structure is proposed, the so-called homeomorphically irreducible tree (HIT) representation. Here a stack is represented as a single pair of matching brackets labeled  $P$  and weighted by the number of base pairs. Correspondingly, a contiguous strain of unpaired bases is shown as one pair of matching brackets labeled  $U$  and weighted by its length. Generally any string consisting of matching brackets and identifiers is equivalent to a plane tree with as many different types of nodes as there are identifiers.

Bruce Shapiro proposed a coarse grained representation [21], which, does not retain the full information of the secondary structure. He represents the different structure elements by single matching brackets and labels them as

- H (hairpin loop),
- I (interior loop),
- B (bulge),
- M (multi-loop), and
- S (stack).

We extend his alphabet by an extra letter for external elements **E**. Again these identifiers may be followed by a weight corresponding to the number of unpaired bases or base pairs in the structure element. All tree representations (except for the dot-bracket form) can be encapsulated into a virtual root (labeled **R**).

The following example illustrates the different linear tree representations used by the package:

Consider the secondary structure represented by the dot-bracket string (full tree) `. ( ( . . ( ( . . . ) ) ) . . ( ( . . ) ) ) ) .` which is the most convenient condensed notation used by our programs and library functions.

Then, the following tree representations are equivalent:

- Expanded tree:  
`((U)((U)(U)((U)(U)(U)P)P)P)(U)(U)((U)(U)P)P)P)(U)R)`
- HIT representation (Fontana et al. 1993 [8]):  
`((U1)((U2)((U3)P3)(U2)((U2)P2)P2)(U1)R)`
- Coarse Grained **Tree** Representation (Shapiro 1988 [21]):
  - Short (with root node **R**, without stem nodes **S**):  
`((H)((H)M)R)`
  - Full (with root node **R**):  
`(((((H)S)((H)S)M)S)R)`
  - Extended (with root node **R**, with external nodes **E**):  
`(((((H)S)((H)S)M)S)E)R)`
  - Weighted (with root node **R**, with external nodes **E**):  
`(((((H3)S3)((H2)S2)M4)S2)E2)R)`

The Expanded tree is rather clumsy and mostly included for the sake of completeness. The different versions of Coarse Grained **Tree** Representations are variations of Shapiro's linear tree notation.

For the output of aligned structures from string editing, different representations are needed, where we put the label on both sides. The above examples for tree representations would then look like:

```
* a) (UU) (P (P (P (P (UU) (UU) (P (P (UU) (UU) (UU) P) P) P) (UU) (UU) (P (P (UU) (U. . .
* b) (UU) (P2 (P2 (U2U2) (P2 (U3U3) P3) (U2U2) (P2 (U2U2) P2) P2) (UU) P2) (UU)
* c) (B (M (HH) (HH) M) B)
*   (S (B (S (M (S (HH) S) (S (HH) S) M) S) B) S)
*   (E (S (B (S (M (S (HH) S) (S (HH) S) M) S) B) S) E)
* d) (R (E2 (S2 (B1 (S2 (M4 (S3 (H3) S3) ((H2) S2) M4) S2) B1) S2) E2) R)
*
```

Aligned structures additionally contain the gap character `_`.

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#), [vrna\\_tree\\_string\\_unweight\(\)](#), [vrna\\_tree\\_string\\_to\\_db\(\)](#)

## 4.1.2 Examples for Structure Parsing and Conversion

### 4.1.3 Structure Parsing and Conversion API

Several functions are provided for parsing structures and converting to different representations.

```
char *expand_Full(const char *structure)
```

Convert the full structure from bracket notation to the expanded notation including root.

```
char *b2HIT (const char *structure)
```

Converts the full structure from bracket notation to the HIT notation including root.

```
char *b2C (const char *structure)
```

Converts the full structure from bracket notation to the a coarse grained notation using the 'H' 'B' 'I' 'M' and 'R' identifiers.

```
char *b2Shapiro (const char *structure)
```

Converts the full structure from bracket notation to the *weighted* coarse grained notation using the 'H' 'B' 'I' 'M' 'S' 'E' and 'R' identifiers.

```
char *expand_Shapiro (const char *coarse);
```

Inserts missing 'S' identifiers in unweighted coarse grained structures as obtained from [b2C\(\)](#).

```
char *add_root (const char *structure)
```

Adds a root to an un-rooted tree in any except bracket notation.

```
char *unexpand_Full (const char *ffull)
```

Restores the bracket notation from an expanded full or HIT tree, that is any tree using only identifiers 'U' 'P' and 'R'.

```
char *unweight (const char *wcoarse)
```

Strip weights from any weighted tree.

```
void unexpand_aligned_F (char *align[2])
```

Converts two aligned structures in expanded notation.

```
void parse_structure (const char *structure)
```

Collects a statistic of structure elements of the full structure in bracket notation.

See also

[RNAstruct.h](#) for prototypes and more detailed description

## 4.2 File Formats

### 4.2.1 File formats for Multiple Sequence Alignments (MSA)

#### 4.2.1.1 ClustalW format

The *ClustalW* format is a relatively simple text file containing a single multiple sequence alignment of DNA, RNA, or protein sequences. It was first used as an output format for the *clustalw* programs, but nowadays it may also be generated by various other sequence alignment tools. The specification is straight forward:

- The first line starts with the words

```
CLUSTAL W
```

or

```
CLUSTALW
```

- After the above header there is at least one empty line
- Finally, one or more blocks of sequence data are following, where each block is separated by at least one empty line

Each line in a blocks of sequence data consists of the sequence name followed by the sequence symbols, separated by at least one whitespace character. Usually, the length of a sequence in one block does not exceed 60 symbols. Optionally, an additional whitespace separated cumulative residue count may follow the sequence symbols. Optionally, a block may be followed by a line depicting the degree of conservation of the respective alignment columns.

Note

Sequence names and the sequences must not contain whitespace characters! Allowed gap symbols are the hyphen ("-"), and dot (".").



```
>AL031296.1/85969-86120
CUGCCUCACAACGUUUGGCCUCAGUUACCCGUGAUGUAGUGAGGGUAACAAUACUUAC
UCUCGUUGGUGUAAGGAACAGCU
>AANU01225121.1/438-603
CUGCCUCACAACAUUUGGCCUCAGUUACUCAUAGAUGUAGUGAGGGUGACAAUACUUAC
UCUCGUUGGUGUAAGGAACAGCU
>AAWR02037329.1/29294-29150
---CUCGACACCACU---GCCUCGGUUACCCAUCGGUGCAGUGCGGGUAGUAGUACCAAU
GCUAAUAGUUGUGAGGACCAACU
```

#### 4.2.1.4 MAF format

The multiple alignment format (MAF) is usually used to store multiple alignments on DNA level between entire genomes. It consists of independent blocks of aligned sequences which are annotated by their genomic location. Consequently, an MAF formatted MSA file may contain multiple records. MAF files start with a line

```
##maf
```

which is optionally extended by whitespace delimited key=value pairs. Lines starting with the character ("#") are considered comments and usually ignored.

A MAF block starts with character ("a") at the beginning of a line, optionally followed by whitespace delimited key=value pairs. The next lines start with character ("s") and contain sequence information of the form

```
s src start size strand srcSize sequence
```

where

- *src* is the name of the sequence source
- *start* is the start of the aligned region within the source (0-based)
- *size* is the length of the aligned region without gap characters
- *strand* is either "+" or "-", depicting the location of the aligned region relative to the source
- *srcSize* is the size of the entire sequence source, e.g. the full chromosome
- *sequence* is the aligned sequence including gaps depicted by the hyphen ("-")

Here is an example alignment in MAF format (bluntly taken from the [UCSC Genome browser website](#)):

```
##maf version=1 scoring=tba.v8
# tba.v8 ((human chimp) baboon) (mouse rat))
# multiz.v7
# maf_project.v5 _tba_right.maf3 mouse _tba_C
# single_cov2.v4 single_cov2 /dev/stdin

a score=23262.0
s hg16.chr7 27578828 38 + 158545518 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s panTro1.chr6 28741140 38 + 161576975 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s baboon 116834 38 + 4622798 AAA-GGGAATGTTAACCAAATGA---GTTGTCTCTTATGGTG
s mm4.chr6 53215344 38 + 151104725 -AATGGGAATGTTAAGCAAACGA---ATTGTCTCTCAGTGTG
s rn3.chr4 81344243 40 + 187371129 -AA-GGGGATGCTAAGCCAATGAGTTGTTGTCTCTCAATGTG

a score=5062.0
s hg16.chr7 27699739 6 + 158545518 TAAAGA
s panTro1.chr6 28862317 6 + 161576975 TAAAGA
s baboon 241163 6 + 4622798 TAAAGA
s mm4.chr6 53303881 6 + 151104725 TAAAGA
s rn3.chr4 81444246 6 + 187371129 taagga

a score=6636.0
s hg16.chr7 27707221 13 + 158545518 gcagctgaaaaca
s panTro1.chr6 28869787 13 + 161576975 gcagctgaaaaca
s baboon 249182 13 + 4622798 gcagctgaaaaca
s mm4.chr6 53310102 13 + 151104725 ACAGCTGAAAATA
```

## 4.2.2 File formats to manipulate the RNA folding grammar

### 4.2.2.1 Command Files

The RNAlib and many programs of the ViennaRNA Package can parse and apply data from so-called command files. These commands may refer to structure constraints or even extensions of the RNA folding grammar (such as [Unstructured Domains](#)). Commands are given as a line of whitespace delimited data fields. The syntax we use extends the constraint definitions used in the `mfold` / `UNAFold` software, where each line begins with a command character followed by a set of positions.

However, we introduce several new commands, and allow for an optional loop type context specifier in form of a sequence of characters, and an orientation flag that enables one to force a nucleotide to pair upstream, or downstream.

**4.2.2.1.1 Constraint commands** The following set of commands is recognized:

- `F ...` Force
- `P ...` Prohibit
- `C ...` Conflicts/Context dependency
- `A ...` Allow (for non-canonical pairs)
- `E ...` Soft constraints for unpaired position(s), or base pair(s)

### 4.2.2.1.2 RNA folding grammar extensions

- `UD ...` Add ligand binding using the [Unstructured Domains](#) feature

**4.2.2.1.3 Specification of the loop type context** The optional loop type context specifier [LOOP] may be a combination of the following:

- `E ...` Exterior loop
- `H ...` Hairpin loop
- `I ...` Interior loop
- `M ...` Multibranch loop
- `A ...` All loops

For structure constraints, we additionally allow one to address base pairs enclosed by a particular kind of loop, which results in the specifier [WHERE] which consists of [LOOP] plus the following character:

- `i ...` enclosed pair of an Interior loop
- `m ...` enclosed pair of a Multibranch loop

If no [LOOP] or [WHERE] flags are set, all contexts are considered (equivalent to `A` )

**4.2.2.1.4 Controlling the orientation of base pairing** For particular nucleotides that are forced to pair, the following [ORIENTATION] flags may be used:

- `U ...` Upstream
- `D ...` Downstream

If no [ORIENTATION] flag is set, both directions are considered.

**4.2.2.1.5 Sequence coordinates** Sequence positions of nucleotides/base pairs are 1— based and consist of three positions  $i$ ,  $j$ , and  $k$ . Alternatively, four positions may be provided as a pair of two position ranges  $[i : j]$ , and  $[k : l]$  using the '-' sign as delimiter within each range, i.e.  $i - j$ , and  $k - l$ .

**4.2.2.1.6 Valid constraint commands** Below are resulting general cases that are considered *valid* constraints:

1. **"Forcing a range of nucleotide positions to be paired":**

Syntax:

`F i 0 k [WHERE] [ORIENTATION]`

Description:

Enforces the set of  $k$  consecutive nucleotides starting at position  $i$  to be paired. The optional loop type specifier [WHERE] allows to force them to appear as closing/enclosed pairs of certain types of loops.

2. **"Forcing a set of consecutive base pairs to form":**

Syntax:

`F i j k [WHERE]`

Description:

Enforces the base pairs  $(i, j), \dots, (i + (k - 1), j - (k - 1))$  to form. The optional loop type specifier [WHERE] allows to specify in which loop context the base pair must appear.

3. **"Prohibiting a range of nucleotide positions to be paired":**

Syntax:

`P i 0 k [WHERE]`

Description:

Prohibit a set of  $k$  consecutive nucleotides to participate in base pairing, i.e. make these positions unpaired. The optional loop type specifier [WHERE] allows to force the nucleotides to appear within the loop of specific types.

4. **"Prohibiting a set of consecutive base pairs to form":**

Syntax:

`P i j k [WHERE]`

Description:

Prohibit the base pairs  $(i, j), \dots, (i + (k - 1), j - (k - 1))$  to form. The optional loop type specifier [WHERE] allows to specify the type of loop they are disallowed to be the closing or an enclosed pair of.

5. **"Prohibiting two ranges of nucleotides to pair with each other":**

Syntax:

`P i-j k-l [WHERE]`

Description:

Prohibit any nucleotide  $p \in [i : j]$  to pair with any other nucleotide  $q \in [k : l]$ . The optional loop type specifier [WHERE] allows to specify the type of loop they are disallowed to be the closing or an enclosed pair of.

6. **"Enforce a loop context for a range of nucleotide positions":**

Syntax:

`C i 0 k [WHERE]`

Description:

This command enforces nucleotides to be unpaired similar to *prohibiting* nucleotides to be paired, as described above. It too marks the corresponding nucleotides to be unpaired, however, the [WHERE] flag can be used to enforce specific loop types the nucleotides must appear in.

7. **"Remove pairs that conflict with a set of consecutive base pairs":**

Syntax:

`C i j k`

Description:

Remove all base pairs that conflict with a set of consecutive base pairs  $(i, j), \dots, (i + (k - 1), j - (k - 1))$ . Two base pairs  $(i, j)$  and  $(p, q)$  conflict with each other if  $i < p < j < q$ , or  $p < i < q < j$ .

#### 8. "Allow a set of consecutive (non-canonical) base pairs to form":

Syntax:

```
A i j k [WHERE]
```

Description:

This command enables the formation of the consecutive base pairs  $(i, j), \dots, (i + (k - 1), j - (k - 1))$ , no matter if they are *canonical*, or *non-canonical*. In contrast to the above  $\mathbb{F}$  and  $\mathbb{W}$  commands, which remove conflicting base pairs, the  $\mathbb{A}$  command does not. Therefore, it may be used to allow *non-canonical* base pair interactions. Since the RNAlib does not contain free energy contributions  $E_{ij}$  for non-canonical base pairs  $(i, j)$ , they are scored as the *maximum* of similar, known contributions. In terms of a *Nussinov* like scoring function the free energy of non-canonical base pairs is therefore estimated as

$$E_{ij} = \min \left[ \max_{(i,k) \in \{GC, CG, AU, UA, GU, UG\}} E_{ik}, \max_{(k,j) \in \{GC, CG, AU, UA, GU, UG\}} E_{kj} \right].$$

The optional loop type specifier [WHERE] allows to specify in which loop context the base pair may appear.

#### 9. "Apply pseudo free energy to a range of unpaired nucleotide positions":

Syntax:

```
E i 0 k e
```

Description:

Use this command to apply a pseudo free energy of  $e$  to the set of  $k$  consecutive nucleotides, starting at position  $i$ . The pseudo free energy is applied only if these nucleotides are considered unpaired in the recursions, or evaluations, and is expected to be given in *kcal/mol*.

#### 10. "Apply pseudo free energy to a set of consecutive base pairs":

Syntax

```
E i j k e
```

Use this command to apply a pseudo free energy of  $e$  to the set of base pairs  $(i, j), \dots, (i + (k - 1), j - (k - 1))$ . Energies are expected to be given in *kcal/mol*.

#### 4.2.2.1.7 Valid domain extensions commands

##### 1. "Add ligand binding to unpaired motif (a.k.a. unstructured domains)":

Syntax:

```
UD m e [LOOP]
```

Description:

Add ligand binding to unpaired sequence motif  $m$  (given in IUPAC format, capital letters) with binding energy  $e$  in particular loop type(s).

Example:

```
UD AAA -5.0 A
```

The above example applies a binding free energy of  $-5 \text{ kcal/mol}$  for a motif AAA that may be present in all loop types.

## 4.3 Plotting

Create Plots of Secondary Structures, Feature Motifs, and Sequence Alignments

### 4.3.1 Producing secondary structure graphs

```
int PS_rna_plot ( char *string,
                  char *structure,
                  char *file)
```

Produce a secondary structure graph in PostScript and write it to 'filename'.



```
int PS_rna_plot_a (
    char *string,
    char *structure,
    char *file,
    char *pre,
    char *post)
```

Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.

```
int gmlRNA (char *string,
    char *structure,
    char *ssfile,
    char option)
```

Produce a secondary structure graph in Graph Meta Language (gml) and write it to a file.

```
int ssv_rna_plot (char *string,
    char *structure,
    char *ssfile)
```

Produce a secondary structure graph in SStructView format.

```
int svg_rna_plot (char *string,
    char *structure,
    char *ssfile)
```

Produce a secondary structure plot in SVG format and write it to a file.

```
int xrna_plot ( char *string,
    char *structure,
    char *ssfile)
```

Produce a secondary structure plot for further editing in XRNA.

```
int rna_plot_type
```

Switch for changing the secondary structure layout algorithm.

Two low-level functions provide direct access to the graph layouting algorithms:

```
int simple_xy_coordinates ( short *pair_table,
    float *X,
    float *Y)
```

Calculate nucleotide coordinates for secondary structure plot the *Simple way*

```
int naview_xy_coordinates ( short *pair_table,
    float *X,
    float *Y)
```

See also

[PS\\_dot.h](#) and [naview.h](#) for more detailed descriptions.

### 4.3.2 Producing (colored) dot plots for base pair probabilities

```
int PS_color_dot_plot ( char *string,
    cpair *pi,
    char *filename)

int PS_color_dot_plot_turn (char *seq,
    cpair *pi,
    char *filename,
    int winSize)

int PS_dot_plot_list (char *seq,
    char *filename,
    plist *pl,
    plist *mf,
    char *comment)
```

Produce a postscript dot-plot from two pair lists.

```
int PS_dot_plot_turn (char *seq,
    struct plist *pl,
    char *filename,
    int winSize)
```

See also

[PS\\_dot.h](#) for more detailed descriptions.

### 4.3.3 Producing (colored) alignments

```
int PS_color_aln (  
    const char *structure,  
    const char *filename,  
    const char *seqs[],  
    const char *names[])
```

Produce PostScript sequence alignment color-annotated by consensus structure.

## Chapter 5

# Basic Data Structures

- [Sequence and Structure Data](#) shows the most common types for sequence or structure data
- [The 'Fold Compound'](#) is the basic, central container for our implementations of prediction-, evaluation, and other algorithms
- [Model Details](#) provides the means to store the different model parameters

### 5.1 Sequence and Structure Data

See also

[Secondary Structure Utilities](#)

### 5.2 The 'Fold Compound'

See also

[The Fold Compound](#)

### 5.3 Model Details

See also

[Fine-tuning of the Implemented Models](#)



## Chapter 6

# API Features

- [RNAlib API v3.0](#)
- [Callback Functions](#)
- [Scripting Language interface\(s\)](#)

## 6.1 RNAlib API v3.0

### 6.1.1 Introduction

With version 2.2 we introduce the new API that will take over the old one in the future version 3.0. By then, backwards compatibility will be broken, and third party applications using RNAlib need to be ported. This switch of API became necessary, since many new features found their way into the RNAlib where a balance between threadsafety and easy-to-use library functions is hard or even impossible to establish. Furthermore, many old functions of the library are present as slightly modified copies of themselves to provide a crude way to overload functions.

Therefore, we introduce the new v3.0 API very early in our development stage such that developers have enough time to migrate to the new functions and interfaces. We also started to provide encapsulation of the RNAlib functions, data structures, typedefs, and macros by prefixing them with *vrna\_* and *VRNA\_*, respectively. Header files should also be included using the *ViennaRNA/* namespace, e.g.

```
#include <ViennaRNA/fold.h>
```

instead of just using

```
#include <fold.h>
```

as required for RNAlib 1.x and 2.x.

This eases the work for programmers of third party applications that would otherwise need to put much effort into renaming functions and data types in their own implementations if their names appear in our library. Since we still provide backward compatibility up to the last version of RNAlib 2.x, this advantage may be fully exploited only starting from v3.0 which will be released in the future. However, our plan is to provide the possibility for an early switch-off mechanism of the backward compatibility in one of our next releases of ViennaRNA Package 2.x.

### 6.1.2 What are the major changes?

...

### 6.1.3 How to port your program to the new API

...

### 6.1.4 Some Examples using RNAlib API v3.0

Examples on how to use the new v3.0 API can be found in the [First Steps with the Fold Compound](#) section.

## 6.2 Callback Functions

With the new [RNAlib API v3.0](#) we introduce so-called callback mechanisms for several functions.

### 6.2.1 The purpose of Callback mechanisms

Using callback mechanisms, our library enables users not only to retrieve computed data without the need for parsing complicated data structures, but also allows one to tweak our implementation to do additional tasks without the requirement of a re-implementation of basic algorithms.

Our implementation of the callback mechanisms always follows the same scheme: The user:

- defines a function that complies with the interface we've defined, and
- passes a pointer to said function to our implementations

In addition to the specific arguments of our callback interfaces, virtually all callbacks receive an additional *pass-through-pointer* as their last argument. This enables one to:

- encapsulate data, and
- provide thread-safe operations,

since this pointer is simply passed through by our library functions. It may therefore hold the address of an arbitrary, user-defined data structure.

### 6.2.2 List of available Callbacks

Below, you find an enumeration of the individual callback functions that are available in *RNAlib*.

#### Global [vrna\\_boltzmann\\_sampling\\_callback](#) (const char \*structure, void \*data)

This function will be called for each secondary structure that has been successfully backtraced from the partition function DP matrices.

#### Global [vrna\\_callback\\_free\\_auxdata](#) (void \*data)

This callback is supposed to free memory occupied by an auxiliary data structure. It will be called when the [vrna\\_fold\\_compound\\_t](#) is erased from memory through a call to [vrna\\_fold\\_compound\\_free\(\)](#) and will be passed the address of memory previously bound to the [vrna\\_fold\\_compound\\_t](#) via [vrna\\_fold\\_compound\\_add\\_auxdata\(\)](#).

#### Global [vrna\\_callback\\_hc\\_evaluate](#) (int i, int j, int k, int l, unsigned char d, void \*data)

This callback enables one to over-rule default hard constraints in secondary structure decompositions.

#### Global [vrna\\_callback\\_recursion\\_status](#) (unsigned char status, void \*data)

This function will be called to notify a third-party implementation about the status of a currently ongoing recursion. The purpose of this callback mechanism is to provide users with a simple way to ensure pre- and post conditions for auxiliary mechanisms attached to our implementations.

#### Global [vrna\\_callback\\_sc\\_backtrack](#) (int i, int j, int k, int l, unsigned char d, void \*data)

This callback enables one to add auxiliary base pairs in the backtracking steps of hairpin- and interior loops.

#### Global [vrna\\_callback\\_sc\\_energy](#) (int i, int j, int k, int l, unsigned char d, void \*data)

This callback enables one to add (pseudo-)energy contributions to individual decompositions of the secondary structure.

#### Global [vrna\\_callback\\_sc\\_exp\\_energy](#) (int i, int j, int k, int l, unsigned char d, void \*data)

This callback enables one to add (pseudo-)energy contributions to individual decompositions of the secondary structure (Partition function variant, i.e. contributions must be returned as Boltzmann factors).

#### Global [vrna\\_callback\\_ud\\_energy](#) (vrna\_fold\_compound\_t \*vc, int i, int j, unsigned int loop\_type, void \*data)

This function will be called to determine the additional energy contribution of a specific unstructured domain, e.g. the binding free energy of some ligand.

Global **`vrna_callback_ud_exp_energy`** (`vrna_fold_compound_t *vc`, `int i`, `int j`, `unsigned int loop_type`, `void *data`)

This function will be called to determine the additional energy contribution of a specific unstructured domain, e.g. the binding free energy of some ligand (Partition function variant, i.e. the Boltzmann factors instead of actual free energies).

Global **`vrna_callback_ud_exp_production`** (`vrna_fold_compound_t *vc`, `void *data`)

The production rule for the unstructured domain grammar extension (Partition function variant)

Global **`vrna_callback_ud_probs_add`** (`vrna_fold_compound_t *vc`, `int i`, `int j`, `unsigned int loop_type`, `FLT_OR_DBL exp_energy`, `void *data`)

A callback function to store equilibrium probabilities for the unstructured domain feature

Global **`vrna_callback_ud_probs_get`** (`vrna_fold_compound_t *vc`, `int i`, `int j`, `unsigned int loop_type`, `int motif`, `void *data`)

A callback function to retrieve equilibrium probabilities for the unstructured domain feature

Global **`vrna_callback_ud_production`** (`vrna_fold_compound_t *vc`, `void *data`)

The production rule for the unstructured domain grammar extension

Global **`vrna_heat_capacity_callback`** (`float temp`, `float heat_capacity`, `void *data`)

This function will be called for each evaluated temperature in the heat capacity prediction.

Global **`vrna_mfe_window_callback`** (`int start`, `int end`, `const char *structure`, `float en`, `void *data`)

This function will be called for each hit in a sliding window MFE prediction.

Global **`vrna_probs_window_callback`** (`FLT_OR_DBL *pr`, `int pr_size`, `int i`, `int max`, `unsigned int type`, `void *data`)

This function will be called for each probability data set in the sliding window probability computation implementation of `vrna_probs_window()`. The argument *type* specifies the type of probability that is passed to this function.

Global **`vrna_subopt_callback`** (`const char *structure`, `float energy`, `void *data`)

This function will be called for each suboptimal secondary structure that is successfully backtraced.

## 6.3 Scripting Language interface(s)

### 6.3.1 Introduction

For an easy integration into scripting languages, we provide an automatically generated interface to the RNAlib C-library, generated with SWIG.

### 6.3.2 Function Renaming

To provide a namespace-like separation of function symbols from our C library and third-party code, we use the prefix `vrna_` or `VRNA_` whenever possible. This, however, is not necessary for the scripting language interface, as it uses the separate namespace or package `RNA` anyway. Consequently, symbols that appear to have the `vrna_` or `VRNA_` prefix in the C-library have the corresponding prefix stripped away.

For instance, the C code

```
mfe = vrna_fold(sequence, structure);
```

translates to

```
my ($structure, $mfe) = RNA::fold($sequence)
```

in the Perl 5 interface, and

```
structure,mfe = RNA.fold(sequence)
```

for Python. Note, that in this example we also make use of the possibility to return multiple data at once in the scripting language, while the C library function uses additional parameters to return multiple data.

Functions that are dedicated to work on specific data structures only, e.g. the `vrna_fold_compound_t`, are usually not exported at all. Instead, they are attached as object methods of a corresponding class (see [Object oriented Interface for Data Structures](#) for detailed information).

### 6.3.2.1 Global Variables

For the Python interface(s) SWIG places global variables of the C-library into an additional namespace `cvar`. For instance, changing the global temperature variable thus becomes

```
RNA.cvar.temperature = 25
```

## 6.3.3 Object oriented Interface for Data Structures

For data structures, typedefs, and enumerations the `vrna_` prefixes are dropped as well, together with their suffixes `_s`, `_t`, and `_e`, respectively. Furthermore, data structures are usually transformed into classes and relevant functions of the C-library are attached as methods.

### 6.3.4 Examples

Examples on the basic usage of the scripting language interfaces can be found in the [Perl5 Examples](#) and [Python Examples](#) section.

### 6.3.5 SWIG generated Wrapper notes

Special notes on how functions, structures, enums, and macro definitions are actually wrapped, can be found below

#### Global `vrna_abstract_shapes` (const char \*structure, unsigned int level)

This function is available as an overloaded function `abstract_shapes()` where the optional second parameter `level` defaults to 5.

#### Global `vrna_abstract_shapes_pt` (const short \*pt, unsigned int level)

This function is available as an overloaded function `abstract_shapes()` where the optional second parameter `level` defaults to 5.

#### Global `vrna_aln_conservation_col` (const char \*\*alignment, const vrna\_md\_t \*md\_p, unsigned int options)

This function is available in an overloaded form where the last two parameters may be omitted, indicating `md = NULL`, and `options = VRNA_MEASURE_SHANNON_ENTROPY`, respectively.

#### Global `vrna_aln_conservation_struct` (const char \*\*alignment, const char \*structure, const vrna\_md\_t \*md)

This function is available in an overloaded form where the last parameter may be omitted, indicating `md = NULL`

#### Global `vrna_backtrack5` (vrna\_fold\_compound\_t \*fc, unsigned int length, char \*structure)

This function is attached as overloaded method `backtrack()` to objects of type `fold_compound` with default parameter `length` equal to the total length of the RNA.

#### Global `vrna_boustrophedon` (size\_t start, size\_t end)

This function is available as overloaded global function `boustrophedon()`.

#### Global `vrna_boustrophedon_pos` (size\_t start, size\_t end, size\_t pos)

This function is available as overloaded global function `boustrophedon()`. Omitting the `pos` argument yields the entire sequence from `start` to `end`.

#### Global `vrna_bp_distance` (const char \*str1, const char \*str2)

This function is available as an overloaded method `bp_distance()`. Note that the SWIG wrapper takes two structure in dot-bracket notation and converts them into pair tables using `vrna_ptable_from_string()`. The resulting pair tables are then internally passed to `vrna_bp_distance_pt()`. To control which kind of matching brackets will be used during conversion, the optional argument `options` can be used. See also the description of `vrna_ptable_from_string()` for available options. (default: `VRNA_BRACKETS_RND`).

#### Global `vrna_bp_distance_pt` (const short \*pt1, const short \*pt2)

This function is available as an overloaded method `bp_distance()`.

#### Global `vrna_db_flatten` (char \*structure, unsigned int options)

This function flattens an input structure string in-place! The second parameter is optional and defaults to `VRNA_BRACKETS_DEFAULT`.

An overloaded version of this function exists, where an additional second parameter can be passed to specify the target brackets, i.e. the type of matching pair characters all brackets will be flattened to. Therefore, in the scripting language interface this function is a replacement for `vrna_db_flatten_to()`.



**Global `vrna_db_flatten_to` (char \*string, const char target[3], unsigned int options)**

This function is available as an overloaded version of `vrna_db_flatten()`

**Global `vrna_db_from_probs` (const FLT\_OR\_DBL \*pr, unsigned int length)**

This function is available as parameter-less method `db_from_probs()` bound to objects of type `fold_compound`. Parameters `pr` and `length` are implicitly taken from the `fold_compound` object the method is bound to. Upon missing base pair probabilities, this method returns an empty string.

**Global `vrna_db_pk_remove` (const char \*structure, unsigned int options)**

This function is available as an overloaded function `db_pk_remove()` where the optional second parameter `options` defaults to `VRNA_BRACKETS_ANY`.

**Global `vrna_ensemble_defect` (vrna\_fold\_compound\_t \*fc, const char \*structure)**

This function is attached as method `ensemble_defect()` to objects of type `fold_compound`. Note that the SWIG wrapper takes a structure in dot-bracket notation and converts it into a pair table using `vrna_ptable_from_string()`. The resulting pair table is then internally passed to `vrna_ensemble_defect_pt()`. To control which kind of matching brackets will be used during conversion, the optional argument `options` can be used. See also the description of `vrna_ptable_from_string()` for available options. (default: `VRNA_BRACKETS_RND`).

**Global `vrna_ensemble_defect_pt` (vrna\_fold\_compound\_t \*fc, const short \*pt)**

This function is attached as overloaded method `ensemble_defect()` to objects of type `fold_compound`.

**Global `vrna_enumerate_necklaces` (const unsigned int \*type\_counts)**

This function is available as global function `enumerate_necklaces()` which accepts lists input, and produces list of lists output.

**Global `vrna_eval_circ_consensus_structure` (const char \*\*alignment, const char \*structure)**

This function is available through an overloaded version of `vrna_eval_circ_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**Global `vrna_eval_circ_consensus_structure_v` (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)**

This function is available through an overloaded version of `vrna_eval_circ_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_circ_gquad_consensus_structure` (const char \*\*alignment, const char \*structure)**

This function is available through an overloaded version of `vrna_eval_circ_gquad_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**Global `vrna_eval_circ_gquad_consensus_structure_v` (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)**

This function is available through an overloaded version of `vrna_eval_circ_gquad_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_circ_gquad_structure` (const char \*string, const char \*structure)**

In the target scripting language, this function serves as a wrapper for `vrna_eval_circ_gquad_structure_v()` and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_circ_gquad_structure_v` (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)**

This function is available through an overloaded version of `vrna_eval_circ_gquad_structure()`. The last two arguments for this function are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_circ_structure` (const char \*string, const char \*structure)**

In the target scripting language, this function serves as a wrapper for `vrna_eval_circ_structure_v()` and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_circ_structure_v`** (`const char *string`, `const char *structure`, `int verbosity_level`, `FILE *file`)

This function is available through an overloaded version of `vrna_eval_circ_structure()`. The last two arguments for this function are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_consensus_structure_pt_simple`** (`const char **alignment`, `const short *pt`)

This function is available through an overloaded version of `vrna_eval_structure_pt_simple()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**Global `vrna_eval_consensus_structure_pt_simple_v`** (`const char **alignment`, `const short *pt`, `int verbosity_level`, `FILE *file`)

This function is available through an overloaded version of `vrna_eval_structure_pt_simple()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_consensus_structure_pt_simple_verbose`** (`const char **alignment`, `const short *pt`, `FILE *file`)

This function is not available. Use `vrna_eval_consensus_structure_pt_v()` instead!

**Global `vrna_eval_consensus_structure_simple`** (`const char **alignment`, `const char *structure`)

This function is available through an overloaded version of `vrna_eval_structure_simple()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**Global `vrna_eval_consensus_structure_simple_v`** (`const char **alignment`, `const char *structure`, `int verbosity_level`, `FILE *file`)

This function is available through an overloaded version of `vrna_eval_structure_simple()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_consensus_structure_simple_verbose`** (`const char **alignment`, `const char *structure`, `FILE *file`)

This function is not available. Use `vrna_eval_consensus_structure_simple_v()` instead!

**Global `vrna_eval_covar_structure`** (`vrna_fold_compound_t *fc`, `const char *structure`)

This function is attached as method `eval_covar_structure()` to objects of type `fold_compound`

**Global `vrna_eval_gquad_consensus_structure`** (`const char **alignment`, `const char *structure`)

This function is available through an overloaded version of `vrna_eval_gquad_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**Global `vrna_eval_gquad_consensus_structure_v`** (`const char **alignment`, `const char *structure`, `int verbosity_level`, `FILE *file`)

This function is available through an overloaded version of `vrna_eval_gquad_structure()`. Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_gquad_structure`** (`const char *string`, `const char *structure`)

In the target scripting language, this function serves as a wrapper for `vrna_eval_gquad_structure_v()` and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_gquad_structure_v`** (`const char *string`, `const char *structure`, `int verbosity_level`, `FILE *file`)

This function is available through an overloaded version of `vrna_eval_gquad_structure()`. The last two arguments for this function are optional and default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**Global `vrna_eval_hp_loop`** (`vrna_fold_compound_t *fc`, `int i`, `int j`)

This function is attached as method `eval_hp_loop()` to objects of type `fold_compound`

**Global `vrna_eval_int_loop`** (`vrna_fold_compound_t *fc`, `int i`, `int j`, `int k`, `int l`)

This function is attached as method `eval_int_loop()` to objects of type `fold_compound`

**Global `vrna_eval_loop_pt`** (`vrna_fold_compound_t *fc`, `int i`, `const short *pt`)

This function is attached as method `eval_loop_pt()` to objects of type `fold_compound`

Global [vrna\\_eval\\_move](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, int m1, int m2)

This function is attached as method [eval\\_move\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_eval\\_move\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, short \*pt, int m1, int m2)

This function is attached as method [eval\\_move\\_pt\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_eval\\_structure](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)

This function is attached as method [eval\\_structure\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_eval\\_structure\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt)

This function is attached as method [eval\\_structure\\_pt\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_eval\\_structure\\_pt\\_simple](#) (const char \*string, const short \*pt)

In the target scripting language, this function serves as a wrapper for [vrna\\_eval\\_structure\\_pt\\_v\(\)](#) and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

Global [vrna\\_eval\\_structure\\_pt\\_verbose](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt, FILE \*file)

This function is attached as method [eval\\_structure\\_pt\\_verbose\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_eval\\_structure\\_simple](#) (const char \*string, const char \*structure)

In the target scripting language, this function serves as a wrapper for [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

Global [vrna\\_eval\\_structure\\_simple\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)

This function is available through an overloaded version of [vrna\\_eval\\_structure\\_simple\(\)](#). The last two arguments for this function are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

Global [vrna\\_eval\\_structure\\_simple\\_verbose](#) (const char \*string, const char \*structure, FILE \*file)

This function is not available. Use [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) instead!

Global [vrna\\_eval\\_structure\\_verbose](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, FILE \*file)

This function is attached as method [eval\\_structure\\_verbose\(\)](#) to objects of type *fold\_compound*

Global [vrna\\_exp\\_params\\_rescale](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double \*mfe)

This function is attached to [vrna\\_fc\\_s](#) objects as overloaded [exp\\_params\\_rescale\(\)](#) method.

When no parameter is passed to this method, the resulting action is the same as passing *NULL* as second parameter to [vrna\\_exp\\_params\\_rescale\(\)](#), i.e. default scaling of the partition function. Passing an energy in kcal/mol, e.g. as retrieved by a previous call to the [mfe\(\)](#) method, instructs all subsequent calls to scale the partition function accordingly.

Global [vrna\\_exp\\_params\\_reset](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_md\\_t](#) \*md\_p)

This function is attached to [vrna\\_fc\\_s](#) objects as overloaded [exp\\_params\\_reset\(\)](#) method.

When no parameter is passed to this method, the resulting action is the same as passing *NULL* as second parameter to [vrna\\_exp\\_params\\_reset\(\)](#), i.e. global default model settings are used. Passing an object of type [vrna\\_md\\_s](#) resets the fold compound according to the specifications stored within the [vrna\\_md\\_s](#) object.

Global [vrna\\_exp\\_params\\_subst](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_exp\\_param\\_t](#) \*params)

This function is attached to [vrna\\_fc\\_s](#) objects as overloaded [exp\\_params\\_subst\(\)](#) method.

When no parameter is passed, the resulting action is the same as passing *NULL* as second parameter to [vrna\\_exp\\_params\\_subst\(\)](#), i.e. resetting the parameters to the global defaults.

Class [vrna\\_fc\\_s](#)

This data structure is wrapped as an object *fold\_compound* with several related functions attached as methods.

A new *fold\_compound* can be obtained by calling one of its constructors:

- *fold\_compound(seq)* – Initialize with a single sequence, or two concatenated sequences separated by an ampersand character '&' (for cofolding)

- `fold_compound(aln)` – Initialize with a sequence alignment `aln` stored as a list of sequences (with gap characters)

The resulting object has a list of attached methods which in most cases directly correspond to functions that mainly operate on the corresponding C data structure:

- `type()` – Get the type of the `fold_compound` (See [vrna\\_fc\\_type\\_e](#))
- `length()` – Get the length of the sequence(s) or alignment stored within the `fold_compound`

Global [vrna\\_file\\_commands\\_apply](#) (`vrna_fold_compound_t *vc`, `const char *filename`, `unsigned int options`)

This function is attached as method `file_commands_apply()` to objects of type `fold_compound`

Global [vrna\\_file\\_msa\\_detect\\_format](#) (`const char *filename`, `unsigned int options`)

This function exists as an overloaded version where the `options` parameter may be omitted! In that case, the `options` parameter defaults to [VRNA\\_FILE\\_FORMAT\\_MSA\\_DEFAULT](#).

Global [vrna\\_file\\_msa\\_read](#) (`const char *filename`, `char ***names`, `char ***aln`, `char **id`, `char **structure`, `unsigned int options`)

In the target scripting language, only the first and last argument, `filename` and `options`, are passed to the corresponding function. The other arguments, which serve as output in the C-library, are available as additional return values. Hence, a function call in python may look like this:

Global [vrna\\_file\\_msa\\_read\\_record](#) (`FILE *fp`, `char ***names`, `char ***aln`, `char **id`, `char **structure`, `unsigned int options`)

In the target scripting language, only the first and last argument, `fp` and `options`, are passed to the corresponding function. The other arguments, which serve as output in the C-library, are available as additional return values. Hence, a function call in python may look like this:

Global [vrna\\_file\\_msa\\_write](#) (`const char *filename`, `const char ***names`, `const char **aln`, `const char *id`, `const char *structure`, `const char *source`, `unsigned int options`)

In the target scripting language, this function exists as a set of overloaded versions, where the last four parameters may be omitted. If the `options` parameter is missing the options default to ([VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#) | [VRNA\\_FILE\\_FORMAT\\_MSA\\_APPEND](#)).

Global [vrna\\_file\\_PS\\_aln](#) (`const char *filename`, `const char **seqs`, `const char **names`, `const char *structure`, `unsigned int columns`)

This function is available as overloaded function `file_PS_aln()` with three additional parameters `start`, `end`, and `offset` before the `columns` argument. Thus, it resembles the [vrna\\_file\\_PS\\_aln\\_slice\(\)](#) function. The last four arguments may be omitted, indicating the default of `start = 0`, `end = 0`, `offset = 0`, and `columns = 60`.

Global [vrna\\_file\\_PS\\_aln\\_slice](#) (`const char *filename`, `const char **seqs`, `const char **names`, `const char *structure`, `unsigned int start`, `unsigned int end`, `int offset`, `unsigned int columns`)

This function is available as overloaded function `file_PS_aln()` where the last four parameter may be omitted, indicating `start = 0`, `end = 0`, `offset = 0`, and `columns = 60`.

Global [vrna\\_hc\\_add\\_from\\_db](#) (`vrna_fold_compound_t *vc`, `const char *constraint`, `unsigned int options`)

This function is attached as method `hc_add_from_db()` to objects of type `fold_compound`

Global [vrna\\_hc\\_init](#) (`vrna_fold_compound_t *vc`)

This function is attached as method `hc_init()` to objects of type `fold_compound`

Global [vrna\\_heat\\_capacity](#) (`vrna_fold_compound_t *fc`, `float T_min`, `float T_max`, `float T_increment`, `unsigned int mpoints`)

This function is attached as overloaded method `heat_capacity()` to objects of type `fold_compound`. If the optional function arguments `T_min`, `T_max`, `T_increment`, and `mpoints` are omitted, they default to 0.0, 100.0, 1.0 and 2, respectively.

Global [vrna\\_heat\\_capacity\\_cb](#) (`vrna_fold_compound_t *fc`, `float T_min`, `float T_max`, `float T_increment`, `unsigned int mpoints`, `vrna_heat_capacity_callback *cb`, `void *data`)

This function is attached as method `heat_capacity_cb()` to objects of type `fold_compound`

Global **vrna\_heat\_capacity\_simple** (const char \*sequence, float T\_min, float T\_max, float T\_increment, unsigned int mpoints)

This function is available as overloaded function **heat\_capacity()**. If the optional function arguments T\_min, T\_max, T\_increment, and mpoints are omitted, they default to 0.0, 100.0, 1.0 and 2, respectively.

Global **vrna\_init\_rand\_seed** (unsigned int seed)

This function is available as an overloaded function **init\_rand()** where the argument seed is optional.

Global **vrna\_maximum\_matching** (vrna\_fold\_compound\_t \*fc)

This function is attached as method **maximum\_matching()** to objects of type *fold\_compound* (i.e. *vrna\_fold\_compound\_t*).

Global **vrna\_maximum\_matching\_simple** (const char \*sequence)

This function is available as global function **maximum\_matching()**.

Class **vrna\_md\_s**

This data structure is wrapped as an object **md** with multiple related functions attached as methods.

A new set of default parameters can be obtained by calling the constructor of **md**:

- *md()* – Initialize with default settings

The resulting object has a list of attached methods which directly correspond to functions that mainly operate on the corresponding C data structure:

- *reset()* – *vrna\_md\_set\_default()*
- *set\_from\_globals()* – *set\_model\_details()*
- *option\_string()* – *vrna\_md\_option\_string()*

Note, that default parameters can be modified by directly setting any of the following global variables. Internally, getting/setting default parameters using their global variable representative translates into calls of the following functions, therefore these wrappers for these functions do not exist in the scripting language interface(s):

Global **vrna\_MEA** (vrna\_fold\_compound\_t \*fc, double gamma, float \*mea)

This function is attached as overloaded method **MEA**(gamma = 1.) to objects of type *fold\_compound*. Note, that it returns the MEA structure and MEA value as a tuple (MEA\_structure, MEA)

Global **vrna\_MEA\_from\_plist** (vrna\_ep\_t \*plist, const char \*sequence, double gamma, vrna\_md\_t \*md, float \*mea)

This function is available as overloaded function **MEA\_from\_plist**(gamma = 1., md = NULL). Note, that it returns the MEA structure and MEA value as a tuple (MEA\_structure, MEA)

Global **vrna\_mean\_bp\_distance** (vrna\_fold\_compound\_t \*vc)

This function is attached as method **mean\_bp\_distance()** to objects of type *fold\_compound*

Global **vrna\_mfe** (vrna\_fold\_compound\_t \*vc, char \*structure)

This function is attached as method **mfe()** to objects of type *fold\_compound*

Global **vrna\_mfe\_dimer** (vrna\_fold\_compound\_t \*vc, char \*structure)

This function is attached as method **mfe\_dimer()** to objects of type *fold\_compound*

Global **vrna\_mfe\_window** (vrna\_fold\_compound\_t \*vc, FILE \*file)

This function is attached as method **mfe\_window()** to objects of type *fold\_compound*

Global **vrna\_neighbors** (vrna\_fold\_compound\_t \*vc, const short \*pt, unsigned int options)

This function is attached as an overloaded method *neighbors()* to objects of type *fold\_compound*. The optional parameter options defaults to **VRNA\_MOVESET\_DEFAULT** if it is omitted.

Global **vrna\_params\_load** (const char fname[], unsigned int options)

This function is available as overloaded function **params\_load**(fname="", options=**VRNA\_PARAMETER\_FORMAT\_DEFAULT**). Here, the empty filename string indicates to load default RNA parameters, i.e. this is equivalent to calling *vrna\_params\_load\_defaults()*.



**Global `vrna_params_load_defaults` (void)**

This function is available as overloaded function `params_load()`.

**Global `vrna_params_load_DNA_Mathews1999` (void)**

This function is available as function `params_load_DNA_Mathews1999()`.

**Global `vrna_params_load_DNA_Mathews2004` (void)**

This function is available as function `params_load_DNA_Mathews2004()`.

**Global `vrna_params_load_from_string` (const char \*string, const char \*name, unsigned int options)**

This function is available as overloaded function `params_load_from_string(string, name="", options=VRNA_PARAMETER_FORMAT_DEFAULT)`.

**Global `vrna_params_load_RNA_Andronescu2007` (void)**

This function is available as function `params_load_RNA_Andronescu2007()`.

**Global `vrna_params_load_RNA_Langdon2018` (void)**

This function is available as function `params_load_RNA_Langdon2018()`.

**Global `vrna_params_load_RNA_misc_special_hairpins` (void)**

This function is available as function `params_load_RNA_misc_special_hairpins()`.

**Global `vrna_params_load_RNA_Turner1999` (void)**

This function is available as function `params_load_RNA_Turner1999()`.

**Global `vrna_params_load_RNA_Turner2004` (void)**

This function is available as function `params_load_RNA_Turner2004()`.

**Global `vrna_params_reset` (vrna\_fold\_compound\_t \*vc, vrna\_md\_t \*md\_p)**

This function is attached to `vrna_fc_s` objects as overloaded `params_reset()` method.

When no parameter is passed to this method, the resulting action is the same as passing `NULL` as second parameter to `vrna_params_reset()`, i.e. global default model settings are used. Passing an object of type `vrna_md_s` resets the fold compound according to the specifications stored within the `vrna_md_s` object.

**Global `vrna_params_save` (const char fname[], unsigned int options)**

This function is available as overloaded function `params_save(fname, options=VRNA_PARAMETER_FORMAT_DEFAULT)`.

**Global `vrna_params_subst` (vrna\_fold\_compound\_t \*vc, vrna\_param\_t \*par)**

This function is attached to `vrna_fc_s` objects as overloaded `params_subst()` method.

When no parameter is passed, the resulting action is the same as passing `NULL` as second parameter to `vrna_params_subst()`, i.e. resetting the parameters to the global defaults.

**Global `vrna_path` (vrna\_fold\_compound\_t \*vc, short \*pt, unsigned int steps, unsigned int options)**

This function is attached as an overloaded method `path()` to objects of type `fold_compound`. The optional parameter `options` defaults to `VRNA_PATH_DEFAULT` if it is omitted.

**Global `vrna_path_direct` (vrna\_fold\_compound\_t \*fc, const char \*s1, const char \*s2, vrna\_path\_options\_t options)**

This function is attached as an overloaded method `path_direct()` to objects of type `fold_compound`. The optional parameter `options` defaults to `NULL` if it is omitted.

**Global `vrna_path_direct_ub` (vrna\_fold\_compound\_t \*fc, const char \*s1, const char \*s2, int maxE, vrna\_path\_options\_t options)**

This function is attached as an overloaded method `path_direct()` to objects of type `fold_compound`. The optional parameter `maxE` defaults to `#INT_MAX - 1` if it is omitted, while the optional parameter `options` defaults to `NULL`. In case the function did not find a path with  $E_{\text{saddle}} < E_{\text{max}}$  it returns an empty list.

**Global `vrna_path_findpath` (vrna\_fold\_compound\_t \*fc, const char \*s1, const char \*s2, int width)**

This function is attached as an overloaded method `path_findpath()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted.

**Global `vrna_path_findpath_saddle` (vrna\_fold\_compound\_t \*fc, const char \*s1, const char \*s2, int width)**

This function is attached as an overloaded method `path_findpath_saddle()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted.

Global **`vrna_path_findpath_saddle_ub`** (`vrna_fold_compound_t *fc`, `const char *s1`, `const char *s2`, `int width`, `int maxE`)

This function is attached as an overloaded method `path_findpath_saddle()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted, while the optional parameter `maxE` defaults to `INF`. In case the function did not find a path with  $E_{saddle} < E_{max}$  the function returns a `NULL` object, i.e. `undef` for Perl and `None` for Python.

Global **`vrna_path_findpath_ub`** (`vrna_fold_compound_t *fc`, `const char *s1`, `const char *s2`, `int width`, `int maxE`)

This function is attached as an overloaded method `path_findpath()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted, while the optional parameter `maxE` defaults to `INF`. In case the function did not find a path with  $E_{saddle} < E_{max}$  the function returns an empty list.

Global **`vrna_path_gradient`** (`vrna_fold_compound_t *vc`, `short *pt`, `unsigned int options`)

This function is attached as an overloaded method `path_gradient()` to objects of type `fold_compound`. The optional parameter `options` defaults to `VRNA_PATH_DEFAULT` if it is omitted.

Global **`vrna_path_options_findpath`** (`int width`, `unsigned int type`)

This function is available as overloaded function `path_options_findpath()`. The optional parameter `width` defaults to 10 if omitted, while the optional parameter `type` defaults to `VRNA_PATH_TYPE_DOT_BRACKET`.

Global **`vrna_path_random`** (`vrna_fold_compound_t *vc`, `short *pt`, `unsigned int steps`, `unsigned int options`)

This function is attached as an overloaded method `path_gradient()` to objects of type `fold_compound`. The optional parameter `options` defaults to `VRNA_PATH_DEFAULT` if it is omitted.

Global **`vrna_pbacktrack`** (`vrna_fold_compound_t *fc`)

This function is attached as overloaded method **`pbacktrack()`** to objects of type `fold_compound`. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack5`** (`vrna_fold_compound_t *fc`, `unsigned int length`)

This function is attached as overloaded method **`pbacktrack5()`** to objects of type `fold_compound`. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack5_cb`** (`vrna_fold_compound_t *fc`, `unsigned int num_samples`, `unsigned int length`, `vrna_boltzmann_sampling_callback *cb`, `void *data`, `unsigned int options`)

This function is attached as overloaded method **`pbacktrack5()`** to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack5_num`** (`vrna_fold_compound_t *fc`, `unsigned int num_samples`, `unsigned int length`, `unsigned int options`)

This function is attached as overloaded method **`pbacktrack5()`** to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack5_resume`** (`vrna_fold_compound_t *vc`, `unsigned int num_samples`, `unsigned int length`, `vrna_pbacktrack_mem_t *nr_mem`, `unsigned int options`)

This function is attached as overloaded method **`pbacktrack5()`** to objects of type `fold_compound`. In addition to the list of structures, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack5_resume_cb`** (`vrna_fold_compound_t *fc`, `unsigned int num_samples`, `unsigned int length`, `vrna_boltzmann_sampling_callback *cb`, `void *data`, `vrna_pbacktrack_mem_t *nr_mem`, `unsigned int options`)

This function is attached as overloaded method **`pbacktrack5()`** to objects of type `fold_compound`. In addition to the number of structures backtraced, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **`vrna_pbacktrack_cb`** (`vrna_fold_compound_t *fc`, `unsigned int num_samples`, `vrna_boltzmann_↔  
sampling_callback *cb`, `void *data`, `unsigned int options`)

This function is attached as overloaded method **`pbacktrack()`** to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_num](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound* where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_resume](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, `vrna_pbacktrack_mem_t *nr_mem`, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound*. In addition to the list of structures, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_resume\\_cb](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, `vrna_boltzmann_sampling_callback *cb`, void \*data, `vrna_pbacktrack_mem_t *nr_mem`, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound*. In addition to the number of structures backtraced, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_sub](#)** (`vrna_fold_compound_t *fc`, unsigned int start, unsigned int end)

This function is attached as overloaded method **[pbacktrack\\_sub\(\)](#)** to objects of type *fold\_compound*. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_sub\\_cb](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, unsigned int start, unsigned int end, `vrna_boltzmann_sampling_callback *cb`, void \*data, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound* where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_sub\\_num](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, unsigned int start, unsigned int end, unsigned int options)

This function is attached as overloaded method **[pbacktrack\\_sub\(\)](#)** to objects of type *fold\_compound* where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_sub\\_resume](#)** (`vrna_fold_compound_t *vc`, unsigned int num\_samples, unsigned int start, unsigned int end, `vrna_pbacktrack_mem_t *nr_mem`, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound*. In addition to the list of structures, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pbacktrack\\_sub\\_resume\\_cb](#)** (`vrna_fold_compound_t *fc`, unsigned int num\_samples, unsigned int start, unsigned int end, `vrna_boltzmann_sampling_callback *bs_cb`, void \*data, `vrna_pbacktrack_mem_t *nr_mem`, unsigned int options)

This function is attached as overloaded method **[pbacktrack\(\)](#)** to objects of type *fold\_compound*. In addition to the number of structures backtraced, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

Global **[vrna\\_pf](#)** (`vrna_fold_compound_t *vc`, char \*structure)

This function is attached as method **[pf\(\)](#)** to objects of type *fold\_compound*

Global **[vrna\\_pf\\_dimer](#)** (`vrna_fold_compound_t *vc`, char \*structure)

This function is attached as method **[pf\\_dimer\(\)](#)** to objects of type *fold\_compound*

Global **[vrna\\_positional\\_entropy](#)** (`vrna_fold_compound_t *fc`)

This function is attached as method **[positional\\_entropy\(\)](#)** to objects of type *fold\_compound*

Global **[vrna\\_pr\\_energy](#)** (`vrna_fold_compound_t *vc`, double e)

This function is attached as method **[pr\\_energy\(\)](#)** to objects of type *fold\_compound*

Global **[vrna\\_pr\\_structure](#)** (`vrna_fold_compound_t *fc`, const char \*structure)

This function is attached as method **[pr\\_structure\(\)](#)** to objects of type *fold\_compound*



**Global `vrna_ptable` (`const char *structure`)**

This functions is wrapped as overloaded function `ptable()` that takes an optional argument `options` to specify which type of matching brackets should be considered during conversion. The default set is round brackets, i.e. `VRNA_BRACKETS_RND`.

**Global `vrna_ptable_from_string` (`const char *structure`, `unsigned int options`)**

This functions is wrapped as overloaded function `ptable()` that takes an optional argument `options` to specify which type of matching brackets should be considered during conversion. The default set is round brackets, i.e. `VRNA_BRACKETS_RND`.

**Global `vrna_rotational_symmetry` (`const char *string`)**

This function is available as global function `rotational_symmetry()`. See `vrna_rotational_symmetry_pos()` for details.

**Global `vrna_rotational_symmetry_db` (`vrna_fold_compound_t *fc`, `const char *structure`)**

This function is attached as method `rotational_symmetry_db()` to objects of type `fold_compound` (i.e. `vrna_fold_compound_t`). See `vrna_rotational_symmetry_db_pos()` for details.

**Global `vrna_rotational_symmetry_db_pos` (`vrna_fold_compound_t *fc`, `const char *structure`, `unsigned int **positions`)**

This function is attached as method `rotational_symmetry_db()` to objects of type `fold_compound` (i.e. `vrna_fold_compound_t`). Thus, the first argument must be omitted. In contrast to our C-implementation, this function doesn't simply return the order of rotational symmetry of the secondary structure, but returns the list `position` of cyclic permutation shifts that result in a rotationally symmetric structure. The length of the list then determines the order of rotational symmetry.

**Global `vrna_rotational_symmetry_num` (`const unsigned int *string`, `size_t string_length`)**

This function is available as global function `rotational_symmetry()`. See `vrna_rotational_symmetry_pos()` for details. Note, that in the target language the length of the list `string` is always known a-priori, so the parameter `string_length` must be omitted.

**Global `vrna_rotational_symmetry_pos` (`const char *string`, `unsigned int **positions`)**

This function is available as overloaded global function `rotational_symmetry()`. It merges the functionalities of `vrna_rotational_symmetry()`, `vrna_rotational_symmetry_pos()`, `vrna_rotational_symmetry_num()`, and `vrna_rotational_symmetry_pos_num()`. In contrast to our C-implementation, this function doesn't return the order of rotational symmetry as a single value, but returns a list of cyclic permutation shifts that result in a rotationally symmetric string. The length of the list then determines the order of rotational symmetry.

**Global `vrna_rotational_symmetry_pos_num` (`const unsigned int *string`, `size_t string_length`, `unsigned int **positions`)**

This function is available as global function `rotational_symmetry()`. See `vrna_rotational_symmetry_pos()` for details. Note, that in the target language the length of the list `string` is always known a-priori, so the parameter `string_length` must be omitted.

**Global `vrna_sc_add_bp` (`vrna_fold_compound_t *vc`, `int i`, `int j`, `FLT_OR_DBL energy`, `unsigned int options`)**

This function is attached as an overloaded method `sc_add_bp()` to objects of type `fold_compound`. The method either takes arguments for a single base pair (i,j) with the corresponding energy value:

**Global `vrna_sc_add_bt` (`vrna_fold_compound_t *vc`, `vrna_callback_sc_backtrack *f`)**

This function is attached as method `sc_add_bt()` to objects of type `fold_compound`

**Global `vrna_sc_add_data` (`vrna_fold_compound_t *vc`, `void *data`, `vrna_callback_free_auxdata *free_data`)**

This function is attached as method `sc_add_data()` to objects of type `fold_compound`

**Global `vrna_sc_add_exp_f` (`vrna_fold_compound_t *vc`, `vrna_callback_sc_exp_energy *exp_f`)**

This function is attached as method `sc_add_exp_f()` to objects of type `fold_compound`

**Global `vrna_sc_add_f` (`vrna_fold_compound_t *vc`, `vrna_callback_sc_energy *f`)**

This function is attached as method `sc_add_f()` to objects of type `fold_compound`

**Global `vrna_sc_add_hi_motif` (`vrna_fold_compound_t *fc`, `const char *seq`, `const char *structure`, `FLT_OR_DBL energy`, `unsigned int options`)**

This function is attached as method `sc_add_hi_motif()` to objects of type `fold_compound`

Global **`vrna_sc_add_SHAPE_deigan`** (`vrna_fold_compound_t *vc`, `const double *reactivities`, `double m`, `double b`, `unsigned int options`)

This function is attached as method **`sc_add_SHAPE_deigan()`** to objects of type *fold\_compound*

Global **`vrna_sc_add_SHAPE_deigan_ali`** (`vrna_fold_compound_t *vc`, `const char **shape_files`, `const int *shape_file_association`, `double m`, `double b`, `unsigned int options`)

This function is attached as method **`sc_add_SHAPE_deigan_ali()`** to objects of type *fold\_compound*

Global **`vrna_sc_add_SHAPE_zarringhalam`** (`vrna_fold_compound_t *vc`, `const double *reactivities`, `double b`, `double default_value`, `const char *shape_conversion`, `unsigned int options`)

This function is attached as method **`sc_add_SHAPE_zarringhalam()`** to objects of type *fold\_compound*

Global **`vrna_sc_add_up`** (`vrna_fold_compound_t *vc`, `int i`, `FLT_OR_DBL energy`, `unsigned int options`)

This function is attached as an overloaded method **`sc_add_up()`** to objects of type *fold\_compound*. The method either takes arguments for a single nucleotide *i* with the corresponding energy value:

Global **`vrna_sc_init`** (`vrna_fold_compound_t *vc`)

This function is attached as method **`sc_init()`** to objects of type *fold\_compound*

Global **`vrna_sc_remove`** (`vrna_fold_compound_t *vc`)

This function is attached as method **`sc_remove()`** to objects of type *fold\_compound*

Global **`vrna_sc_set_bp`** (`vrna_fold_compound_t *vc`, `const FLT_OR_DBL **constraints`, `unsigned int options`)

This function is attached as method **`sc_set_bp()`** to objects of type *fold\_compound*

Global **`vrna_sc_set_up`** (`vrna_fold_compound_t *vc`, `const FLT_OR_DBL *constraints`, `unsigned int options`)

This function is attached as method **`sc_set_up()`** to objects of type *fold\_compound*

Global **`vrna_seq_encode`** (`const char *sequence`, `vrna_md_t *md`)

In the target scripting language, this function is wrapped as overloaded function *seq\_encode()* where the last parameter, the *model\_details* data structure, is optional. If it is omitted, default model settings are applied, i.e. default nucleotide letter conversion. The wrapped function returns a list/tuple of integer representations of the input sequence.

Global **`vrna_strtrim`** (`char *string`, `const char *delimiters`, `unsigned int keep`, `unsigned int options`)

Since many scripting languages treat strings as immutable objects, this function does not modify the input string directly. Instead, it returns the modified string as second return value, together with the number of removed delimiters.

The scripting language interface provides an overloaded version of this function, with default parameters *delimiters=NULL*, *keep=0*, and *options=VRNA\_TRIM\_DEFAULT*.

Global **`vrna_subopt`** (`vrna_fold_compound_t *fc`, `int delta`, `int sorted`, `FILE *fp`)

This function is attached as method **`subopt()`** to objects of type *fold\_compound*

Global **`vrna_subopt_cb`** (`vrna_fold_compound_t *fc`, `int delta`, `vrna_subopt_callback *cb`, `void *data`)

This function is attached as method **`subopt_cb()`** to objects of type *fold\_compound*

Global **`vrna_subopt_zuker`** (`vrna_fold_compound_t *fc`)

This function is attached as method **`subopt_zuker()`** to objects of type *fold\_compound*

Global **`vrna_ud_remove`** (`vrna_fold_compound_t *vc`)

This function is attached as method **`ud_remove()`** to objects of type *fold\_compound*

Global **`vrna_ud_set_data`** (`vrna_fold_compound_t *vc`, `void *data`, `vrna_callback_free_auxdata *free_cb`)

This function is attached as method **`ud_set_data()`** to objects of type *fold\_compound*

Global **`vrna_ud_set_exp_prod_rule_cb`** (`vrna_fold_compound_t *vc`, `vrna_callback_ud_exp_production *pre_cb`, `vrna_callback_ud_exp_energy *exp_e_cb`)

This function is attached as method **`ud_set_exp_prod_rule_cb()`** to objects of type *fold\_compound*

Global **`vrna_ud_set_prob_cb`** (`vrna_fold_compound_t *vc`, `vrna_callback_ud_probs_add *setter`, `vrna_callback_ud_probs_get *getter`)

This function is attached as method **`ud_set_prob_cb()`** to objects of type *fold\_compound*

Global `vrna_ud_set_prod_rule_cb` (`vrna_fold_compound_t *vc`, `vrna_callback_ud_production *pre_cb`, `vrna_callback_ud_energy *e_cb`)

This function is attached as method `ud_set_prod_rule_cb()` to objects of type *fold\_compound*



## Chapter 7

# Additional Utilities



## Chapter 8

# Examples

- [C Examples](#)
- [Perl5 Examples](#)
- [Python Examples](#)

### 8.1 C Examples

#### 8.1.1 Hello World Examples

##### helloworld\_mfe.c

The following is an example showing the minimal requirements to compute the Minimum Free Energy (MFE) and corresponding secondary structure of an RNA sequence

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/fold.h>
#include <ViennaRNA/Utils/basic.h>
int
main()
{
    /* The RNA sequence */
    char *seq = "GAGUAGUGGAACCCAGGCUAUGUUUGUGACUCGCAGACUAACA";
    /* allocate memory for MFE structure (length + 1) */
    char *structure = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* predict Minimum Free Energy and corresponding secondary structure */
    float mfe = vrna_fold(seq, structure);
    /* print sequence, structure and MFE */
    printf("%s\n%s [ %6.2f ]\n", seq, structure, mfe);
    /* cleanup memory */
    free(structure);
    return 0;
}
```

See also

examples/helloworld\_mfe.c in the source code tarball

##### helloworld\_mfe\_comparative.c

Instead of using a single sequence as done above, this example predicts a consensus structure for a multiple sequence alignment

```
#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/alifold.h>
#include <ViennaRNA/Utils/basic.h>
#include <ViennaRNA/Utils/alignments.h>
int
main()
{
    /* The RNA sequence alignment */
    const char *sequences[] = {
        "CUGCCUCACAACGUUUUGUGCCUCAGUUACCCGUAGAUGUAGUGAGGGU",
        "CUGCCUCACAACAUAUUUGUGCCUCAGUUACUCAUAGAUGUAGUGAGGGU",
    };
}
```

```

    "---CUCGACACCACU---GCCUCGGUUAACCAUCGGUGCAGUGCGGGU",
    NULL /* indicates end of alignment */
};
/* compute the consensus sequence */
char *cons = consensus(sequences);
/* allocate memory for MFE consensus structure (length + 1) */
char *structure = (char *)vrna_alloc(sizeof(char) * (strlen(sequences[0]) + 1));
/* predict Minimum Free Energy and corresponding secondary structure */
float mfe = vrna_alifold(sequences, structure);
/* print consensus sequence, structure and MFE */
printf("%s\n%s [ %.2f ]\n", cons, structure, mfe);
/* cleanup memory */
free(cons);
free(structure);
return 0;
}

```

#### See also

examples/helloworld\_mfe\_comparative.c in the source code tarball

### helloworld\_probabilities.c

This example shows how to compute the partition function and base pair probabilities with minimal implementation effort.

```

#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/fold.h>
#include <ViennaRNA/part_func.h>
#include <ViennaRNA/Utils/basic.h>
int
main()
{
    /* The RNA sequence */
    char *seq = "GAGUAGUGGAACAGGCUAUGUUUGUGACUCGCAGACUAACA";
    /* allocate memory for pairing propensity string (length + 1) */
    char *propensity = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* pointers for storing and navigating through base pair probabilities */
    vrna_ep_t *ptr, *pair_probabilities = NULL;
    float en = vrna_pf_fold(seq, propensity, &pair_probabilities);
    /* print sequence, pairing propensity string and ensemble free energy */
    printf("%s\n%s [ %.2f ]\n", seq, propensity, en);
    /* print all base pairs with probability above 50% */
    for (ptr = pair_probabilities; ptr->i != 0; ptr++)
        if (ptr->p > 0.5)
            printf("p(%d, %d) = %g\n", ptr->i, ptr->j, ptr->p);
    /* cleanup memory */
    free(pair_probabilities);
    free(propensity);
    return 0;
}

```

#### See also

examples/helloworld\_probabilities.c in the source code tarball

## 8.1.2 First Steps with the Fold Compound

### fold\_compound\_mfe.c

Instead of calling the simple MFE folding interface `vrna_fold()`, this example shows how to first create a `vrna_fold_compound_t` container with the RNA sequence to finally compute the MFE using this container. This is especially useful if non-default model settings are applied or the dynamic programming (DP) matrices of the MFE prediction are required for post-processing operations, or other tasks on the same sequence will be performed.

```

#include <stdlib.h>
#include <stdio.h>
#include <ViennaRNA/fold_compound.h>
#include <ViennaRNA/Utils/basic.h>
#include <ViennaRNA/Utils/strings.h>
#include <ViennaRNA/mfe.h>
int
main()
{
    /* initialize random number generator */
    vrna_init_rand();
    /* Generate a random sequence of 50 nucleotides */
    char *seq = vrna_random_string(50, "ACGU");
    /* Create a fold compound for the sequence */
    vrna_fold_compound_t *fc = vrna_fold_compound(seq, NULL, VRNA_OPTION_DEFAULT);
}

```



```

/* allocate memory for MFE structure (length + 1) */
char      *structure = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
/* predict Minimum Free Energy and corresponding secondary structure */
float      mfe = vrna_mfe(fc, structure);
/* print sequence, structure and MFE */
printf("%s\n%s [ %6.2f ]\n", seq, structure, mfe);
/* cleanup memory */
free(seq);
free(structure);
vrna_fold_compound_free(fc);
return 0;
}

```

See also

examples/fold\_compound\_mfe.c in the source code tarball

## fold\_compound\_md.c

In the following, we change the model settings (model details) to a temperature of 25 Degree Celcius, and activate G-Quadruplex prediction.

```

#include <stdlib.h>
#include <stdio.h>
#include <string.h>
#include <ViennaRNA/model.h>
#include <ViennaRNA/fold_compound.h>
#include <ViennaRNA/utils/basic.h>
#include <ViennaRNA/utils/strings.h>
#include <ViennaRNA/mfe.h>
int
main()
{
    /* initialize random number generator */
    vrna_init_rand();
    /* Generate a random sequence of 50 nucleotides */
    char      *seq = vrna_random_string(50, "ACGU");
    /* allocate memory for MFE structure (length + 1) */
    char      *structure = (char *)vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* create a new model details structure to store the Model Settings */
    vrna_md_t md;
    /* ALWAYS set default model settings first! */
    vrna_md_set_default(&md);
    /* change temperature and activate G-Quadruplex prediction */
    md.temperature = 25.0; /* 25 Deg Celcius */
    md.gquad       = 1;    /* Turn-on G-Quadruples support */
    /* create a fold compound */
    vrna_fold_compound_t *fc = vrna_fold_compound(seq, &md, VRNA_OPTION_DEFAULT);
    /* predict Minimum Free Energy and corresponding secondary structure */
    float      mfe = vrna_mfe(fc, structure);
    /* print sequence, structure and MFE */
    printf("%s\n%s [ %6.2f ]\n", seq, structure, mfe);
    /* cleanup memory */
    free(structure);
    vrna_fold_compound_free(fc);
    return 0;
}

```

See also

examples/fold\_compound\_md.c in the source code tarball

## 8.1.3 Writing Callback Functions

### callback\_subopt.c

Here is a basic example how to use the callback mechanism in `vrna_subopt_cb()`. It simply defines a callback function (see interface definition for `vrna_subopt_callback`) that prints the result and increases a counter variable.

```

#include <stdlib.h>
#include <stdio.h>
#include <ViennaRNA/fold_compound.h>
#include <ViennaRNA/utils/basic.h>
#include <ViennaRNA/utils/strings.h>
#include <ViennaRNA/subopt.h>
void
subopt_callback(const char *structure,
               float      energy,
               void      *data)
{
    /* simply print the result and increase the counter variable by 1 */
    if (structure)
        printf("%d.\t%s\t%6.2f\n", ((int *)data)++, structure, energy);
}

```

```

}
int
main()
{
    /* initialize random number generator */
    vrna_init_rand();
    /* Generate a random sequence of 50 nucleotides */
    char *seq = vrna_random_string(50, "ACGU");
    /* Create a fold compound for the sequence */
    vrna_fold_compound_t *fc = vrna_fold_compound(seq, NULL, VRNA_OPTION_DEFAULT);
    int counter = 0;
    /*
     * call subopt to enumerate all secondary structures in an energy band of
     * 5 kcal/mol of the MFE and pass it the address of the callback and counter
     * variable
     */
    vrna_subopt_cb(fc, 500, &subopt_callback, (void *)&counter);
    /* cleanup memory */
    free(seq);
    vrna_fold_compound_free(fc);
    return 0;
}

```

See also

examples/callback\_subopt.c in the source code tarball

## 8.1.4 Application of Soft Constraints

### soft\_constraints\_up.c

In this example, a random RNA sequence is generated to predict its MFE under the constraint that a particular nucleotide receives an additional bonus energy if it remains unpaired.

```

#include <stdlib.h>
#include <stdio.h>
#include <ViennaRNA/fold_compound.h>
#include <ViennaRNA/utils/basic.h>
#include <ViennaRNA/utils/strings.h>
#include <ViennaRNA/constraints/soft.h>
#include <ViennaRNA/mfe.h>
int
main()
{
    /* initialize random number generator */
    vrna_init_rand();
    /* Generate a random sequence of 50 nucleotides */
    char *seq = vrna_random_string(50, "ACGU");
    /* Create a fold compound for the sequence */
    vrna_fold_compound_t *fc = vrna_fold_compound(seq, NULL, VRNA_OPTION_DEFAULT);
    /* Add soft constraint of -1.7 kcal/mol to nucleotide 5 whenever it appears in an unpaired context */
    vrna_sc_add_up(fc, 5, -1.7, VRNA_OPTION_DEFAULT);
    /* allocate memory for MFE structure (length + 1) */
    char *structure = (char *)vrna_alloc(sizeof(char) * 51);
    /* predict Minimum Free Energy and corresponding secondary structure */
    float mfe = vrna_mfe(fc, structure);
    /* print sequence, structure and MFE */
    printf("%s\n%s [ %.2f ]\n", seq, structure, mfe);
    /* cleanup memory */
    free(seq);
    free(structure);
    vrna_fold_compound_free(fc);
    return 0;
}

```

See also

examples/soft\_constraints\_up.c in the source code tarball

## 8.1.5 Other Examples

### example1.c

A more extensive example including MFE, Partition Function, and Centroid structure prediction.

```

#include <stdio.h>
#include <stdlib.h>
#include <string.h>
#include <ViennaRNA/data_structures.h>
#include <ViennaRNA/params/basic.h>
#include <ViennaRNA/utils/basic.h>
#include <ViennaRNA/eval.h>
#include <ViennaRNA/fold.h>

```

```

#include <ViennaRNA/part_func.h>
int
main(int argc,
      char *argv[])
{
    char          *seq =
        "AGACGACAAGGUUGAAUCGCACCCACAGUCUAUGAGUCGGUGACAACAUAUACGAAAGGCUGUAAAAUCAUUUAUACACACAGGGGGCCCCCGUGUCUAG";
    char          *mfe_structure = vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    char          *prob_string   = vrna_alloc(sizeof(char) * (strlen(seq) + 1));
    /* get a vrna_fold_compound with default settings */
    vrna_fold_compound_t *vc = vrna_fold_compound(seq, NULL, VRNA_OPTION_DEFAULT);
    /* call MFE function */
    double         mfe = (double)vrna_mfe(vc, mfe_structure);
    printf("%s\n%s (%6.2f)\n", seq, mfe_structure, mfe);
    /* rescale parameters for Boltzmann factors */
    vrna_exp_params_rescale(vc, &mfe);
    /* call PF function */
    FLT_OR_DBL en = vrna_pf(vc, prob_string);
    /* print probability string and free energy of ensemble */
    printf("%s (%6.2f)\n", prob_string, en);
    /* compute centroid structure */
    double dist;
    char      *cent = vrna_centroid(vc, &dist);
    /* print centroid structure, its free energy and mean distance to the ensemble */
    printf("%s (%6.2f d=%6.2f)\n", cent, vrna_eval_structure(vc, cent), dist);
    /* free centroid structure */
    free(cent);
    /* free pseudo dot-bracket probability string */
    free(prob_string);
    /* free mfe structure */
    free(mfe_structure);
    /* free memory occupied by vrna_fold_compound */
    vrna_fold_compound_free(vc);
    return EXIT_SUCCESS;
}

```

See also

examples/example1.c in the source code tarball

### 8.1.6 Deprecated Examples

```

#include <stdio.h>
#include <stdlib.h>
#include <math.h>
#include <string.h>
#include "utils.h"
#include "fold_vars.h"
#include "fold.h"
#include "part_func.h"
#include "inverse.h"
#include "RNAstruct.h"
#include "treedist.h"
#include "stringdist.h"
#include "profiledist.h"
void
main()
{
    char          *seq1 = "CGCAGGGAUACCGCG", *seq2 = "GCGCCCAUAGGGACGC",
        *struct1, *struct2, *xstruc;
    float         e1, e2, tree_dist, string_dist, profile_dist, kT;
    Tree          *T1, *T2;
    swString      *S1, *S2;
    float         *pf1, *pf2;
    FLT_OR_DBL    *bppm;
    /* fold at 30C instead of the default 37C */
    temperature = 30.; /* must be set *before* initializing */
    /* allocate memory for structure and fold */
    struct1 = (char *)space(sizeof(char) * (strlen(seq1) + 1));
    e1 = fold(seq1, struct1);
    struct2 = (char *)space(sizeof(char) * (strlen(seq2) + 1));
    e2 = fold(seq2, struct2);
    free_arrays(); /* free arrays used in fold() */
    /* produce tree and string representations for comparison */
    xstruc = expand_Full(struct1);
    T1 = make_tree(xstruc);
    S1 = Make_swString(xstruc);
    free(xstruc);
    xstruc = expand_Full(struct2);
    T2 = make_tree(xstruc);
    S2 = Make_swString(xstruc);
    free(xstruc);
    /* calculate tree edit distance and aligned structures with gaps */
    edit_backtrack = 1;
    tree_dist = tree_edit_distance(T1, T2);
}

```

```

free_tree(T1);
free_tree(T2);
unexpand_aligned_F(aligned_line);
printf("%s\n%s  %3.2f\n", aligned_line[0], aligned_line[1], tree_dist);
/* same thing using string edit (alignment) distance */
string_dist = string_edit_distance(S1, S2);
free(S1);
free(S2);
printf("%s  mfe=%5.2f\n%s  mfe=%5.2f  dist=%3.2f\n",
       aligned_line[0], e1, aligned_line[1], e2, string_dist);
/* for longer sequences one should also set a scaling factor for
 * partition function folding, e.g: */
kT      = (temperature + 273.15) * 1.98717 / 1000.; /* kT in kcal/mol */
pf_scale = exp(-e1 / kT / strlen(seq1));
/* calculate partition function and base pair probabilities */
e1 = pf_fold(seq1, struct1);
/* get the base pair probability matrix for the previous run of pf_fold() */
bppm = export_bppm();
pf1 = Make_bp_profile_bppm(bppm, strlen(seq1));
e2 = pf_fold(seq2, struct2);
/* get the base pair probability matrix for the previous run of pf_fold() */
bppm = export_bppm();
pf2 = Make_bp_profile_bppm(bppm, strlen(seq2));
free_pf_arrays(); /* free space allocated for pf_fold() */
profile_dist = profile_edit_distance(pf1, pf2);
printf("%s  free energy=%5.2f\n%s  free energy=%5.2f  dist=%3.2f\n",
       aligned_line[0], e1, aligned_line[1], e2, profile_dist);
free_profile(pf1);
free_profile(pf2);
}

```

See also

examples/example\_old.c in the source code tarball

## 8.2 Perl5 Examples

### Hello World Examples

#### Using the flat interface

- MFE prediction
 

```

use RNA;
# The RNA sequence
my $seq = "GAGUAGUGGAACCGGCUAUGUUUGACUCGCAGACUAACA";
# compute minimum free energy (MFE) and corresponding structure
my ($ss, $mfe) = RNA::fold($seq);
# print output
printf "%s\n%s [ %6.2f ]\n", $seq, $ss, $mfe;

```
- comparative MFE prediction for sequence alignments
 

```

use RNA;
# The RNA sequence alignment
my @sequences = (
    "CUGCCUCACACGUAUUGGCCUCAGUUACCGUAGAUGUAGUGAGGGU",
    "CUGCCUCACACAUUUGGCCUCAGUUACUACAUAGAUGUAGUGAGGGU",
    "---CUCGACACACU---GCCUCGGUACCAUCGGUGCAGUGCGGGU"
);
# compute the consensus sequence
my $cons = RNA::consensus(\@sequences);
# predict Minimum Free Energy and corresponding secondary structure
my ($ss, $mfe) = RNA::alifold(\@sequences);
# print output
printf "%s\n%s [ %6.2f ]\n", $cons, $ss, $mfe;

```

#### Using the object oriented interface

- MFE prediction
 

```

#!/usr/bin/perl
use warnings;
use strict;
use RNA;
my $seq1 = "CGCAGGGAUACCGCG";
# create new fold_compound object
my $fc = new RNA::fold_compound($seq1);
# compute minimum free energy (mfe) and corresponding structure
my ($ss, $mfe) = $fc->mfe();
# print output
printf "%s [ %6.2f ]\n", $ss, $mfe;

```

## Changing the Model Settings

### Using the object oriented interface

- MFE prediction at different temperature and dangle model
- ```
use RNA;
# The RNA sequence
my $seq = "GAGUAGUGGAACCGGCUAUGUUUGUGACUCGACAGACUAACA";
# create a new model details structure
my $md = new RNA::md();
# change temperature and dangle model
$md->{temperature} = 20.0; # 20 Deg Celcius
$md->{dangles} = 1; # Dangle Model 1
# create a fold compound
my $fc = new RNA::fold_compound($seq, $md);
# predict Minmum Free Energy and corresponding secondary structure
my ($ss, $mfe) = $fc->mfe();
# print sequence, structure and MFE
printf "%s\n%s [ %6.2f ]\n", $seq, $ss, $mfe;
```

## 8.3 Python Examples

### MFE Prediction (flat interface)

```
import RNA
# The RNA sequence
seq = "GAGUAGUGGAACCGGCUAUGUUUGUGACUCGACAGACUAACA"
# compute minimum free energy (MFE) and corresponding structure
(ss, mfe) = RNA.fold(seq)
# print output
print("{}\n{} [ {:.2f} ]".format(seq, ss, mfe))
```

### MFE Prediction (object oriented interface)

```
import RNA;
sequence = "CGCAGGGAUACCCGCG"
# create new fold_compound object
fc = RNA.fold_compound(sequence)
# compute minimum free energy (mfe) and corresponding structure
(ss, mfe) = fc.mfe()
# print output
print("{} [ {:.2f} ]".format(ss, mfe))
```

### Suboptimal Structure Prediction

```
import RNA
sequence = "GGGGAAAACCCC"
# Set global switch for unique ML decomposition
RNA.cvar.uniq_ML = 1
subopt_data = { 'counter' : 1, 'sequence' : sequence }
# Print a subopt result as FASTA record
def print_subopt_result(structure, energy, data):
    if not structure == None:
        print(">subopt {}:d".format(data['counter']))
        print("{}\n{} [ {:.2f} ]".format(data['sequence'], structure, energy))
        # increase structure counter
        data['counter'] = data['counter'] + 1
# Create a 'fold_compound' for our sequence
a = RNA.fold_compound(sequence)
# Enumerate all structures 500 docal/mol = 5 kcal/mol around
# the MFE and print each structure using the function above
a.subopt_cb(500, print_subopt_result, subopt_data);
```

### Boltzmann Sampling (a.k.a. Probabilistic Backtracing)

```
import RNA
sequence =
    "UGGGAAUAGUCUCUCCGAGUCUCGCGGGCGACGGGCGAUCUUCGAAAGUGGAAUCCGUACUUAUACCGCCUGUGCGGACUACUAUCCUGACCACAUAGU"
def store_structure(s, data):
    """
    A simple callback function that stores
    a structure sample into a list
    """
    if s:
        data.append(s)
"""
First we prepare a fold_compound object
"""
```

```

# create model details
md = RNA.md()
# activate unique multibranch loop decomposition
md.uniq_ML = 1
# create fold compound object
fc = RNA.fold_compound(sequence, md)
# compute MFE
(ss, mfe) = fc.mfe()
# rescale Boltzmann factors according to MFE
fc.exp_params_rescale(mfe)
# compute partition function to fill DP matrices
fc.pf()
"""
Now we are ready to perform Boltzmann sampling
"""
# 1. backtrack a single sub-structure of length 10
print("{}".format(fc.pbacktrack5(10)))
# 2. backtrack a single sub-structure of length 50
print("{}".format(fc.pbacktrack5(50)))
# 3. backtrack multiple sub-structures of length 10 at once
for s in fc.pbacktrack5(20, 10):
    print("{}".format(s))
# 4. backtrack multiple sub-structures of length 50 at once
for s in fc.pbacktrack5(100, 50):
    print("{}".format(s))
# 5. backtrack a single structure (full length)
print("{}".format(fc.pbacktrack()))
# 6. backtrack multiple structures at once
for s in fc.pbacktrack(100):
    print("{}".format(s))
# 7. backtrack multiple structures non-redundantly
for s in fc.pbacktrack(100, RNA.PBACKTRACK_NON_REDUNDANT):
    print("{}".format(s))
# 8. backtrack multiple structures non-redundantly (with resume option)
num_samples = 500
iterations = 15
d = None # pbacktrack memory object
s_list = []
for i in range(0, iterations):
    d, ss = fc.pbacktrack(num_samples, d, RNA.PBACKTRACK_NON_REDUNDANT)
    s_list = s_list + list(ss)
for s in s_list:
    print("{}".format(s))
# 9. backtrack multiple sub-structures of length 50 in callback mode
ss = []
i = fc.pbacktrack5(100, 50, store_structure, ss)
for s in ss:
    print("{}".format(s))
# 10. backtrack multiple full-length structures in callback mode
ss = list()
i = fc.pbacktrack(100, store_structure, ss)
for s in ss:
    print("{}".format(s))
# 11. non-redundantly backtrack multiple full-length structures in callback mode
ss = list()
i = fc.pbacktrack(100, store_structure, ss, RNA.PBACKTRACK_NON_REDUNDANT)
for s in ss:
    print("{}".format(s))
# 12. non-redundantly backtrack multiple full length structures
# in callback mode with resume option
ss = []
d = None # pbacktrack memory object
for i in range(0, iterations):
    d, i = fc.pbacktrack(num_samples, store_structure, ss, d, RNA.PBACKTRACK_NON_REDUNDANT)
for s in ss:
    print("{}".format(s))
# 13. backtrack a single substructure from the sequence interval [10:50]
print("{}".format(fc.pbacktrack_sub(10, 50)))
# 14. backtrack multiple substructures from the sequence interval [10:50]
for s in fc.pbacktrack_sub(100, 10, 50):
    print("{}".format(s))
# 15. backtrack multiple substructures from the sequence interval [10:50] non-redundantly
for s in fc.pbacktrack_sub(100, 10, 50, RNA.PBACKTRACK_NON_REDUNDANT):
    print("{}".format(s))

```

## RNAfold -p –MEA equivalent

```

#!/usr/bin/python
#
import RNA
seq = "AUUUCACUAGAGAAGGUCUAGAGUGUUUGUCGUAAGUCCUAUUCAGGUACGAACACGGUGGAUAUGUUCGACGACAGGAUCGGCGCACUA"
# create fold_compound data structure (required for all subsequently applied algorithms)
fc = RNA.fold_compound(seq)
# compute MFE and MFE structure
(mfe_struct, mfe) = fc.mfe()
# rescale Boltzmann factors for partition function computation

```

```

fc.exp_params_rescale(mfe)
# compute partition function
(pp, pf) = fc.pf()
# compute centroid structure
(centroid_struct, dist) = fc.centroid()
# compute free energy of centroid structure
centroid_en = fc.eval_structure(centroid_struct)
# compute MEA structure
(MEA_struct, MEA) = fc.MEA()
# compute free energy of MEA structure
MEA_en = fc.eval_structure(MEA_struct)
# print everything like RNAfold -p --MEA
print("{}\n{} ({}:6.2f)".format(seq, mfe_struct, mfe))
print("{} [{}:6.2f]".format(pp, pf))
print("{} [{}:6.2f] d={}:.2f)".format(centroid_struct, centroid_en, dist))
print("{} [{}:6.2f] MEA={}:.2f)".format(MEA_struct, MEA_en, MEA))
print(" frequency of mfe structure in ensemble {}:g; ensemble diversity
      {}:6.2f)".format(fc.pr_structure(mfe_struct), fc.mean_bp_distance()))

```

## Fun with Soft Constraints

```

import RNA
seq1 = "CUCGUCGCCUUAUCCAGUGCGGGCGCUAGACAUCUAGUUAUCGCCGCAA"
# Turn-off dangles globally
RNA.cvar.dangles = 0
# Data structure that will be passed to our MaximumMatching() callback with two components:
# 1. a 'dummy' fold_compound to evaluate loop energies w/o constraints, 2. a fresh set of energy parameters
mm_data = { 'dummy': RNA.fold_compound(seq1), 'params': RNA.param() }
# Nearest Neighbor Parameter reversal functions
revert_NN = {
    RNA.DECOMP_PAIR_HP:      lambda i, j, k, l, f, p: - f.eval_hp_loop(i, j) - 100,
    RNA.DECOMP_PAIR_IL:      lambda i, j, k, l, f, p: - f.eval_int_loop(i, j, k, l) - 100,
    RNA.DECOMP_PAIR_ML:      lambda i, j, k, l, f, p: - p.MLclosing - p.MLintern[0] - (j - i - k + l - 2) *
        p.MLbase - 100,
    RNA.DECOMP_ML_ML_STEM:   lambda i, j, k, l, f, p: - p.MLintern[0] - (l - k - 1) * p.MLbase,
    RNA.DECOMP_ML_STEM:      lambda i, j, k, l, f, p: - p.MLintern[0] - (j - i - k + l) * p.MLbase,
    RNA.DECOMP_ML_ML:        lambda i, j, k, l, f, p: - (j - i - k + l) * p.MLbase,
    RNA.DECOMP_ML_ML_ML:     lambda i, j, k, l, f, p: 0,
    RNA.DECOMP_ML_UP:        lambda i, j, k, l, f, p: - (j - i + l) * p.MLbase,
    RNA.DECOMP_EXT_STEM:     lambda i, j, k, l, f, p: - f.eval_ext_stem(k, l),
    RNA.DECOMP_EXT_EXT:      lambda i, j, k, l, f, p: 0,
    RNA.DECOMP_EXT_STEM_EXT: lambda i, j, k, l, f, p: - f.eval_ext_stem(i, k),
    RNA.DECOMP_EXT_EXT_STEM: lambda i, j, k, l, f, p: - f.eval_ext_stem(l, j),
}
# Maximum Matching callback function (will be called by RNAlib in each decomposition step)
def MaximumMatching(i, j, k, l, d, data):
    return revert_NN[d](i, j, k, l, data['dummy'], data['params'])
# Create a 'fold_compound' for our sequence
fc = RNA.fold_compound(seq1)
# Add maximum matching soft-constraints
fc.sc_add_f(MaximumMatching)
fc.sc_add_data(mm_data, None)
# Call MFE algorithm
(s, mm) = fc.mfe()
# print result
print("{}\n{} (MM: {}:d)".format(seq1, s, int(-mm)))

```





## Chapter 9

# Contributing to the ViennaRNA Package

### Contents

- General Remarks
- Reporting Bugs
- Pull Request Process
- Contributors License Agreement (CLA)

### General Remarks

The ViennaRNA Package is developed by humans and consequently may contain bugs that prevent proper operation of the implemented algorithms. If you think you have found any of those nasty animals, please help us to improve our software by reporting the bug to us.

The ViennaRNA Package also is open-source software, which means that everybody can have a closer look into our implementations to understand and potentially extend its functionality. If you implemented any novel feature into the ViennaRNA Package that might be of interest to a larger community, please don't hesitate to ask for merging of your code into our official source tree. See the Pull Request Process section below to find information on how to do that.

Please note that we have a code of conduct. Please follow it in all your interactions with this project.

If you wish to contribute to this project, please first discuss any proposed changes with the owners and main developers. You may do that either through making an issue at [our official GitHub presence](#), [by email](#), or any other personal communication with the core developer team.

More importantly, if you wish to contribute any files or software, you need to agree to our ViennaRNA Package Contributors License Agreement (CLA)! Otherwise, your contributions can't be merged into our source tree. See below for further information and the full CLA details.

### Reporting Bugs

1. Please make an issue at GitHub or notify us by emailing to [rna@tbi.univie.ac.at](mailto:rna@tbi.univie.ac.at)
2. In your report, include as much information as possible, such that we are able to reproduce it. If possible, find a minimal example that triggers the bug.
3. Include the version number for the ViennaRNA Package you experience the bug with.
4. Include at least some minimal information regarding your operating system (Linux, Mac OS X, Windows, etc.)

### Pull Request Process

1. Ensure that you have not checked-in any files that are automatically build!

2. When contributing C source code, follow our code formatting guide lines. You may use the tool `uncrustify` together with our config located in `misc/uncrustify.cfg` to accomplish that.
3. Only expose symbols (functions, variables, etc.) to the libraries interface that are absolutely necessary! Hide all other symbols in the corresponding object file(s) by declaring them as `static`.
4. Use the prefixes `vrna_` for any symbol you add to the API of our library! Preprocessor macros in header files require the prefix in capital letters, i.e. `VRNA_`.
5. Use C-style comments at any place necessary to make sure your implementation can still be understood and followed in the future.
6. Add test cases for any new implementation! The test suite is located in the `tests` directory and is split into tests for the C-library, executable programs, and the individual scripting language interfaces.
7. Run `make check` to ensure that all other test suites still run properly with your applied changes!
8. When contributing via GitHub, make a personal fork of our project and create a separate branch for your changes. Then make a pull request to our `user-contrib` branch. Pull requests to the `master` branch will be rejected to keep its history clean.
9. Pull requests that have been successfully merged into the `user-contrib` branch usually find their way into the next release of the ViennaRNA Package. However, please note that the core developers may decide to include your changes in a later version.

## Contributors License Agreement

Thank you for your interest in contributing to the ViennaRNA Package ("We" or "Us").

Before contributing, please note that we adopted a standard Contributors License Agreement (CLA) agreement provided by [Project Harmony](#), a community-centered group focused on contributor agreements for free and open source software (FOSS).

This contributor agreement ("Agreement") documents the rights granted by contributors to Us. To make this document effective, please sign it and send it to Us by email to [rna@tbi.univie.ac.at](mailto:rna@tbi.univie.ac.at).

The respective CLA PDF documents are available in the [doc/CLA directory](#) of the distribution tarball, and online at our [official ViennaRNA Website](#).

# Chapter 10

## Changelog

Below, you'll find a list of notable changes for each version of the ViennaRNA Package.

### Unreleased

### Version 2.5.x

#### Version 2.5.1 (Release date: 2022-06-02)

##### Programs

- Refactor `ct2db` program to allow for pseudoknots in output structure

##### Library

- API: Fix MEA computation for G-quadruplex predictions
- API: Fix memory leak in hard constraints container
- API: Fix RNApuzzler edge-case that resulted in segmentation faults
- API: Fix invalid memory access in `vrna_strjoin()`
- API: Revisit generic soft constraints for sliding-window base pair probability computations
- API: Enable to overwrite automatic unpaired probability determination in MEA computation
- API: Add `#VRNA_PLIST_TYPE_UNPAIRED` and `#VRNA_PLIST_TYPE_TRIPLE` identifiers for `vrna_ep_t`
- API: Add `vrna_init_rand_seed()` to initialize RNG with seed
- API: Add `vrna_zsc_compute_raw()` to obtain mean and sd for Z-score computation
- API: Add `vrna_file_connect_read_record()` function to parse connectivity table (\*.ct) files
- API: Add `vrna_strtrim()` function
- API: Update sanity checks for input in `vrna_pbacktrack_sub*()`
- API: Allow for pseudo-knots in `vrna_db_from_ptable()`
- API: Do not use `min_loop_size = 0` for multi strand interaction prediction
- API: Remove unnecessary uses of `min_loop_size` at multiple locations
- API: Deprecate cutpoint member of `vrna_fold_compound_t` and prepare for 5'/3' encoding
- API: Refactor sequence addition/preparation for `vrna_fold_compound_t`
- DOC: Update documentation

- SWIG: Add simple dot-plot file wrapper `plot_dp_EPS()`
- SWIG: Add `sequence`, `sequence_encoding` and `sequence_encoding2` attributes to `fold_compound` objects
- SWIG: Fix RNG wrapping and initialize RNG upon module load and update associated functions
- SWIG: Add more access to member variable arrays for various objects used throughout the library
- SWIG: Add memory efficient wrapper for dynamically allocated arrays and matrices
- SWIG: Shadow pair table data structure for efficient interactions between C and target languages
- SWIG: Expose hard constraints members in `fold_compound` objects
- SWIG: Add `exp_E_ext_stem()` method (`vrna_exp_E_ext_stem()`) to `fold_compound` objects
- SWIG: Expose DP matrices within `fold_compound` objects
- SWIG: Fix memory leak in wrapper for `vrna_db_from_ptable()`

### Package

- Update dlib to version 19.23
- DOC: Update doxygen.conf for version 1.9.2
- AUTOCONF: Factor-out Naview layout algorithm to allow for deactivating the Naview layout algorithm at configure-time
- AUTOCONF: Make LaTeX checks more portable and update LaTeX package checks
- AUTOCONF: Check whether we can build the swig interface when SVM support is deactivated
- AUTOCONF: Fix condition check for CLA build

## Version 2.5.0 (Release date: 2021-11-08)

### Programs

- Add `RNAmultifold` program to compute secondary structures for multiple interacting RNAs
- Add multistrand capabilities to `RNAeval`
- Add multistrand capabilities to `RNAsubopt`
- Replace `RNAcofold` with a wrapper to `RNAmultifold`
- Fix computation of BB homodimer base pair probabilities in `RNAcofold`

### Library

- API: Fix use of undefined values in deprecated function `PS_dot_plot()`
- API: Fix probability computations for unstructured domains within multibranch loops
- API: Fix index error in ensemble defect computations
- API: Fix hard constraints behavior on non-specific base pairing
- API: Fix segmentation fault for short input sequences in `vrna_hx_from_ptable()`
- API: Fix memory leak in static `rna_layout()` function
- API: Fix corner-case in covariance score computation on sequence alignments that determines which alignment columns may pair and which don't
- API: Add MFE computations for multiple interacting strands

- API: Add partition function computations for multiple interacting strands
- API: Add base pair probability computations for multiple interacting strands
- API: Add suboptimal structure prediction for multiple interacting strands
- API: Add multistrand capabilities to `vrna_eval*()` functions
- API: Add new function `vrna_equilibrium_conc()` for concentration dependency computations of multiple interacting strands with `dlib` backend
- API: Add `vrna_equilibrium_constants()` function to obtain equilibrium constants for different complexes of multiple interacting strands
- API: Add function `vrna_pf_add()` to add ensemble free energies of two ensembles
- API: Add function `vrna_pf_substrands()` to get ensemble free energies for complexes up to a specific number of interacting strands
- API: Add function `vrna_n_multichoose_k()` to obtain a list of k-combinations with repetition
- API: Add `vrna_cstr_discard()` function to allow for discarding char streams prior to flushing
- API: Add `vrna_bp_distance_pt()` function to allow for base pair distance computation with pseudoknots
- API: Add functions `vrna_pbacktrack_sub*()` to allow for stochastic backtracking within arbitrary sequence intervals
- API: Add functions `vrna_boustrophedon()` and `vrna_boustrophedon_pos()` to generate lists of or obtain values from sequences of Boustrophedon distributed integer numbers
- API: Add `vrna_pscore()` and `vrna_pscore_freq()` functions to obtain covariance score for particular alignment columns
- API: Rewrite Zuker suboptimals implementation
- API: Remove old cofold implementations
- API: Make `type` attribute of `vrna_mx_mfe_t` and `vrna_mx_pf_t` a constant
- API: Guard more functions in `utils/structure_utils.c` against `NULL` input
- API: Rename `vrna_E_ext_loop()` to `vrna_eval_ext_stem()`
- API: Use v3 typedefs in dot-plot function declarations
- SWIG: Fix Python 3 file handle as optional argument in `eval*` functions and methods
- SWIG: Add wrapper for `vrna_pf_add()`
- SWIG: Add wrapper for `vrna_hx_from_ptable()`
- SWIG: Add wrapper for `vrna_db_from_probs()`

## Package

- Update `libsvm` to version 3.25
- Make Python 3.x the default Python for the scripting language interfaces
- Add Python3 capability for Mac OS X installer builds
- TESTS: Create TAP driver output for all unit tests (library, executables, SWIG interfaces)
- Remove compile-time switch to deactivate Boustrophedon backtracking scheme (this is the status-quo now)
- Add Contributors License Agreement (CLA) to the Package in `doc/CLA/`

## Version 2.4.x

### Version 2.4.18 (Release date: 2021-04-22)

#### Programs

- Fix and refactor `RNApkplex` program
- Fix occasional backtracing errors in `RNALalifold`
- Restrict available dangling end models in `RNALalifold` to 0 and 2
- Prevent segmentation faults upon bogus input data in `RNAfold`, `RNAalifold`, `RNAcofold`, `RNAheat`, and `RNAeval`
- Free MFE DP matrices in `RNAsubopt` Boltzmann sampling when not required anymore

#### Library

- API: Add `vrna_abstract_shapes()` and `vrna_abstract_shapes_pt()` functions to convert secondary structures into their respective abstract shape notation ala Giegerich et al. 2004
- API: Add functions `vrna_seq_reverse()` and `vrna_DNA_complement()` to create reverse complements of a sequence
- API: Add more soft constraint handling to comparative structure prediction
- API: Add generic soft constraints for sliding window comparative MFE backtracing
- API: Add `vrna_ensemble_defect_pt()` that accepts pair table input instead of dot-bracket string to allow for non-nested reference structures
- API: Add failure/success return values to generic soft constraints application functions
- API: Refactor `RNApkplex` implementation by better using constraints framework and moving out many parts from `RNApkplex.c` into `RNAlib` as separate re-usable functions
- API: Fix energy contributions used in `RNApkplex` implementations
- API: Fix energy evaluation for cofolding with dangle model 1
- API: Fix wrong arithmetic usage for PF variant of combined generic and simple soft constraints applied to external loops
- API: Fix memory size in `vrna_fold_compound_t` initialization
- API: Fix bogus memory access for comparative prediction when preparing hard constraints
- API: Fix wrong index usage in hard constraints for comparative base pair probability computations of internal loops
- API: Fix G-Quadruplex contributions as part of multibranch loops in single sequence base pair probability computations
- API: Fix multibranch loop MFE decomposition step for multiple strand cases
- API: Fix external loop generic hard constraint index updating for partition function computations
- API: Fix memory allocation for auxiliary grammar data structure
- API: Fix incorporation of auxiliary grammar contrib for closing pairs in sliding-window MFE computation
- API: Fix DP matrix initialization in sliding window MFE computations (fixes occasional backtracing issues in comparative sliding-window MFE computations)
- API: Make `vrna_sc_t.type` attribute a constant
- API: Remove upper-triangular hard constraint matrix in favor of full matrix

- API: Always ensure sane base pair span settings after `vrna_fold_compound_prepare()`
- API: Return INF on predictions of `vrna_mfe_dimer()` that fail due to unsatisfiable constraints
- API: Rename internally used hard and soft constraints API symbols
- API: Fix header file inclusions to prevent `#include` cycles
- SWIG: Add wrapper for `vrna_file_fasta_read_record()`
- SWIG: Fix memory leak in wrapper for `vrna_probs_window()`
- SWIG: Refactor and therefore fix soft constraint binding functions for use in comparative structure predictions
- SWIG: Fix typo that prevented properly wrapping `vrna_params_load_RNA_Andronesescu2007()`
- SWIG: Unify wrappers for `vrna_ptable()` and `vrna_ptable_from_string()`

## Package

- REFMAN: Refactored structure annotation documentation
- REFMAN: Update Mac OS X install section
- Replace DEF placeholders in energy parameter files with their value of -50
- Update `RNAlocmin` subpackage to properly compile with more stringent C++ compilers
- Update `RNAforester` subpackage to properly compile with more stringent C++ compilers
- Update autotools framework, e.g. checks for pthreads
- Update universal binary build instructions for Mac OS X builds to enable ARM compilation for M1 CPUs

## Version 2.4.17 (Release date: 2020-11-25)

## Programs

- Fix `RNAup -b` mode with shorter sequence first
- Add `--backtrack-global` option to `RNAfold` (currently only available for `dangles == 2 | 0`)
- Add `--zscore-pre-filter` and `--zscore-report-subsumed` options to `RNAfold`

## Library

- API: Fix multiloop backtracing with soft constraints for unpaired positions in `vrna_subopt()` and `vrna_subopt_cb()`
- API: Fix parameter parse in `vrna_params_load_from_string()`
- API: Add `vrna_heat_capacity()` and `vrna_head_capacity_cb()` functions to `RNAlib`
- API: Add backtracing function `vrna_backtrack_window()` for global MFE structure to sliding-window predictions
- API: Add SVG support for `RNApuzzler` structure layouts
- API: Make `vrna_md_t` argument to `vrna_fold_compound()` a constant pointer
- API: Remove missing symbols from header file `ViennaRNA/params/default.h`
- API: Refactor z-score threshold filter handling for sliding-window MFE prediction
- SWIG: Fix typo in interface functions to load DNA parameters
- SWIG: Add python-3.9 autoconf checks

- SWIG: Add `vrna_head_capacity*()` wrappers
- SWIG: Add access to raw energy parameters
- SWIG: Add `alias` and `pair` attribute to objects of type `md`
- SWIG: Add out/varout typemaps for 2-dimensional int-like arrays
- SWIG: Add all data fields to objects of type 'param' and 'exp\_param'

### Package

- Fix Debian and Windows installer files

## Version 2.4.16 (Release date: 2020-10-09)

### Programs

- Fix backtracing errors in `RNAalifold` for alignments with more than 32768 columns
- Fix backtracing errors in `RNAalifold` and `RNAalifold` for rare cases when two alignment columns may pair due to covariance score threshold but still yield infinite energies due to energy model
- Refactored manpages/help options for `RNAplfold`, `RNAplot`, `RNApvmmin`, `RNAsubopt`, and `RNAup`

### Library

- API: Fix undefined behavior due to short int overflows when accessing alignment lengths with alignments larger than 32768 columns. This fixes occasional backtracing errors in `RNAalifold` and `vrna_mfe_window()`
- API: Fix adding pscore to base pairs that yield INF energy in comparative global and local MFE prediction
- API: Add `vrna_convert_kcal_to_dcal()` and vice-versa function for safely converting integer to float representations of energy values
- SWIG: Add a reasonable Python interface for objects of type `vrna_path_t`
- SWIG: Add a wrapper for `vrna_seq_encode()`

### Package

- Move `units.h` include file to `ViennaRNA/utils/units.h`

## Version 2.4.15 (Release date: 2020-08-18)

### Programs

- Fix compilation of `Kinfold` with GCC 10
- Add `--en-only` flag to `RNAsubopt` to allow for sorting by energy only
- Prevent `RNAcofold` to process input with more than two strands
- Add cutpoint marker to dot-plots created with `RNAcofold -a`
- Update `Kinfold` to version 1.4



## Library

- API: Fix removal of strand delimiter in `vrna_plot_dp_PS_list()`
- API: Fix `vrna_enumerate_necklaces()`
- API: Fix bogus backtracing for co-folded structures in `vrna_subopt()` and `vrna_subopt_cb()`
- API: Fix storing co-folded structures for sorted output in `vrna_subopt()`
- API: Fix multibranch loop component hard constraints for multi-strand cases
- API: Prevent adding internal loop energy contributions to enclosed parts with `energy=INF`
- API: Adapt `vrna_db_pack()` / `vrna_db_unpack()` functions to produce comparable strings
- API: Add sorting modes `VRNA_UNSORTED`, `VRNA_SORT_BY_ENERGY_LEXICOGRAPHIC_ASC`, and `VRNA_SORT_BY_ENERGY_ASC` to `vrna_subopt()`
- API: Add `vrna_strjoin()` function
- API: Add missing case to external loop hard constraints
- API: Make hard constraints strand-aware
- SWIG: Fix invalid memory access when using `MEA_from_plist()` in Perl 5 or Python
- SWIG: Enable keyword argument features in Python interface of constructors for `fold_compound`, `md`, `move`, `param`, and `exp_param` objects
- SWIG: Enable autodoc feature for Python interface of constructors for `fold_compound`, `md`, and `move` objects
- SWIG: Enable `toString` conversion for Python interface for objects of type `fold_compound`, `md`, `move`, `params`, `exp_params`, and `subopt_solution`
- SWIG: Add (read-only) attributes `type`, `length`, `strands`, `params`, and `exp_params` to objects of type `fold_compound`
- SWIG: Make attributes of objects of type `param` and `exp_param` read-only
- Add array of strand nicks to EPS dot plot files instead of single cutpoint
- Draw separator line for each strand nick in EPS dot-plots
- Update `libsvm` to version 3.24

## Package

- Disable Link-Time-Optimization (LTO) for third-party programs linking against `RNAlib` using `pkg-config`
- TESTS: Fix results dir path for out-of-tree builds
- TESTS: Set default timeout for library tests to 20s

## Version 2.4.14 (Release date: 2019-08-13)

## Programs

- Fix `RNApvmin` pertubation vector computation
- Add non-redundant sampling option to `RNApvmin`
- Add `RNA DOS` program to compute density of states
- Add `-P DNA` convenience command line parameter to most programs to quickly load DNA parameters without any input file
- MAN: Add example section to man-page of `RNAalifold`

## Library

- API: Fix memory leak in `vrna_path_gradient()`
- API: Fix release of memory for `vrna_sequence_remove_all()`
- API: Fix soft-constraints application in `vrna_sc_minimize_perturbation()` that prevented proper computation of the perturbation vector
- API: Add 5' and 3' neighbor nucleotide encoding arrays and name string to `vrna_seq_t`
- API: Add new data structure for multiple sequence alignments
- API: Add `vrna_sequence_order_update()` function
- API: Add non-redundant sampling mode to `vrna_sc_minimize_perturbation()` through passing negative sample-sizes
- API: Add v3.0 API functions for maximum expected accuracy (MEA) computation
- API: Include energy parameter sets into RNAlib and provide functions to load them at runtime
- API: Prepare sequence data in `vrna_fold_compound_t` with `vrna_sequence_add()`
- API: Use `vrna_pbacktrack_num()` instead of `vrna_pbacktrack()` in `vrna_sc_minimize_perturbation()` to speed-up sample generation
- Reduce use of global variable `cut_point` in RNAlib
- SWIG: Use `importlib` in favor of `imp` to determine Python 3 tag extension
- SWIG: Update various wrapper functions
- SWIG: Add wrappers for MEA computation with `vrna_MEA()` and `vrna_MEA_from_plist`
- SWIG: Add wrappers for `vrna_pr_structure()` and `vrna_pr_energy()`

## Package

- REFMAN: Fix LaTeX code in `units.h` that prevented proper compilation with `pdflatex`
- Add an R script to create 2D landscape plots from RNA2Dfold output
- Add `gengetopt` to configure-time requirements to build man-pages
- Add new energy parameter file `rna_misc_special_hairpins.par` with additional UV-melting derived parameters for Tri- and Tetra-loops
- Update RNA Tutorial
- Colorize final configure script message
- REFMAN: Always use `pdflatex` to compile reference manual and tutorial
- EXAMPLES: Add Python script that performs computations equivalent to `RNAfold -p --MEA`

## Version 2.4.13 (Release date: 2019-05-30)

## Programs

- Fix centroid structure prediction for `RNAcofold`
- Fix `--noLP` option for `RNAIalifold`

## Library

- API: Refactor and fix collision handling in `vrna_hash_table_t`
- API: Fix one access using wrong index for odd dangles in `loops/external.c`
- API: Add two missing `MLbase` contributions for MFE prediction in `loops/multibranch.c`
- API: Refactor multiloop MFE backtracking for odd dangles
- API: Add function `vrna_backtrack5()` to allow for MFE backtracking of sub-sequences starting at the 5'-end
- API: Reduce usage of global macro `TURN` by replacing it with `min_loop_size` field of `vrna_md_t`
- API: Add functions `vrna_path_direct()` and `vrna_path_direct_ub()` that may also return move lists instead of dot-bracket lists
- API: Add functions `vrna_pt_pk_remove()` and `vrna_db_pk_remove()` that remove pseudoknots from an input structure
- API: Fix invalid memory access for lonely pair mode (`--noLP`) in comparative sliding-window MFE prediction
- SWIG: Fix access to global variable `pf_smooth` and `pf_smooth` attribute in `model_details` object
- SWIG: Fix Python reference counting for `Py_None` in `interfaces/findpath.i` wrapper
- SWIG: Refactor reference counting for all Python2 and Python3 wrappers
- REFMAN: Larger updates and restructuring of reference manual

## Package

- Install example scripts and source code files, e.g. to `$prefix/share/ViennaRNA/examples`
- Properly pass `GSL`, `PTHREADS`, and `MPFR` flags to sub-projects
- Fix `RNApuzzler` header file installation
- SWIG: Include Python 3.7 and 3.8 in list of autoconf-probed python interpreters
- SWIG: Fix wrapper building for `swig >= 4.0.0`

## Version 2.4.12 (Release date: 2019-04-16)

## Programs

- Add non-redundant stochastic backtracing option for `RNAalifold`
- Add `--noDP` option to suppress dot-plot output in `RNAfold` and `RNAalifold`
- Add `RNApuzzler` (4) and `RNAturtle` (3) secondary structure layout algorithm options to `RNAfold` and `RNAplot`
- Update help/man page of `RNAfold`
- Allow for multiple input files and parallel input processing in `RNAheat`

## Library

- API: Fix declaration of `vrna_move_apply_db()`
- API: Fix `vrna_path()` lexicographical ordering in gradient walks
- API: Enable non-redundant stochastic backtracing for comparative structure prediction
- API: Enable stochastic backtracing for circular comparative structure prediction
- API: Enable stochastic backtracing of subsequences (5' prefixes) for comparative structure prediction
- API: Add `pf_smooth` attribute to `vrna_md_t` data structure to allow for disabling Boltzmann factor energy smoothing
- API: Add functions to allow for resuming non-redundant stochastic backtracing
- API: Add functions to retrieve multiple stochastically backtraced structures (list and callback variants)
- API: Add `vrna_positional_entropy` to compute vector of positional entropies
- API: Add `RNApuzzler` and `RNAturtle` secondary structure layout algorithm (Wiegreffe et al. 2018)
- API: Add v3.0 API for secondary structure layout/coordinate algorithms
- API: Add more helper/utility functions for `vrna_move_t` data structures
- API: Add callback-based neighborhood update function for (subsequent) `vrna_move_t` application
- API: Add abstract heap data structure available as `<ViennaRNA/datastructures/heap.h>`
- API: Refactor and speed-up gradient walk implementation available as `vrna_path_gradient()`
- API: Substitute `vrna_file_PS_aln_sub()` alignment plot function by `vrna_file_PS_aln_slice()` that actually slices out a sub-alignment
- API: Rename `vrna_annotate_covar_struct()` to `vrna_annotate_covar_db()` and add new function `vrna_annotate_covar_db_extended()` to support more bracket types
- API: Calling `vrna_params_reset()` now implies a call to `vrna_exp_params_reset()` as well
- API: Move landscape implementations into separate directory, thus headers should be included as `<ViennaRNA/landscape/move.h>`, `<ViennaRNA/landscape/neighbor.h>`, etc.
- Ensure proper rescaling of energy parameters upon temperature changes
- Refactor soft constraints implementation in stochastic backtracing
- SWIG: Wrap all non-redundant stochastic backtracing functions to scripting language interface(s)
- SWIG: Refactor stochastic backtracing interface(s)
- SWIG: Add proper constructor for objects of type `vrna_ep_t`
- SWIG: Sanitize alignment plot function interface(s)

## Package

- Update Ubuntu/Debian and OpenSUSE build instructions
- Reduce intra-package dependency on non-v3.0 API

## Version 2.4.11 (Release date: 2018-12-17)

## Programs

- Add `--commands` option to `RNAsubopt`
- Add non-redundant Boltzmann sampling mode for `RNAsubopt`

## Library

- API: Fix wrong access to base pair soft constraints in equilibrium probability computations
- API: Fix behavior of `vrna_nucleotide_encode()` with lowercase characters in sequence
- API: Fix behavior of `encode_char()` with lowercase characters in sequence
- API: Fix forbidden GU pairs behavior in pscore computation for comparative folding
- API: Fix potential errors due to uninitialized next pointers in `vrna_move_t` of `vrna_eval_move_t` ↔ `shift_pt`
- API: Add AVX 512 optimized version of MFE multibranch loop decomposition
- API: Add functions for CPU SIMD feature detection
- API: Add dispatcher to automatically delegate exterior-/multibranch loop MFE decomposition to supported SIMD optimized implementation
- API: Add function `vrna_dist_mountain()` to compute mountain distance between two structures
- API: Add function `vrna_ensemble_defect()` to compute ensemble defect given a target structure
- API: Add non-redundant Boltzmann sampling
- API: Change behavior of `vrna_cstr_free()` and `vrna_cstr_close()` to always flush output before unregistering the stream
- SWIG: Add interface for `vrna_loopidx_from_ptable()`

## Package

- Activate compilation for compile-time supported SIMD optimized implementations by default
- Replace `--enable-sse` configure script option with `--disable-simd`

## Version 2.4.10 (Release date: 2018-09-26)

## Programs

- Fix wrong output filename for binary opening energies in `RNAplfold`
- Enable G-Quadruplex support for partition function computation in `RNAalifold`

## Library

- Fix broken SSE4.1 support for multibranch loop MFE computation that resulted in increased run times
- Fix redundant output issue in subopt backtracking with unusually high delta energies ( $\geq \text{INF}$ )
- Restore default behavior of '|' symbol in dot-bracket hard constraint strings that got lost with version 2.2.0
- Add faster (cache-optimized) version of Nussinov Maximum Matching algorithm
- Change default linker- and loop length computations for G-Quadruplex predictions in comparative prediction modes
- Add hard constraints warning for base pairs that violate the `min_loop_size` of the model
- Update `libsvm` to version 3.23
- API: Add functions to set auxiliary grammar extension rules
- API: Replace upper-triangular hard constraints matrix with full matrix for cache-optimized access
- API: Add G-Quadruplex prediction support for comparative partition function
- API: Remove `VRNA_GQUAD_MISMATCH_PENALTY` and `VRNA_GQUAD_MISMATCH_NUM_ALI` macros
- SWIG: Fix invalid memory access in `subopt()` method of `fold_compound` object when writing to file
- SWIG: Add wrapper for Nussinov Maximum Matching algorithm

**Package**

- Add `-ftree-vectorize` compile flag by default if supported

**Version 2.4.9 (Release date: 2018-07-11)****Programs**

- Fix interactive mode behavior for multiple sequence alignment input in `RNAalifold`, `RNAalifold`
- Allow for Stockholm formatted multiple sequence alignment input in `RNAeval` and `RNAplot`
- Allow for multiple input files in `RNAeval` and `RNAplot`
- Allow for parallel processing of input batch jobs in `RNAeval` and `RNAplot`
- Add `-g` option to activate G-Quadruplex support in `RNAheat`
- Warn on unsatisfiable hard constraints from dot-bracket string input in `RNAfold`, `RNAcofold`, and `RNAalifold`

**Library**

- Fix parameter order bug in `vrna_path_findpath*` functions that resulted in too large search widths
- Fix wrong application of base pair soft constraints in partition function computations
- Fix position ruler string in EPS alignment output files
- Fix MFE backtracking errors that might appear under specific hard constrained base pair patterns
- Refrain from reading anything other than `#=GC SS_cons` to retrieve structures when parsing Stockholm 1.0 format
- Complete soft constraints additions to Boltzmann sampling implementation for single sequences
- Allow for disabling alignment wrapping in `vrna_file_PS_aln*` functions
- Do not remove G-Quadruplex annotation from WUSS formatted structure strings upon calls to `vrna_db_↵  
from_WUSS`
- Enable G-Quadruplex related average loop energy correction terms in verbose output of `vrna_eval_*` functions
- Speed-up backward compatibility layer for energy evaluation functions that unnecessarily slowed down third-party tools using the old API
- Allow for passing dot-bracket strings with `"&'strand-end identifier to simplevrna_eval_↵  
*functions`
- Remove `implicitexit()` calls from global MFE backtracking implementation.

**Version 2.4.8 (Release date: 2018-06-23)****Programs**

- Fix compilation of `RNAforester` with C++17 standard
- Fix tty input detection in `RNAcofold`
- Fix bad memory access with `RNAcofold -p`

## Library

- API: Fix incorrect unpaired probability computations in [vrna\\_probs\\_window\(\)](#)
- API: Fix potential out-of-bounds access situations (for circular RNA folding) in `eval.c`
- API: Fix comparative exterior internal loop partition function computation for `circfold`
- SWIG: Fix false-positive use of uninitialized value in `Python3/file_py3.i`

## Package

- TESTS: Add tests for special features in `RNAalifold`
- TESTS: Add test case for `RNAcofold -p`

## Version 2.4.7 (Release date: 2018-06-13)

- Allow for parallel processing across multiple input files in `RNAfold`
- Allow for arbitrary number of input files in `RNAalifold`
- Allow for parallel processing of input data in `RNAalifold`
- Allow for arbitrary number of input files in `RNAcofold`
- Allow for parallel processing of input data in `RNAcofold`
- Enable parallel processing in `RNAfold`, `RNAcofold`, `RNAalifold` for MS Windows build
- Add centroid and MEA structure computation to `RNAcofold`
- Add configure time check for LTO capabilities of the linker
- Include ligand binding energies in centroid and MEA structure output of `RNAfold`
- Refactor `ct2db` program to process multiple structures from single `.ct` file
- API: Enable processing of comparative `fold_compound` with `vrna_pr_*`() functions
- API: Refactor `vrna_ostream_t` to enable NULL input in [vrna\\_ostream\\_provide\(\)](#)
- API: Major refactoring in loop energy evaluations (MFE and PF)
- API: Make `vrna_mx_pf_aux_el_t` and `vrna_mx_pf_aux_ml_s` opaque pointers
- API: Make `fold_compound` field `type` a const attribute
- API: Refactor MFE post-processing for circular RNAs
- API: Add motif name/id support for unstructured domains
- API: Remove major part of implicit `exit()` calls in `RNAlib`
- API: Add implementations of Boyer-Moore-Horspool search algorithm
- API: Add implementations to determine number of rotational symmetry for strings (of objects)
- API: Make `vrna_cmd_t` an opaque pointer
- API: Move headers for constraints, datastructures, io, loop energy evaluation, energy parameters, plotting, search, and utilities into separate subdirectories (backward compatibility is maintained)
- API: Add hash table data structure
- API: Fix discrepancy between comparative and single sequence `--noLP` predictions
- API: Add functions to replace 'old API' interface of [RNAstruct.h](#)

- API: Add functions to replace 'old API' interface of [aln\\_util.h](#)
- API: Add generic soft constraints support to suboptimal structure prediction sensu Wuchty et al.
- SWIG: Refactor callback execution for Python 2 / 3 interface to reduce overhead
- SWIG: Fix configure-time check for Python 3 interface build
- SWIG: Fix Python 3 IO file stream to C FILE \* conversion
- Cosmetic changes in final configure notice
- Major changes in source tree structure of the library
- Add autoconf checks for maintainer tools
- Generate C strings from static PostScript files at configure time (for structure- and dot plots)
- REFMAN: Large updates in API documentation and structure of reference manual

### Version 2.4.6 (Release date: 2018-04-19)

- Stabilize rounding of free energy output in RNAalifold
- API: Fix potential rounding errors for comparative free energies in eval.c and mfe.c
- API: Fix regression in exterior loop dangling end contributions for comparative base pair probabilities and Boltzmann sampling (introduced with v2.4.4)
- API: Fix regression with hard constrained base pairs for comparative structure prediction (introduced with v2.4.4)
- TESTS: Add basic tests for RNAalifold executable
- TESTS: Ignore 'frequency of MFE structure' in RNAcifold partition function checks

### Version 2.4.5 (Release date: 2018-04-17)

- Allow for arbitrary number of input files in RNAfold
- Allow for parallel processing of input data in RNAfold (UNIX only, no Windows support yet)
- Add SHAPE reactivity support through commandline options for RNApIfold
- Fix unstructured domain motif detection in MFE, centroid, and MEA structures computed by RNAfold
- Limit allowed set of commands in command file for RNAcifold to hard and soft constraints
- API: Add functions to compute equilibrium probability of particular secondary structures
- API: Add dynamic string stream data type and associated functions
- API: Add priority-queue like data structure with unordered fill capability and ordered output callback execution
- API: Add functions to detect unstructured domain motifs in MFE, centroid, and MEA structures
- API: Fix bug in sliding-window partition function computation with SHAPE reactivity and Deigan et al. conversion method
- API: Fix application of '<' and '>' constraint symbols in dot-bracket provided constraints (was broken since v2.4.2)
- API: Fix MEA structure computation in the presence of unstructured domains
- API: Stabilize order of probability entries in EPS dot-plot files
- Fix compiler warnings on wrong type of printf() in naview.c



- Define VRNA\_VERSION macro as string literal and add macros for major, minor, and patch numbers
- Stabilize parallel make of Mac OS X installer
- Add energy parameter set from Langdon et al. 2018
- Add autoconf checks for POSIX threads compiler/linker support
- SWIG: Fix 'next' is a perl keyword warnings for Perl5 wrapper
- SWIG: Catch errors and throw exceptions whenever scripting language provided callback functions are not applicable or fail
- SWIG: Add keyword arguments and autodoc feature for Python/Python3 wrappers

### Version 2.4.4 (Release date: 2018-03-06)

- Change verbose output for soft-constraints derived ligand binding motifs in RNAfold
- Allow for lowercase letters in ct2db input
- Fix bug in interior-like G-Quadruplex MFE computation for single sequences
- Fix autoconf switch to enable deprecation warnings
- Fix bug in eval\_int\_loop() that prevented propagation of energy evaluation for loops with nick in strands
- Fix several bugs for SHAPE reactivity related comparative partition function computations
- Fix annotation of PostScript output for soft-constraint derived ligand binding motifs in RNAfold
- Fix constraint indices for multibranch loops in unpaired probability computations of LPfold.c
- Fix dangling end contributions in comparative partition function for exterior loops
- API: Add simplified interface for [vrna\\_pf\\_dimer\(\)](#)
- API: Move concentraton dependent implementation for co-folding to separate compile unit
- API: Add new API functions for exterior loop evaluations
- API: Add simplified interfaces for energy evaluation with G-Quadruplexes and circular RNAs
- API: Add findpath functions that allow for specification of an upper bound for the saddle point
- Add configure-time linker check for Python3 interface
- Add automatic CPP suggestions for deprecated function substitutes
- Major restructuring and constraints feature additions in loop type dependent energy evaluation functions
- Major restructuring in MFE implementations
- Major restructuring in PF implementations
- Minor fixes in Boltzmann sampling implementation
- SWIG: Fix wrappers for findpath() implementation
- SWIG: Add tons of energy evaluation wrappers
- SWIG: Fix configure-time check of Perl5 interface build capabilities
- SWIG: Wrap functions from walk.c and neighbor.c
- DOC: Add some missing references to manpages of executable programs
- REFMAN: Heavy re-ordering of the RNAlib reference manual

**Version 2.4.3 (Release date: 2017-11-14)**

- Fix handling of dangling end contribution at sequence boundaries for sliding window base pair probability computations
- Fix handling of base pair hard constraints in sliding-window implementations
- Fix sliding-window pair probability computations with multibranch-loop unpaired constraints
- Fix sliding-window non-specific base pair hard constraint implementation
- Fix probability computation for stochastic backtracking in RNAsubopt `–stochBT_en` output
- Fix regression in comparative structure prediction for circular RNAs
- Fix LDFLAGS for scripting language interfaces in corresponding Makefiles
- Stabilize partition function scaling by always using `sfact` scaling factor from model details
- Add `–pf_scale` commandline parameter to RNAplfold
- Add constraint framework for single sequence circular RNA structure prediction
- Add RNAfold test suite to check for working implementation of constraints for circular RNAs
- Add a brief contribution guideline CONTRIBUTING.md
- Prevent RNAplfold from creating `inf/-inf` output when solution set is empty with particular hard constraints
- Include RNAforester v2.0.1

**Version 2.4.2 (Release date: 2017-10-13)**

- Fix G-Quadruplex energy corrections in comparative structure energy evaluations
- Fix discrepancy in comparative exterior loop dangling end contribution of eval vs. MFE predictions
- Fix regression in RNAup unstructuredness and interaction energy computations
- Fix sequence length confusions when FASTA input contains carriage returns
- Fix build problems of RNALocmin with older compilers
- Fix sliding-window hard constraints where single nucleotides are prohibited from pairing
- Fix dot-bracket output string length in sliding-window MFE with G-Quadruplexes
- Fix unpaired probability computations for separate individual loop types in LPfold.c
- Fix bad memory access in RNAsubopt with dot-bracket constraint
- Add full WUSS support for `–SS_cons` constraint option in RNAalifold
- Add commandline option to RNALalifold that enables splitting of energy contributions into separate parts
- Add missing hard constraint cases to sliding-window partition function implementation
- Add CSV output option to RNAcofold
- Use the same model details for SCI computations in RNAalifold
- Abort computations in `vrna_eval_structure_v()` if structure has unexpected length
- Use original MSA in all output generated by RNAalifold and RNALalifold
- API: Add new functions to convert dot-bracket like structure annotations
- API: Add various new utility functions for alignment handling and comparative structure predictions
- API: Add function `vrna_strsplit()` to split string into tokens

- API: Do not convert sequences of input MSA to uppercase letters in [vrna\\_file\\_msa\\_read\\_record\(\)](#)
- API: Rename `vrna_annotate_bp_covar()` and `vrna_annotate_pr_covar()`
- API: Add new noLP neighbor generation
- SWIG: Add wrapper for functions in `file_utils_msa.h`
- SWIG: Add wrappers for [vrna\\_pbacktrack\(\)](#) and [vrna\\_pbacktrack5\(\)](#)
- SWIG: Add [vrna\\_db\\_to\\_element\\_string\(\)](#) to scripting language interface
- REFMAN: Fix formula to image conversion in HTML output

### Version 2.4.1 (Release date: 2017-08-23)

- Fix memory leak in `fold_compound` methods of SWIG interface
- Fix memory leaks in double `**` returning functions of SWIG Perl5 interface
- Fix memory leak in `vrna_ep_t` to-string() function of SWIG interface
- Regression: Fix reverting `pf_scale` to defaults after [vrna\\_exp\\_params\\_rescale\(\)](#)
- Regression: Fix homo-dimer partition function computation in RNAcofold
- Add unit tests for RNAcofold executable
- Add SHAPE reactivity support to RNAcofold
- Add SHAPE reactivity support to RNALali

### Version 2.4.0 (Release date: 2017-08-01)

- Bump libsvm to version 3.22
- Print G-Quadruplex corrections in verbose mode of RNAeval
- Change behavior of RNAfold `-outfile` option to something more predictable
- Unify `max_bp_span` usage among sliding window prediction algorithms: RNAplfold, RNALfold, and RNALali-fold now consider any base pair (i,j) with  $(j - i + 1) \leq \text{max\_bp\_span}$
- Add SHAPE reactivity data support to RNALfold
- Add commands-file support for RNALfold, RNAplfold (hard/soft constraints)
- Add RNALocmin - Calculate local minima from structures via gradient walks
- Add RNA Bioinformatics tutorial (PDF version)
- Add hard constraints to sliding-window MFE implementations (RNALfold, RNALali
- Add hard constraints to sliding-window PF implementations (RNAplfold)
- Add soft constraints to sliding-window MFE implementation for single sequences (RNALfold)
- Add soft constraints to sliding-window PF implementations (RNAplfold)
- Add SWIG interfaces for sliding-window MFE/PF implementations
- Add proper SWIG interface for alignment and structure plotting functions
- Add proper SWIG interface for `duplexfold`, `duplex_subopt`, and its comparative variants
- Add SWIG wrapper for [vrna\\_exp\\_params\\_rescale\(\)](#)
- Add explicit destructor for SWIG generated `vrna_md_t` objects

- Add SWIG perl5 typemap for simple nested STL vectors
- Add dummy field in [vrna\\_structured\\_domains\\_s](#)
- Add note about SSE optimized code in reference manual
- Add SWIG interface for findpath implementation
- Add prepare() functions for ptypes-arrays and `vrna_(exp_)param_t`
- Add warnings for ignored commands in function [vrna\\_commands\\_apply\(\)](#)
- Add callback featured functions for sliding window MFE and PF implementations
- Change default behavior of adding soft constraints to a `vrna_fold_compound_t` (store only)
- Several fixes with respect to G-Quadruplex prediction in sliding-window MFE recursions (single sequence and comparative implementation)
- Replace comparative sliding-window MFE recursions (All hits are reported to callback and can be filtered in a post-processing step)
- API: Remove `E_mb_loop_stack()` and introduce new function [vrna\\_E\\_mb\\_loop\\_stack\(\)](#) as a replacement
- API: change data type of all constraint bit-flags from `char` to `unsigned char`
- API: change data type of `a2s` array in comparative structure prediction from `unsigned short` to `unsigned int`
- API: Change function parameter order in [vrna\\_probs\\_window\(\)](#) to follow the style of other callback-aware functions in RNAlib
- Move sliding-window MFE implementations to new file `mfe_window.c`
- Fix building PDF Reference manual with non-standard executable paths
- Fix redefinition of macro `ON_SAME_STRAND()` in `subopt.c`
- Fix dangling end issues in sliding-window MFE implementations
- Fix regression for `-canonicalBPonly` switch in [RNAfold/RNAcofold/RNAsubopt](#)
- Fix building sliding-window MFE implementation without SVM support
- Fix parsing of STOCKHOLM 1.0 MSA files that contain MSA spanning multiple blocks
- Fix Alidot link in RNAalifold manpage
- Fix wrong pre-processor flags when enabling single-precision PF computations
- Fix unit testing perl5 interface by including `builddir/tests` in `PERL5LIB` path
- Fix buffer overflow in hairpin loop sequence motif extraction for circular RNAs
- Fix out-of-bounds memory access in `neighbor.c`
- Restore capability to compile stand-alone findpath utility
- Restore capability to use non-standard alphabets for structure prediction
- Restore old-API random number functions in SWIG interface
- Allow additional control characters in MAF MSA input that do not end a block
- Improve reference manual
- Make functions in [pair\\_mat.h](#) static inline
- Prevent users from adding out-of-range base pair soft constraints

- Inline print functions in color\_output.inc
- Start documenting callback features in reference manual
- Re-write large portions of sliding-window PF implementation
- Introduce soft-constraint state flag
- Clean-up SWIG unit test framework
- Remove obsolete scripts ct2b.pl and colorrna.pl from src/Utils directory
- Remove old RNAfold tutorial

## Version 2.3.x

### Version 2.3.5 (Release date: 2017-04-14)

- Fix duplication of output filename prefix in RNAfold
- Add V3.0 API for sliding window partition function (a.k.a. RNAPLfold)
- Add G-Quadruplex prediction to RNALalifold
- Add SWIG wrappers for callback-based sliding window comparative MFE prediction
- Add SSE4.1 multiloop decomposition for single sequence MFE prediction
- Enable RNAfold unit tests to run in parallel
- Enable users to turn-off base pair probability computations in RNACofold with -a option
- Split move set in neighbor.c

### Version 2.3.4 (Release date: 2017-03-10)

- Fix G-Quadruplex probability computation for single sequences
- Fix double-free when using SHAPE reactivity data in RNAalifold
- Fix out-of-bounds access in strand\_number array
- Fix weighting of SHAPE reactivity data in consensus structure prediction when fewer data than sequences are present
- Fix z-score output in RNALfold
- Substitute field name 'A0'/'B0' in data structure `vrna_dimer_conc_s` by 'Ac\_start'/'Bc\_start' to avoid clashes with `termios.h` (Mac OSX Python wrapper bug)
- Minimize usage of 'unsafe' `sprintf()` calls
- Enhance auto-id feature in executable programs
- Always sanitize output file names to avoid problems due to strange FASTA headers
- Lift restrictions of FASTA header length in RNAfold, RNACofold, and RNAeval
- Add ViennaRNA/config.h with pre-processor definitions of configure time choices
- Add test-suite for RNAfold
- Add functions to produce colored EPS structure alignments
- Add function to write Stockholm 1.0 formatted alignments
- Add function to sanitize file names

- Add callback based implementation for sliding-window MFE prediction (single sequences, comparative structure prediction)
- Add fast API 3.0 implementations to generate structural neighbors and perform steepest descent / random walks (Thanks to Gregor!)
- Add parameter option to RNALalifold for colored EPS structure alignment and structure plot output
- Add parameter option to RNALalifold to write hits into Stockholm file
- Add parameter option to RNAalifold to write Stockholm 1.0 formatted output
- Add parameter option to RNAalifold to suppress stderr spam
- Add auto-id feature to RNAplot, RNALfold, RNAsubopt, RNApfold, RNAheat
- Add SHAPE reactivity derived pseudo-energies as separate output in RNAalifold
- Add colored output to RNA2Dfold, RNALalifold, RNALfold, RNAduplex, RNAheat, RNAinverse, RNApfold, and RNAsubopt
- Add command line parameters to RNAsubopt to allow for specification of input/output files

### Version 2.3.3 (Release date: 2017-01-24)

- Fix multiloop contributions for comparative partition function
- Fix building python2 extension module for OSX

### Version 2.3.2 (Release date: 2017-01-18)

- Fix pair probability plist creation with G-Quadruplexes
- Allow for specification of python2/3-config at configure time
- Fix init of vrna\_md\_t data structure after call to [set\\_model\\_details\(\)](#)
- Fix bug in consensus partition function with hard constraints that force nucleotides to be paired
- Fix compilation of functions that use ellipsis/va\_list
- Enable generic hard constraints by default
- Fix init of partition function DP matrices for unusually short RNAs
- Fix behavior of RNApfold for unusually short RNAs
- Report SCI of 0 in RNAalifold when sum of single sequence MFEs is 0
- Avoid multiple includes of [pair\\_mat.h](#)
- Add configure flag to build entirely static executables

### Version 2.3.1 (Release date: 2016-11-15)

- Add description for how to use unstructured domains through command files to reference manual and RNAfold manpage
- Fix compilation issue for Windows platforms with MingW
- Add missing newline in non-TTY-color output of [vrna\\_message\\_info\(\)](#)
- Fix regression in [vrna\\_md\\_update\(\)](#) that resulted in incomplete init of reverse-basepair type array
- Extend coverage of generic hard constraints for partition function computations
- Fix scaling of secondary structure in EPS plot such that it always fits into bounding box
- Several fixes and improvements for SWIG generated scripting language interface(s)

### Version 2.3.0 (Release date: 2016-11-01)

- Add grammar extension with structured and unstructured domains
- Add default implementation for unstructured domains to allow for ligand/protein binding to unpaired structure segments (MFE and PF for single sequences)
- Introduced command files that subsume constraint definition files (currently used in RNAfold and RNAcifold)
- Replace explicit calls to `asprintf()` with portable equivalent functions in the library
- Fix configure script to deal with situations where Perl module can't be build
- Fix bug in `doc/Makefile.am` that prevented HTML installation due to long argument list
- Added utility functions that deal with conversion between different units
- Bugfix in SWIG wrapped generic soft constraint feature
- Add `subopt()` and `subopt_zuker()` methods to SWIG wrapped `fold_compound` objects
- Bugfix multiloop decomposition in MFE for circular RNAs
- Add separate function to compute pscore for alignments
- Renamed `VRNA_VC_TYPE_*` macros to `VRNA_FC_TYPE_*`
- Bugfix regression that prevented programs to fail on too long input sequences
- Extend EPS dot-plot in RNAfold to include motif/binding probabilities from unstructured domains
- Add variadic functions for error/warning/info message
- Add ID manipulation feature to RNAeval
- Extend API for soft constraint feature for more fine-grained control
- Add section on SWIG wrapped functions in reference manual
- Fix bug in interior loop computations when hard constraints result in non-canonical base pairs

## Version 2.2.x

### Version 2.2.10 (Release date: 2016-09-06)

- Do not 'forget' subopt results when output is not written to file handle and sorting is switched off
- Fix bad memory access in `vrna_subopt()` with sorted output
- Add SWIG wrappers for `vrna_subopt_cb()`
- Correctly show if C11 features are activated in configure status
- Fix autoconf checks to allow for cross compilation again

### Version 2.2.9 (Release date: 2016-09-01)

- Fix bug in partition function scaling for backward compatibility of `ali_pf_fold()`
- Stabilize v3.0 API when building RNAlib and third party program linking against it with compilers that use different C/C++ standards
- Add details on how to link against RNAlib to the reference manual
- Fix RNAlib2.pc
- Fix bug for temperature setting in RNAplfold

- Use -fflat-lto-objects for static RNALib library to allow linking without LTO
- Fix interpretation of 'P' hard constraint for single nucleotides in constraint definition files
- Add 'A' command for hard constraints
- Fix several hard constraint corner-cases in MFE and partition function computation when nucleotides must not be unpaired
- Fix order of hard constraints when read from input file
- Allow for non-canonical base pairs in MFE and partition function computations if hard constraints demand it
- Fix behavior of `--without-swig` configure script option
- Fix bug in hard constraints usage of exterior loop MFE prediction with odd dangles
- Add parsers for Clustal, Stockholm, FASTA, and MAF formatted alignment files
- Enable RNAalifold to use Clustal, Stockholm, FASTA, or MAF alignments as input
- Lift restriction of sequence number in alignments for RNAalifold
- Enable ANSI colors for TTY output in RNAfold, RNAcifold, RNAalifold, RNAsubopt, and warnings/errors issued by RNALib
- Add various new commandline options to manipulate sequence/alignment IDs in RNAfold, RNAcifold and RNAalifold

### Version 2.2.8 (Release date: 2016-08-01)

- Fix bad memory access in RNAalifold
- Fix regression in RNAalifold to restore covariance contribution ratio determination for circular RNA alignments
- Changed output of RNAsubopt in energy-band enumeration mode to print MFE and energy range in kcal/mol instead of 10cal/mol
- Include latest Kinfold sources that make use of v3.0 API, therefore speeding up runtime substantially
- Re-activate warnings in RNAeval when non-canonical base pairs are encountered
- Fix syntactic incompatibilities that potentially prevented compilation with compilers other than gcc
- dd function to compare nucleotides encoded in IUPAC format
- Fix regression in energy evaluation for circular RNA sequences
- Fix regression in suboptimal structure enumeration for circular RNAs
- Allow for P i-j k-l commands in constraint definition files
- Make free energy evaluation functions polymorphic
- Add free energy evaluation functions that allow for specifying verbosity level
- Secure functions in alphabet.c against NULL pointer arguments
- Fix incompatibility with swig  $\geq 3.0.9$
- Fix memory leak in swig-generated scripting language interface(s) for user-provided target language soft-constraint callbacks
- Expose additional functions to swig-generated scripting language interface(s)
- Build Python3 interface by default
- Start of more comprehensive scripting language interface documentation



- Fix linking of python2/python3 interfaces when libpython is in non-standard directory
- Restructured viennarna.spec for RPM based distributions
- Several syntactic changes in the implementation to minimize compiler warnings
- Fix `--with-*/--without-*` and `--enable-*/--disable-*` configure script behavior

### Version 2.2.7 (Release date: 2016-06-30)

- Fix partition function scaling for long sequences in RNAfold, RNAalifold, and RNAup
- Fix backtracking issue in RNAcofold when `--noLP` option is activated
- Fix hard constraints issue for circular RNAs in generating suboptimal structures
- Rebuild reference manual only when actually required

### Version 2.2.6 (Release date: 2016-06-19)

- Plugged memory leak in RNAcofold
- Fixed partition function rescaling bug in RNAup
- Fixed bug in RNALfold with window sizes larger than sequence length
- Re-added SCI parameter for RNAalifold
- Fixed backtracking issue for large G-quadruplexes in RNAalifold
- Fixed missing FASTA id in RNAeval output
- Added option to RNAalifold that allows to specify prefix for output files
- Several fixes and additional functions/methods in scripting language interface(s)
- Added version information for scripting language interface(s)
- Some changes to allow for compilation with newer compilers, such as gcc 6.1

### Version 2.2.5 (Release date: 2016-04-09)

- Fixed regression in RNAcofold that prohibited output of concentration computations
- Fixed behavior of RNAfold and RNAcofold when hard constraints create empty solution set (programs now abort with error message)
- Added optional Python 3 interface
- Added RNA::Params Perl 5 sub-package
- Update RNA::Design Perl 5 sub-package
- Simplified usage of v3.0 API with default options
- Wrap more functions of v3.0 API in SWIG generated scripting language interfaces
- Plugged some memory leaks in SWIG generated scripting language interfaces
- Changed parameters of recursion status callback in `vrna_fold_compound_t`
- Enable definition and binding of callback functions from within SWIG target language
- Added optional subpackage Kinwalker
- Added several configure options to ease building and packaging under MacOS X
- Added new utility script RNAdesign.pl

**Version 2.2.4 (Release date: 2016-02-19)**

- Fixed bug in RNAsubopt that occasionally produced cofolded structures twice
- Removed debugging output in preparations of consensus structure prediction datastructures

**Version 2.2.3 (Release date: 2016-02-13)**

- Added postscript annotations for found ligand motifs in RNAfold
- Added more documentation for the constraints features in RNAfold and RNAalifold
- Restore backward compatibility of [get\\_alipf\\_arrays\(\)](#)

**Version 2.2.2 (Release date: 2016-02-08)**

- Fix regression bug that occasionally prevented backtracking with RNAcofold --noLP

**Version 2.2.1 (Release date: 2016-02-06)**

- Fix regression bug that made RNAcofold -a unusable
- Fix regression bug that prohibited RNAfold to compute the MEA structure when G-Quadruplex support was switched on
- Fix bug in Kinfold to enable loading energy parameters from file
- Fix potential use of uninitialized value in RNApdist
- Add manpage for ct2db
- Fix MEA computation when G-Quadruplex support is activated
- Allow for vendor installation of the perl interface using INSTALLDIRS=vendor at configure time
- Install architecture dependent and independent files of the perl and python interface to their correct file system locations

**Version 2.2.0 (Release date: 2016-01-25)**

- RNAforester is now of version 2.0
- New program RNApvmin to compute pseudo-energy perturbation vector that minimizes discrepancy between observed and predicted pairing probabilities
- SHAPE reactivity support for RNAfold, RNAsubopt, and RNAalifold
- Ligand binding to hairpin- and interior-loop motif support in RNAfold
- New commandline option to limit maximum base pair span for RNAfold, RNAsubopt, RNAcofold, and RNAalifold
- Bugfix in RNAheat to remove numerical instabilities
- Bugfix in RNApdex to allow for computation of interactions without length limitation
- Bugfix in RNAplot for simple layouts and hairpins of size 0
- (generic) hard- and soft-constraints for MFE, partition function, base pair probabilities, stochastic backtracking, and suboptimal secondary structures of single sequences, sequence alignments, and sequence dimers
- libsvm version as required for z-scoring in RNALfold is now 3.20
- Stochastic backtracking for single sequences is faster due to usage of Boustrophedon scheme
- First polymorphic functions [vrna\\_mfe\(\)](#), [vrna\\_pf\(\)](#), and [vrna\\_pbacktrack\(\)](#).

- The FLT\_OR\_DBL macro is now a typedef
- New functions to convert between different secondary structure representations, such as helix lists, and RNASHapes abstractions
- First object-oriented interface for new API functions in the scripting language interfaces
- new ViennaRNA-perl submodule that augments the Perl interface to RNALib
- Ligand binding to hairpin- and interior-loop motif support in C-library and scripting language interfaces.
- Libraries are generated using libtool
- Linking of libraries and executables defaults to use Link Time Optimization (LTO)
- Large changes in directory structure of the source code files

## Version 2.1.x

### Version 2.1.9

- Fixed integer underflow bug in RNALfold
- Added Sequence Conservation index (SCI) option to RNAalifold
- Fixed bug in energy evaluation of dangling ends / terminal mismatches of exterior loops and multibranch loops
- Fixed bug in alifold partition function for circular RNAs
- Fixed bug in alifold that scrambled backtracing with activated G-Quadruplex support
- Fixed bug in alifold backtracking for larger G-Quadruplexes

### Version 2.1.8

- Repaired incorporation of RNAinverse user provided alphabet
- Fix missing FASTA ID in RNAeval output
- prevent race condition in parallel calls of [Lfold\(\)](#)
- Fixed memory bug in [Lfold\(\)](#) that occurred using long sequences and activated G-Quad support
- Added latest version of switch.pl

### Version 2.1.7

- Fixed bug in RNALfold -z
- Python and Perl interface are compiling again under MacOSX
- Fixed handling of C arrays in Python interface
- Added latest version of switch.pl
- Make relplot.pl work with RNACofold output

### Version 2.1.6

- New cmdline switches allow for elimination of non-canonical base pairs from constraint structures in RNAfold, RNAalifold and RNAsubopt
- updated moveset functions
- final fix for discrepancy of tri-loop evaluation between partition function and mfe
- pkg-config file now includes the OpenMP linker flag if necessary
- New program ct2db allows for conversion of .ct files into dot-bracket notation (incl. pseudo-knot removal)

### Version 2.1.5

- Fix for discrepancy between special hairpin loop evaluation in partition functions and MFE

### Version 2.1.4

- Fix of G-quadruplex support in [subopt\(\)](#)
- Fix for discrepancy between special hairpin loop evaluation in partition functions and MFE

### Version 2.1.3

- RNAfold: Bugfix for ignoring user specified energy parameter files
- RNACofold: Bugfix for crashing upon constrained folding without specifying a constraint structure
- RNAsubopt: Added G-quadruplex support
- RNAalifold: Added parameter option to specify base pair probability threshold in dotplot
- Fix of several G-quadruplex related bugs
- Added G-quadruplex support in [subopt\(\)](#)

### Version 2.1.2

- RNAfold: Bugfix for randomly missing probabilities in dot-plot during batch job execution
- RNAeval: Bugfix for misinterpreted G-quadruplex containing sequences where the quadruplex starts at nucleotide 1
- RNAsubopt: Slight changes to the output of stochastic backtracking and zucker subopt
- Fix of some memory leaks
- Bugfixes in [zuckersubopt\(\)](#), [assign\\_plist\\_from\\_pr\(\)](#)
- New threadsafe variants of putoutpU\_prob\*() for LPfold()
- Provision of python2 interface support.

### Version 2.1.1

- Bugfix to restore backward compatibility with ViennaRNA Package 1.8.x API (this bug also affected proper usage of the perl interface)

### Version 2.1.0

- G-Quadruplex support in RNAfold, RNACofold, RNALfold, RNAalifold, RNAeval and RNAplot
- LPfold got a new option to output its computations in split-mode
- several G-Quadruplex related functions were introduced with this release
- several functions for moves in an RNA landscape were introduced
- new function in alipfold.c now enables access to the partition function matrices of [alipf\\_fold\(\)](#)
- different numeric approach was implement for concentration dependend co-folding to avoid instabilities which occurred under certain circumstances

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## Version 2.0.x

### Version 2.0.7

- Bugfix for RNAplfold where segfault happened upon usage of -O option
- Corrected misbehavior of RNAeval and RNAplot in tty mode

### Version 2.0.6

- Bugfix for bad type casting with gcc under MacOSX (resulted in accidental "sequence too long" errors)
- Bugfix for disappearing tri-/hexaloop contributions when read in from certain parameter files
- Bugfix for RNALfold that segfaulted on short strange sequences like AT+ repeats
- Change of RNA2Dfold output format for stochastic backtracking

### Version 2.0.5

- Restored z-score computation capabilities in RNALfold

### Version 2.0.4

- Bugfix for RNAcifold partition function
- Perl wrapper compatibility to changed RNALib has been restored
- Backward compatibility for partition function calls has been restored

### Version 2.0.3

- Bugfix for RNAalifold partition function and base pair probabilities in v2.0.3b
- Added Boltzmann factor scaling in RNAsubopt, RNAalifold, RNAplfold and RNAcifold
- Bugfix for alipfold() in v2.0.3b
- Restored threadsafety of folding matrix access in LPfold.c, alipfold.c, part\_func.c, part\_func\_co.c and part\_func\_up.c
- Added several new functions regarding threadsafe function calls in terms of concurrently changing the model details
- Added pkg-config file in the distribution to allow easy checks for certain RNALib2 versions, compiler flags and linker flags.

### Version 2.0.2

- added support for Boltzmann factor scaling in RNAfold
- fixed fastaheader to filename bug
- plugged some memory leaks

### Version 2.0.1

- First official release of version 2.0
- included latest bugfixes

## History

2011-03-10 Ronny Lorenz [ronny@tbi.univie.ac.at](mailto:ronny@tbi.univie.ac.at)

- new naming scheme for all shipped energy parameter files
- fixed bugs that appear while compiling with gcc under MacOS X
- fixed bug in RNAup –interaction-first where the longer of the first two sequences was taken as target
- added full FASTA input support to RNAfold, RNAcofold, RNAheat, RNAplfold, RNALfoldz, RNAsubopt and RNALfold

2010-11-24 Ronny Lorenz [ronny@tbi.univie.ac.at](mailto:ronny@tbi.univie.ac.at)

- first full pre-release of version 2.0

2009-11-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Fix memory corruption in [PS\\_color\\_aln\(\)](#)

2009-09-09 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Fix bug in RNAplfold when -u and -L parameters are equal
- Fix double call to [free\\_arrays\(\)](#) in RNAfold.c
- Improve drawing of cofolded structures

2009-05-14 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Fix occasional segfault in RNAalifold's [print\\_alifold\(\)](#)

2009-02-24 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Add -MEA options to RNAfold and RNAalifold
- change [energy\\_of\\_alifold](#) to return float not void

2009-02-24 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- RNAfold will draw structures unless -noPS is used (no more "structure too long" messages)
- Restore the "alifold.out" output from RNAalifold -p
- RNAalifold -circ did not work due to wrong return type
- Accessibility calculation with RNAplfold would give wrong results for  $u \leq 30$

2008-12-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Add Zuker style suboptimals to RNAsubopt (-z)
- [get\\_line\(\)](#) should be much faster when reading huge sequences (e.g. whole chromosomes for RNALfold)

2008-08-12 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Add Ribosum matrices for covariance scoring in RNAalifold

2008-06-27 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Change RNAalifold to use Berni's new energy evaluation w/o gaps
- Add stochastic backtracking in RNAalifold

2008-07-04 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- modify output of RNAup (again). Program reading RNAup output will have to be updated!

2008-07-02 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- RNAplfold now computes accessibilities for all regions up to a max length simultaneously. Slightly slower when only 1 value is needed, but much faster if all of them are wanted. This entails a new output format. Programs reading accessibility output from RNAplfold need to be updated!

2008-03-31 Stephan Bernhart [berni@tbi.univie.ac.at](mailto:berni@tbi.univie.ac.at)

- add cofolding to RNAsubopt

2008-01-08 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- ensure circfold works even for open chain

2007-12-13 Ulli Mueckstein [ulli@tbi.univie.ac.at](mailto:ulli@tbi.univie.ac.at)

- update RNAup related files RNAup can now include the intramolecular structure of both molecules and handles constraints.

2007-12-05 Ronny Lorenz [ronny@tbi.univie.ac.at](mailto:ronny@tbi.univie.ac.at)

- add circfold variants in part\_func.c alipfold.c subopt.c

2007-09-19 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- compute the centroid structure of the ensemble in RNAfold -p
- fix a missing factor 2 in [mean\\_bp\\_dist\(\)](#). CAUTION ensemble diversities returned by RNAfold -p are now twice as large as in earlier versions.

2007-09-04 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- fix a bug in [Lfold\(\)](#) where base number n-max-4 would never pair

2007-08-26 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add RNAaliduplex the alignment version of RNAduplex
- introduce a minimal distance between hits produced by duplex\_subopt()

2007-07-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add a [loop\\_energy\(\)](#) function to compute energy of a single loop

2007-06-23 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add aliLfold() and RNALalifold, alignment variant of [Lfold\(\)](#)

2007-04-30 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add RNAup to distribution

2007-04-15 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- fix segfault in colorps output (thanks to Andres Varon)

2007-03-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- avoid unnormalized doubles in scale[], big speedup for [pf\\_fold\(\)](#) on very long sequences

2007-02-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- RNAalifold can now produce colored structure plots and alignment plots

2007-02-01 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Fix segfault in RNAplfold because of missing prototype

2006-12-01 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- RNAduplex would segfault when no structure base pairs are possible

2006-08-22 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add computation stacking probabilities using RNAfold -p2
- add -noPS option for RNAfold to suppress drawing structures

2006-08-09 Stephan Bernhart [berni@tbi.univie.ac.at](mailto:berni@tbi.univie.ac.at)

- RNAplfold can now compute probabilities of unpaired regions (scanning version of RNAup)

2006-06-14 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- compile library with -fpic (if available) for use as shared library in the Perl module.
- fix another bug when calling `Lfold()` repeatedly
- fix switch cmdline parsing in RNAalifold (-mis implied -4)
- fix bug in `cofold()` with dangles=0

2006-05-08 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- fix segfault in `Lfold()` when calling repeatedly
- fix structure parsing in RNAstruct.c (thanks to Michael Pheasant for reporting both bugs)
- add duplexfold() and `alifold()` to Perl module
- distinguish window size and max pair span in LPfold

2006-04-05 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- fix performance bug in `co_pf_fold()`
- use relative error for termination of Newton iteration

2006-03-02 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add circular folding in `alifold()`

2006-01-18 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- cleanup berni partition cofold code, including several bug fixes

2006-01-16 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- update RNAplfold to working version
- add `PS_dot_plot_turn()` in `PS_dot.c`

2005-11-07 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add new utilities colorna and coloraln

2005-10-11 Christoph Flamm [xtof@tbi.univie.ac.at](mailto:xtof@tbi.univie.ac.at)

- adapt `PS_rna_plot()` for drawing co-folded structures

2005-07-24 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)



- fix a few memory problems in structure comparison routines

2005-04-30 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add folding of circular RNAs

2005-03-11 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add -mis option to RNAalifold to give "most informative sequence" as consensus

2005-02-10 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- move [alifold\(\)](#) into the library

2004-12-22 Stephan Bernhart [berni@tbi.tbi.univie.ac.at](mailto:berni@tbi.tbi.univie.ac.at)

- add partition function version of RNAcofold

2004-12-23 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add RNAln for fast structural alignments (RNAdist improvement)

2004-08-12 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- fix constrained folding in stochastic backtracking

2004-07-21 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add RNAduplex, to compute hybrid structures without intra-molecular pairs

2004-02-09 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- fix bug in fold that caused segfaults when using Intel compiler
- add computation of ensemble diversity to RNAfold

2003-09-10 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add annotation options to RNAplot

2003-08-04 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- stochastic backtracking finally works. Try e.g. RNAsubopt -p 10

2003-07-18 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add relplot.pl and rotate\_ss.pl utilities for reliability annotation and rotation of rna structure plots

2003-01-29 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- add RNALfold program to compute locally optimal structures with maximum pair span.
- add RNAcofold for computing hybrid structure

2002-11-07 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- change [Make\\_bp\\_profile\(\)](#) and [profile\\_edit\\_distance\(\)](#) to use simple (float \*) arrays; makes Perl access much easier. RNAdist -B now works again

2002-10-28 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- Improved Perl module with pod documentation; allow to write things like (\$structure, \$energy) = RNA $\leftrightarrow$ ::fold(\$seq); Compatibility warning: the ptrvalue() and related functions are gone, see the pod documentation for alternatives.

2002-10-29 Ivo Hofacker [ivo@tbi.tbi.univie.ac.at](mailto:ivo@tbi.tbi.univie.ac.at)

- added svg structure plots in PS\_dot.c and RNAplot

2002-08-15 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- Improve reading of clustal files (alifold)
- add a sample alifold.cgi script

2001-09-18 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- moved suboptimal folding into the library, thus it's now accessible from the Perl module

2001-08-31 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- added co-folding support in [energy\\_of\\_struct\(\)](#), and thus RNAeval

2001-04-30 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- switch from handcrafted makefiles to automake and autoconf

2001-04-05 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- added PS\_rna\_plot\_a to produce structure plots with annotation

2001-03-03 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add alifold; predict consensus structures from alignment

2000-09-28 Ivo Hofacker [ivo@tbi.univie.ac.at](mailto:ivo@tbi.univie.ac.at)

- add -d3 option to RNAfold for co-axial stacking

# Chapter 11

## Deprecated List

Global **alifold** (const char \*\*strings, char \*structure)

Usage of this function is discouraged! Use [vrna\\_alifold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

Global **alimake\_pair\_table** (const char \*structure)

Use [vrna\\_pt\\_ali\\_get\(\)](#) instead!

Global **alipbacktrack** (double \*prob)

Use [vrna\\_pbacktrack\(\)](#) instead!

Global **alipf\_circ\_fold** (const char \*\*sequences, char \*structure, vrna\_ep\_t \*\*pl)

Use [vrna\\_pf\(\)](#) instead

Global **alipf\_fold** (const char \*\*sequences, char \*structure, vrna\_ep\_t \*\*pl)

Use [vrna\\_pf\(\)](#) instead

Global **alipf\_fold\_par** (const char \*\*sequences, char \*structure, vrna\_ep\_t \*\*pl, vrna\_exp\_param\_t \*parameters, int calculate\_bppm, int is\_constrained, int is\_circular)

Use [vrna\\_pf\(\)](#) instead

Global **aliPS\_color\_aln** (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])

Use [vrna\\_file\\_PS\\_aln\(\)](#) instead!

File **aln\_util.h**

Use [ViennaRNA/utis/alignments.h](#) instead

Global **assign\_plist\_from\_db** (vrna\_ep\_t \*\*pl, const char \*struc, float pr)

Use [vrna\\_plist\(\)](#) instead

Global **assign\_plist\_from\_pr** (vrna\_ep\_t \*\*pl, FLT\_OR\_DBL \*probs, int length, double cutoff)

Use [vrna\\_plist\\_from\\_probs\(\)](#) instead!

Global **b2C** (const char \*structure)

See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_SHORT](#) for a replacement

Global **b2HIT** (const char \*structure)

See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_HIT](#) for a replacement

Global **b2Shapiro** (const char \*structure)

See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_WEIGHT](#) for a replacement

Global **base\_pair**

Do not use this variable anymore!

Global **bondT**

Use [vrna\\_bp\\_stack\\_t](#) instead!

Global **bp\_distance** (const char \*str1, const char \*str2)

Use [vrna\\_bp\\_distance](#) instead

Global **bppm\_symbol** (const float \*x)

Use [vrna\\_bpp\\_symbol\(\)](#) instead!

Global **bppm\_to\_structure** (char \*structure, FLT\_OR\_DBL \*pr, unsigned int length)

Use [vrna\\_db\\_from\\_probs\(\)](#) instead!

Global **centroid** (int length, double \*dist)

This function is deprecated and should not be used anymore as it is not threadsafe!

File **char\_stream.h**

Use [ViennaRNA/datastructures/char\\_stream.h](#) instead

Global **circularfold** (const char \*\*strings, char \*structure)

Usage of this function is discouraged! Use [vrna\\_alicircfold\(\)](#), and [vrna\\_mfe\(\)](#) instead!

Global **circfold** (const char \*sequence, char \*structure)

Use [vrna\\_circfold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

Global **co\_pf\_fold** (char \*sequence, char \*structure)

{Use [vrna\\_pf\\_dimer\(\)](#) instead!}

Global **co\_pf\_fold\_par** (char \*sequence, char \*structure, vrna\_exp\_param\_t \*parameters, int calculate\_bppm, int is\_constrained)

Use [vrna\\_pf\\_dimer\(\)](#) instead!

Global **cofold** (const char \*sequence, char \*structure)

use [vrna\\_mfe\\_dimer\(\)](#) instead

Global **cofold\_par** (const char \*string, char \*structure, vrna\_param\_t \*parameters, int is\_constrained)

use [vrna\\_mfe\\_dimer\(\)](#) instead

Global **compute\_BPdifferences** (short \*pt1, short \*pt2, unsigned int turn)

Use [vrna\\_refBPdist\\_matrix\(\)](#) instead

Global **compute\_probabilities** (double FAB, double FEA, double FEB, vrna\_ep\_t \*prAB, vrna\_ep\_t \*prA, vrna\_ep\_t \*prB, int Alength)

{ Use [vrna\\_pf\\_dimer\\_probs\(\)](#) instead!}

Global **constrain\_ptypes** (const char \*constraint, unsigned int length, char \*ptype, int \*BP, int min\_loop\_size, unsigned int idx\_type)

Do not use this function anymore! Structure constraints are now handled through [vrna\\_hc\\_t](#) and related functions.

File **constraints.h**

Use [ViennaRNA/constraints/basic.h](#) instead

File **constraints\_hard.h**

Use [ViennaRNA/constraints/hard.h](#) instead

File **constraints\_ligand.h**

Use [ViennaRNA/constraints/ligand.h](#) instead

File **constraints\_SHAPE.h**

Use [ViennaRNA/constraints/SHAPE.h](#) instead

File **constraints\_soft.h**

Use [ViennaRNA/constraints/soft.h](#) instead

File **convert\_epars.h**

Use [ViennaRNA/params/convert.h](#) instead

Global **copy\_pair\_table** (const short \*pt)

Use [vrna\\_ptable\\_copy\(\)](#) instead

Global **cpair**

Use [vrna\\_cpair\\_t](#) instead!

**Global `cv_fact`**

See `vrna_md_t.cv_fact`, and `vrna_mfe()` to avoid using global variables

**File `data_structures.h`**

Use `ViennaRNA/datastructures/basic.h` instead

**Global `destroy_TwoDfold_variables` (`TwoDfold_vars` \*`our_variables`)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_↵_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `destroy_TwoDpfold_variables` (`TwoDpfold_vars` \*`vars`)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_↵_TwoD()`, `vrna_pf_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `E_Stem` (int `type`, int `si1`, int `sj1`, int `extLoop`, `vrna_param_t` \*`P`)**

Please use one of the functions `vrna_E_ext_stem()` and `E_MLstem()` instead! Use the former for cases where `extLoop` != 0 and the latter otherwise.

**File `energy_const.h`**

Use `ViennaRNA/params/constants.h` instead

**Global `energy_of_alistruct` (const char \*\*`sequences`, const char \*`structure`, int `n_seq`, float \*`energy`)**

Usage of this function is discouraged! Use `vrna_eval_structure()`, and `vrna_eval_covar_structure()` instead!

**Global `energy_of_circ_struct` (const char \*`string`, const char \*`structure`)**

This function is deprecated and should not be used in future programs Use `energy_of_circ_structure()` instead!

**Global `energy_of_circ_struct_par` (const char \*`string`, const char \*`structure`, `vrna_param_t` \*`parameters`, int `verbosity_level`)**

Use `vrna_eval_structure()` or `vrna_eval_structure_verbose()` instead!

**Global `energy_of_circ_structure` (const char \*`string`, const char \*`structure`, int `verbosity_level`)**

Use `vrna_eval_structure()` or `vrna_eval_structure_verbose()` instead!

**Global `energy_of_move` (const char \*`string`, const char \*`structure`, int `m1`, int `m2`)**

Use `vrna_eval_move()` instead!

**Global `energy_of_move_pt` (short \*`pt`, short \*`s`, short \*`s1`, int `m1`, int `m2`)**

Use `vrna_eval_move_pt()` instead!

**Global `energy_of_struct` (const char \*`string`, const char \*`structure`)**

This function is deprecated and should not be used in future programs! Use `energy_of_structure()` instead!

**Global `energy_of_struct_par` (const char \*`string`, const char \*`structure`, `vrna_param_t` \*`parameters`, int `verbosity_level`)**

Use `vrna_eval_structure()` or `vrna_eval_structure_verbose()` instead!

**Global `energy_of_struct_pt` (const char \*`string`, short \*`ptable`, short \*`s`, short \*`s1`)**

This function is deprecated and should not be used in future programs! Use `energy_of_structure_pt()` instead!

**Global `energy_of_struct_pt_par` (const char \*`string`, short \*`ptable`, short \*`s`, short \*`s1`, `vrna_param_↵_t` \*`parameters`, int `verbosity_level`)**

Use `vrna_eval_structure_pt()` or `vrna_eval_structure_pt_verbose()` instead!

**Global `energy_of_structure` (const char \*`string`, const char \*`structure`, int `verbosity_level`)**

Use `vrna_eval_structure()` or `vrna_eval_structure_verbose()` instead!

**Global `energy_of_structure_pt` (const char \*`string`, short \*`ptable`, short \*`s`, short \*`s1`, int `verbosity_level`)**

Use `vrna_eval_structure_pt()` or `vrna_eval_structure_pt_verbose()` instead!

**File `energy_par.h`**

Use `ViennaRNA/params/default.h` instead

**Global `exp_E_ExtLoop` (int `type`, int `si1`, int `sj1`, `vrna_exp_param_t` \*`P`)**

Use `vrna_exp_E_ext_stem()` instead!

Global **expHairpinEnergy** (int u, int type, short si1, short sj1, const char \*string)

Use [exp\\_E\\_Hairpin\(\)](#) from [loop\\_energies.h](#) instead

Global **expLoopEnergy** (int u1, int u2, int type, int type2, short si1, short sj1, short sp1, short sq1)

Use [exp\\_E\\_IntLoop\(\)](#) from [loop\\_energies.h](#) instead

Global **export\_ali\_bppm** (void)

Usage of this function is discouraged! The new [vrna\\_fold\\_compound\\_t](#) allows direct access to the folding matrices, including the pair probabilities! The pair probability array returned here reflects the one of the latest call to [vrna\\_pf\(\)](#), or any of the old API calls for consensus structure partition function folding.

Global **export\_circfold\_arrays** (int \*Fc\_p, int \*FcH\_p, int \*Fcl\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)

See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

Global **export\_circfold\_arrays\_par** (int \*Fc\_p, int \*FcH\_p, int \*Fcl\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, vrna\_param\_t \*\*P\_p)

See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

Global **export\_co\_bppm** (void)

This function is deprecated and will be removed soon! The base pair probability array is available through the [vrna\\_fold\\_compound\\_t](#) data structure, and its associated [vrna\\_mx\\_pf\\_t](#) member.

Global **export\_cofold\_arrays** (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*indx\_p, char \*\*ptype\_p)

folding matrices now reside within the [vrna\\_fold\\_compound\\_t](#). Thus, this function will only work in conjunction with a prior call to the deprecated functions [cofold\(\)](#) or [cofold\\_par\(\)](#)

Global **export\_cofold\_arrays\_ggq** (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*ggg\_p, int \*\*indx\_p, char \*\*ptype\_p)

folding matrices now reside within the fold compound. Thus, this function will only work in conjunction with a prior call to [cofold\(\)](#) or [cofold\\_par\(\)](#)

Global **export\_fold\_arrays** (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)

See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

Global **export\_fold\_arrays\_par** (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, vrna\_param\_t \*\*P\_p)

See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

File **exterior\_loops.h**

Use [ViennaRNA/loops/external.h](#) instead

File **file\_formats.h**

Use [ViennaRNA/io/file\\_formats.h](#) instead

File **file\_formats\_msa.h**

Use [ViennaRNA/io/file\\_formats\\_msa.h](#) instead

File **file\_utils.h**

Use [ViennaRNA/io/utils.h](#) instead

Global **filecopy** (FILE \*from, FILE \*to)

Use [vrna\\_file\\_copy\(\)](#) instead!

Global **find\_saddle** (const char \*seq, const char \*s1, const char \*s2, int width)

Use [vrna\\_path\\_findpath\\_saddle\(\)](#) instead!

File **findpath.h**

Use [ViennaRNA/landscape/findpath.h](#) instead

Global **fold** (const char \*sequence, char \*structure)

use [vrna\\_fold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

Global **fold\_par** (const char \*sequence, char \*structure, vrna\_param\_t \*parameters, int is\_constrained, int is\_circular)

use [vrna\\_mfe\(\)](#) instead!

Global **free\_alifold\_arrays** (void)

Usage of this function is discouraged! It only affects memory being free'd that was allocated by an old API function before. Release of memory occupied by the newly introduced [vrna\\_fold\\_compound\\_t](#) is handled by [vrna\\_fold\\_compound\\_free\(\)](#)

Global **free\_alipf\_arrays** (void)

Usage of this function is discouraged! This function only free's memory allocated by old API function calls. Memory allocated by any of the new API calls (starting with vrna\_) will be not affected!

Global **free\_arrays** (void)

See [vrna\\_fold\(\)](#), [vrna\\_circfold\(\)](#), or [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

Global **free\_co\_arrays** (void)

This function will only free memory allocated by a prior call of [cofold\(\)](#) or [cofold\\_par\(\)](#). See [vrna\\_mfe\\_dimer\(\)](#) for how to use the new API

Global **free\_co\_pf\_arrays** (void)

This function will be removed for the new API soon! See [vrna\\_pf\\_dimer\(\)](#), [vrna\\_fold\\_compound\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) for an alternative

Global **free\_path** (vrna\_path\_t \*path)

Use [vrna\\_path\\_free\(\)](#) instead!

Global **free\_pf\_arrays** (void)

See [vrna\\_fold\\_compound\\_t](#) and its related functions for how to free memory occupied by the dynamic programming matrices

Global **get\_alipf\_arrays** (short \*\*\*S\_p, short \*\*\*S5\_p, short \*\*\*S3\_p, unsigned short \*\*\*a2s\_p, char \*\*\*Ss\_p, FLT\_OR\_DBL \*\*qb\_p, FLT\_OR\_DBL \*\*qm\_p, FLT\_OR\_DBL \*\*q1k\_p, FLT\_OR\_DBL \*\*qln↵\_p, short \*\*pscore)

It is discouraged to use this function! The new [vrna\\_fold\\_compound\\_t](#) allows direct access to all necessary consensus structure prediction related variables!

Global **get\_boltzmann\_factor\_copy** (vrna\_exp\_param\_t \*parameters)

Use [vrna\\_exp\\_params\\_copy\(\)](#) instead!

Global **get\_boltzmann\_factors** (double temperature, double betaScale, vrna\_md\_t md, double pf\_scale)

Use [vrna\\_exp\\_params\(\)](#) instead!

Global **get\_boltzmann\_factors\_ali** (unsigned int n\_seq, double temperature, double betaScale, vrna\_md\_t md, double pf\_scale)

Use [vrna\\_exp\\_params\\_comparative\(\)](#) instead!

Global **get\_centroid\_struct\_gquad\_pr** (int length, double \*dist)

This function is deprecated and should not be used anymore as it is not threadsafe!

Global **get\_centroid\_struct\_pl** (int length, double \*dist, vrna\_ep\_t \*pl)

This function was renamed to [vrna\\_centroid\\_from\\_plist\(\)](#)

Global **get\_centroid\_struct\_pr** (int length, double \*dist, FLT\_OR\_DBL \*pr)

This function was renamed to [vrna\\_centroid\\_from\\_probs\(\)](#)

Global **get\_concentrations** (double FEAB, double FEAA, double FEBB, double FEA, double FEB, double \*startconc)

{ Use [vrna\\_pf\\_dimer\\_concentrations\(\)](#) instead! }

Global **get\_line** (FILE \*fp)

Use [vrna\\_read\\_line\(\)](#) as a substitute!

Global **get\_mpi** (char \*Alseq[], int n\_seq, int length, int \*mini)

Use [vrna\\_aln\\_mpi\(\)](#) as a replacement

Global **get\_path** (const char \*seq, const char \*s1, const char \*s2, int width)

Use [vrna\\_path\\_findpath\(\)](#) instead!

Global **get\_plist** (vrna\_ep\_t \*pl, int length, double cut\_off)

{ This function is deprecated and will be removed soon!} use [assign\\_plist\\_from\\_pr\(\)](#) instead!

Global **get\_scaled\_alipf\_parameters** (unsigned int n\_seq)

Use [vrna\\_exp\\_params\\_comparative\(\)](#) instead!

Global **get\_scaled\_parameters** (double temperature, vrna\_md\_t md)

Use [vrna\\_params\(\)](#) instead!

Global **get\_scaled\_pf\_parameters** (void)

Use [vrna\\_exp\\_params\(\)](#) instead!

Global **get\_TwoDfold\_variables** (const char \*seq, const char \*structure1, const char \*structure2, int circ)

Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound↵\\_TwoD\(\)](#), [vrna\\_mfe\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

Global **get\_TwoDpfold\_variables** (const char \*seq, const char \*structure1, char \*structure2, int circ)

Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound↵\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

File **hairpin\_loops.h**

Use [ViennaRNA/loops/hairpin.h](#) instead

Global **HairpinE** (int size, int type, int si1, int sj1, const char \*string)

{This function is deprecated and will be removed soon. Use [E\\_Hairpin\(\)](#) instead!}

Global **hamming** (const char \*s1, const char \*s2)

Use [vrna\\_hamming\\_distance\(\)](#) instead!

Global **hamming\_bound** (const char \*s1, const char \*s2, int n)

Use [vrna\\_hamming\\_distance\\_bound\(\)](#) instead!

Global **iindx**

Do not use this variable anymore!

Global **init\_co\_pf\_fold** (int length)

{ This function is deprecated and will be removed soon!}

Global **init\_pf\_fold** (int length)

This function is obsolete and will be removed soon!

Global **init\_rand** (void)

Use [vrna\\_init\\_rand\(\)](#) instead!

Global **initialize\_cofold** (int length)

{This function is obsolete and will be removed soon!}

Global **initialize\_fold** (int length)

See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

Global **int\_urn** (int from, int to)

Use [vrna\\_int\\_urn\(\)](#) instead!

File **interior\_loops.h**

Use [ViennaRNA/loops/internal.h](#) instead

Global **Lfold** (const char \*string, const char \*structure, int maxdist)

Use [vrna\\_mfe\\_window\(\)](#) instead!

Global **Lfoldz** (const char \*string, const char \*structure, int maxdist, int zsc, double min\_z)

Use [vrna\\_mfe\\_window\\_zscore\(\)](#) instead!



**File [loop\\_energies.h](#)**

Use [ViennaRNA/loops/all.h](#) instead

**Global [loop\\_energy](#) (short \*ptable, short \*s, short \*s1, int i)**

Use [vrna\\_eval\\_loop\\_pt\(\)](#) instead!

**Global [LoopEnergy](#) (int n1, int n2, int type, int type\_2, int si1, int sj1, int sp1, int sq1)**

{This function is deprecated and will be removed soon. Use [E\\_IntLoop\(\)](#) instead!}

**Global [Make\\_bp\\_profile](#) (int length)**

This function is deprecated and will be removed soon! See [Make\\_bp\\_profile\\_bppm\(\)](#) for a replacement

**Global [make\\_pair\\_table](#) (const char \*structure)**

Use [vrna\\_ptable\(\)](#) instead

**Global [make\\_pair\\_table\\_snoop](#) (const char \*structure)**

Use [vrna\\_pt\\_snoop\\_get\(\)](#) instead!

**Global [make\\_referenceBP\\_array](#) (short \*reference\_pt, unsigned int turn)**

Use [vrna\\_refBPcnt\\_matrix\(\)](#) instead

**Global [MEA](#) (plist \*p, char \*structure, double gamma)**

Use [vrna\\_MEA\(\)](#) or [vrna\\_MEA\\_from\\_plist\(\)](#) instead!

**Global [mean\\_bp\\_dist](#) (int length)**

This function is not threadsafe and should not be used anymore. Use [mean\\_bp\\_distance\(\)](#) instead!

**Global [mean\\_bp\\_distance](#) (int length)**

Use [vrna\\_mean\\_bp\\_distance\(\)](#) or [vrna\\_mean\\_bp\\_distance\\_pr\(\)](#) instead!

**Global [mean\\_bp\\_distance\\_pr](#) (int length, FLT\_OR\_DBL \*pr)**

Use [vrna\\_mean\\_bp\\_distance\(\)](#) or [vrna\\_mean\\_bp\\_distance\\_pr\(\)](#) instead!

**File [multibranch\\_loops.h](#)**

Use [ViennaRNA/loops/multibranch.h](#) instead

**File [naview.h](#)**

Use [ViennaRNA/plotting/naview/naview.h](#) instead

**Global [nc\\_fact](#)**

See [vrna\\_md\\_t.nc\\_fact](#), and [vrna\\_mfe\(\)](#) to avoid using global variables

**File [neighbor.h](#)**

Use [ViennaRNA/landscape/neighbor.h](#) instead

**Global [nerror](#) (const char message[])**

Use [vrna\\_message\\_error\(\)](#) instead!

**Global [pack\\_structure](#) (const char \*struc)**

Use [vrna\\_db\\_pack\(\)](#) as a replacement

**Global [PAIR](#)**

Use [vrna\\_basepair\\_t](#) instead!

**Global [pair\\_info](#)**

Use [vrna\\_pinfo\\_t](#) instead!

**File [params.h](#)**

Use [ViennaRNA/params/basic.h](#) instead

**Global [paramT](#)**

Use [vrna\\_param\\_t](#) instead!

**Global [parenthesis\\_structure](#) (char \*structure, vrna\_bp\_stack\_t \*bp, int length)**

use [vrna\\_parenthesis\\_structure\(\)](#) instead

Global **parenthesis\_zuker** (char \*structure, vrna\_bp\_stack\_t \*bp, int length)

use vrna\_parenthesis\_zuker instead

Global **path\_t**

Use vrna\_path\_t instead!

Global **pbacktrack\_circ** (char \*sequence)

Use vrna\_pbacktrack() instead.

Global **pf\_circ\_fold** (const char \*sequence, char \*structure)

Use vrna\_pf() instead!

Global **pf\_fold\_par** (const char \*sequence, char \*structure, vrna\_exp\_param\_t \*parameters, int calculate↵\_bppm, int is\_constrained, int is\_circular)

Use vrna\_pf() instead

Global **pf\_paramT**

Use vrna\_exp\_param\_t instead!

Global **plist**

Use vrna\_ep\_t or vrna\_elem\_prob\_s instead!

File **plot\_aln.h**

Use ViennaRNA/plotting/alignments.h instead

File **plot\_layouts.h**

Use ViennaRNA/plotting/layouts.h instead

File **plot\_structure.h**

Use ViennaRNA/plotting/structures.h instead

File **plot\_utils.h**

Use ViennaRNA/plotting/utils.h instead

Global **pr**

Do not use this variable anymore!

Global **print\_tty\_constraint** (unsigned int option)

Use vrna\_message\_constraints() instead!

Global **print\_tty\_constraint\_full** (void)

Use vrna\_message\_constraint\_options\_all() instead!

Global **print\_tty\_input\_seq** (void)

Use vrna\_message\_input\_seq\_simple() instead!

Global **print\_tty\_input\_seq\_str** (const char \*s)

Use vrna\_message\_input\_seq() instead!

Global **PS\_color\_aln** (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])

Use vrna\_file\_PS\_aln() instead!

File **PS\_dot.h**

Use ViennaRNA/plotting/probabilities.h instead

Global **PS\_dot\_plot** (char \*string, char \*file)

This function is deprecated and will be removed soon! Use PS\_dot\_plot\_list() instead!

Global **PS\_rna\_plot** (char \*string, char \*structure, char \*file)

Use vrna\_file\_PS\_rnaplot() instead!

Global **PS\_rna\_plot\_a** (char \*string, char \*structure, char \*file, char \*pre, char \*post)

Use vrna\_file\_PS\_rnaplot\_a() instead!

Global **PS\_rna\_plot\_a\_gquad** (char \*string, char \*structure, char \*ssfile, char \*pre, char \*post)

Use vrna\_file\_PS\_rnaplot\_a() instead!

Global **random\_string** (int l, const char symbols[])

Use [vrna\\_random\\_string\(\)](#) instead!

File **read\_epars.h**

Use [ViennaRNA/params/io.h](#) instead

Global **read\_parameter\_file** (const char fname[])

Use [vrna\\_params\\_load\(\)](#) instead!

Global **read\_record** (char \*\*header, char \*\*sequence, char \*\*\*rest, unsigned int options)

This function is deprecated! Use [vrna\\_file\\_fasta\\_read\\_record\(\)](#) as a replacment.

Global **scale\_parameters** (void)

Use [vrna\\_params\(\)](#) instead!

Global **sect**

Use [vrna\\_sect\\_t](#) instead!

Global **set\_model\_details** (vrna\_md\_t \*md)

This function will vanish as soon as backward compatibility of RNAlib is dropped (expected in version 3). Use [vrna\\_md\\_set\\_default\(\)](#) instead!

Global **simple\_circplot\_coordinates** (short \*pair\_table, float \*x, float \*y)

Consider switching to [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#) instead!

Global **simple\_xy\_coordinates** (short \*pair\_table, float \*X, float \*Y)

Consider switching to [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#) instead!

Global **SOLUTION**

Use [vrna\\_subopt\\_solution\\_t](#) instead!

Global **space** (unsigned size)

Use [vrna\\_alloc\(\)](#) instead!

Global **st\_back**

set the *uniq\_ML* flag in [vrna\\_md\\_t](#) before passing it to [vrna\\_fold\\_compound\(\)](#).

Global **stackProb** (double cutoff)

Use [vrna\\_stack\\_prob\(\)](#) instead!

Global **str\_DNA2RNA** (char \*sequence)

Use [vrna\\_seq\\_toRNA\(\)](#) instead!

Global **str\_uppercase** (char \*sequence)

Use [vrna\\_seq\\_toupper\(\)](#) instead!

File **stream\_output.h**

Use [ViennaRNA/datastructures/stream\\_output.h](#) instead

File **string\_utils.h**

Use [ViennaRNA/utls/strings.h](#) instead

File **structure\_utils.h**

Use [ViennaRNA/utls/structures.h](#) instead

File **svm\_utils.h**

Use [ViennaRNA/utls/svm.h](#) instead

Global **temperature**

Use [vrna\\_md\\_defaults\\_temperature\(\)](#), and [vrna\\_md\\_defaults\\_temperature\\_get\(\)](#) to change, and read the global default temperature settings

Global **time\_stamp** (void)

Use [vrna\\_time\\_stamp\(\)](#) instead!

**Global `TwoDfold_backtrack_f5` (unsigned int j, int k, int l, `TwoDfold_vars` \*vars)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound↵_TwoD()`, `vrna_mfe_TwoD()`, `vrna_backtrack5_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `TwoDfold_vars`**

This data structure will be removed from the library soon! Use `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `TwoDfoldList` (`TwoDfold_vars` \*vars, int distance1, int distance2)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound↵_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `TwoDpfold_pbacktrack` (`TwoDpfold_vars` \*vars, int d1, int d2)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound↵_TwoD()`, `vrna_pf_TwoD()`, `vrna_pbacktrack_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `TwoDpfold_pbacktrack5` (`TwoDpfold_vars` \*vars, int d1, int d2, unsigned int length)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound↵_TwoD()`, `vrna_pf_TwoD()`, `vrna_pbacktrack5_TwoD()`, and `vrna_fold_compound_free()` instead!

**Class `TwoDpfold_vars`**

This data structure will be removed from the library soon! Use `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_pf_TwoD()`, and `vrna_fold_compound_free()` instead!

**Global `TwoDpfoldList` (`TwoDpfold_vars` \*vars, int maxDistance1, int maxDistance2)**

Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound↵_TwoD()`, `vrna_pf_TwoD()`, and `vrna_fold_compound_free()` instead!

**File `units.h`**

Use `ViennaRNA/utills/units.h` instead

**Global `unpack_structure` (const char \*packed)**

Use `vrna_db_unpack()` as a replacement

**Global `update_alifold_params` (void)**

Usage of this function is discouraged! The new API uses `vrna_fold_compound_t` to lump all folding related necessities together, including the energy parameters. Use `vrna_update_fold_params()` to update the energy parameters within a `vrna_fold_compound_t`.

**Global `update_co_pf_params` (int length)**

Use `vrna_exp_params_subst()` instead!

**Global `update_co_pf_params_par` (int length, `vrna_exp_param_t` \*parameters)**

Use `vrna_exp_params_subst()` instead!

**Global `update_cofold_params` (void)**

See `vrna_params_subst()` for an alternative using the new API

**Global `update_cofold_params_par` (`vrna_param_t` \*parameters)**

See `vrna_params_subst()` for an alternative using the new API

**Global `update_fold_params` (void)**

For non-default model settings use the new API with `vrna_params_subst()` and `vrna_mfe()` instead!

**Global `update_fold_params_par` (`vrna_param_t` \*parameters)**

For non-default model settings use the new API with `vrna_params_subst()` and `vrna_mfe()` instead!

**Global `update_pf_params` (int length)**

Use `vrna_exp_params_subst()` instead

**Global `update_pf_params_par` (int length, `vrna_exp_param_t` \*parameters)**

Use `vrna_exp_params_subst()` instead

**Global `urn` (void)**

Use `vrna_urn()` instead!

**File `utils.h`**

Use [ViennaRNA/utils/basic.h](#) instead

Use [ViennaRNA/utils/basic.h](#) instead

**Global `vrna_cofold` (`const char *sequence, char *structure`)**

This function is obsolete since [vrna\\_mfe\(\)](#)/[vrna\\_fold\(\)](#) can handle complexes multiple sequences since v2.5.0. Use [vrna\\_mfe\(\)](#)/[vrna\\_fold\(\)](#) for connected component MFE instead and compute MFEs of unconnected states separately.

**Global `VRNA_CONSTRAINT_FILE`**

Use 0 instead!

**Global `VRNA_CONSTRAINT_MULTILINE`**

see [vrna\\_extract\\_record\\_rest\\_structure\(\)](#)

**Global `VRNA_CONSTRAINT_NO_HEADER`**

This mode is not supported anymore!

**Global `VRNA_CONSTRAINT_SOFT_MFE`**

This flag has no meaning anymore, since constraints are now always stored!

**Global `VRNA_CONSTRAINT_SOFT_PF`**

Use [VRNA\\_OPTION\\_PF](#) instead!

**Global `vrna_exp_param_s::id`**

This attribute will be removed in version 3

**Global `vrna_extract_record_rest_constraint` (`char **cstruc, const char **lines, unsigned int option`)**

Use [vrna\\_extract\\_record\\_rest\\_structure\(\)](#) instead!

**Global `vrna_fc_s::pscore_pf_compat`**

This attribute will vanish in the future!

**Global `vrna_fc_s::ptype_pf_compat`**

This attribute will vanish in the future! It's meant for backward compatibility only!

**Global `vrna_mfe_dimer` (`vrna_fold_compound_t *vc, char *structure`)**

This function is obsolete since [vrna\\_mfe\(\)](#) can handle complexes multiple sequences since v2.5.0. Use [vrna\\_mfe\(\)](#) for connected component MFE instead and compute MFEs of unconnected states separately.

**File `walk.h`**

Use [ViennaRNA/landscape/walk.h](#) instead

**Global `warn_user` (`const char message[]`)**

Use [vrna\\_message\\_warning\(\)](#) instead!

**Global `write_parameter_file` (`const char fname[]`)**

Use [vrna\\_params\\_save\(\)](#) instead!

**Global `xrealloc` (`void *p, unsigned size`)**

Use [vrna\\_realloc\(\)](#) instead!

**Global `zukersubopt` (`const char *string`)**

use [vrna\\_zukersubopt\(\)](#) instead

**Global `zukersubopt_par` (`const char *string, vrna_param_t *parameters`)**

use [vrna\\_zukersubopt\(\)](#) instead



## Chapter 12

# Bug List

### Module [domains\\_up](#)

Although the additional production rule(s) for unstructured domains as described in [Unstructured Domains](#) are always treated as 'segments possibly bound to one or more ligands', the current implementation requires that at least one ligand is bound. The default implementation already takes care of the required changes, however, upon using callback functions other than the default ones, one has to take care of this fact. Please also note, that this behavior might change in one of the next releases, such that the decomposition schemes as shown above comply with the actual implementation.

### Global [VRNA\\_PROBS\\_WINDOW\\_STACKP](#)

Currently, this flag is a placeholder doing nothing as the corresponding implementation for stack probability computation is missing.

### Global [vrna\\_subopt\\_zuker](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)

Due to resizing, any pre-existing constraints will be lost!





# Chapter 13

## Module Index

### 13.1 The RNALib API

Our library is grouped into several modules, each addressing different aspects of RNA secondary structure related problems. You can find an overview of the different groups below.

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## Chapter 14

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## Chapter 15

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# Chapter 16

## Module Documentation

### 16.1 Free Energy Evaluation

Functions and variables related to free energy evaluation of sequence/structure pairs.

#### 16.1.1 Detailed Description

Functions and variables related to free energy evaluation of sequence/structure pairs.

Several different functions to evaluate the free energy of a particular secondary structure under a particular set of parameters and the Nearest Neighbor Energy model are available. For most of them, two different forms of representations for the secondary structure may be used:

- The Dot-Bracket string
- A pair table representation

Furthermore, the evaluation functions are divided into `basic` and `simplified` variants, where `basic` functions require the use of a `vrna_fold_compound_t` data structure holding the sequence string, and model configuration (settings and parameters). The `simplified` functions, on the other hand, provide often used default model settings that may be called directly with only sequence and structure data.

Finally, `verbose` options exist for some functions that allow one to print the (individual) free energy contributions to some `FILE` stream. Collaboration diagram for Free Energy Evaluation:

#### Modules

- [Energy Evaluation for Individual Loops](#)  
*Functions to evaluate the free energy of particular types of loops.*
- [Energy Evaluation for Atomic Moves](#)  
*Functions to evaluate the free energy change of a structure after application of (a set of) atomic moves.*
- [Deprecated Interface for Free Energy Evaluation](#)  
*Deprecated Energy Evaluation functions.*

#### Files

- file [eval.h](#)  
*Functions and variables related to energy evaluation of sequence/structure pairs.*
- file [all.h](#)  
*Energy evaluation for MFE and partition function calculations.*
- file [external.h](#)  
*Energy evaluation of exterior loops for MFE and partition function calculations.*
- file [hairpin.h](#)  
*Energy evaluation of hairpin loops for MFE and partition function calculations.*
- file [internal.h](#)

*Energy evaluation of interior loops for MFE and partition function calculations.*

- file [multibranch.h](#)

*Energy evaluation of multibranch loops for MFE and partition function calculations.*

## Macros

- `#define VRNA_VERBOSEITY_QUIET -1`  
*Quiet level verbosity setting.*
- `#define VRNA_VERBOSEITY_DEFAULT 1`  
*Default level verbosity setting.*

## Basic Energy Evaluation Interface with Dot-Bracket Structure String

- float [vrna\\_eval\\_structure](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Calculate the free energy of an already folded RNA.*
- float [vrna\\_eval\\_covar\\_structure](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Calculate the pseudo energy derived by the covariance scores of a set of aligned sequences.*
- float [vrna\\_eval\\_structure\\_verbose](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions on a per-loop base.*
- float [vrna\\_eval\\_structure\\_v](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions on a per-loop base.*
- float [vrna\\_eval\\_structure\\_cstr](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, int verbosity\_level, [vrna\\_cstr\\_t](#) output\_stream)

## Basic Energy Evaluation Interface with Structure Pair Table

- int [vrna\\_eval\\_structure\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_verbose](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt, FILE \*file)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_v](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA.*

## Simplified Energy Evaluation with Sequence and Dot-Bracket Strings

- float [vrna\\_eval\\_structure\\_simple](#) (const char \*string, const char \*structure)  
*Calculate the free energy of an already folded RNA.*
- float [vrna\\_eval\\_circ\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the sequence is circular.*
- float [vrna\\_eval\\_gquad\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_circ\\_gquad\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the sequence is circular and the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_structure\\_simple\\_verbose](#) (const char \*string, const char \*structure, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions per loop.*
- float [vrna\\_eval\\_structure\\_simple\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate free energy of a sequence/structure pair, assume sequence to be circular and print contributions per loop.*
- float [vrna\\_eval\\_gquad\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate free energy of a sequence/structure pair, allow for G-Quadruplexes in the structure and print contributions per loop.*

- float [vrna\\_eval\\_circ\\_gquad\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)

*Evaluate free energy of a sequence/structure pair, assume sequence to be circular, allow for G-Quadruplexes in the structure, and print contributions per loop.*

## Simplified Energy Evaluation with Sequence Alignments and Consensus Structure Dot-Bracket String

- float [vrna\\_eval\\_consensus\\_structure\\_simple](#) (const char \*\*alignment, const char \*structure)  
*Calculate the free energy of an already folded RNA sequence alignment.*
- float [vrna\\_eval\\_circ\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequences are circular.*
- float [vrna\\_eval\\_gquad\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequence is circular and the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_consensus\\_structure\\_simple\\_verbose](#) (const char \*\*alignment, const char \*structure, FILE \*file)  
*Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop.*
- float [vrna\\_eval\\_consensus\\_structure\\_simple\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_consensus\\_structure\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences and print contributions per loop.*
- float [vrna\\_eval\\_gquad\\_consensus\\_structure\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate the free energy of a consensus structure for an RNA sequence alignment, allow for annotated G-Quadruplexes in the structure and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences, allow for annotated G-Quadruplexes in the structure and print contributions per loop.*

## Simplified Energy Evaluation with Sequence String and Structure Pair Table

- int [vrna\\_eval\\_structure\\_pt\\_simple](#) (const char \*string, const short \*pt)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_simple\\_verbose](#) (const char \*string, const short \*pt, FILE \*file)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_simple\\_v](#) (const char \*string, const short \*pt, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA.*

## Simplified Energy Evaluation with Sequence Alignment and Consensus Structure Pair Table

- int [vrna\\_eval\\_consensus\\_structure\\_pt\\_simple](#) (const char \*\*alignment, const short \*pt)  
*Evaluate the Free Energy of a Consensus Secondary Structure given a Sequence Alignment.*
- int [vrna\\_eval\\_consensus\\_structure\\_pt\\_simple\\_verbose](#) (const char \*\*alignment, const short \*pt, FILE \*file)
- int [vrna\\_eval\\_consensus\\_structure\\_pt\\_simple\\_v](#) (const char \*\*alignment, const short \*pt, int verbosity\_level, FILE \*file)

## 16.1.2 Function Documentation

### 16.1.2.1 `vrna_eval_structure()`

```
float vrna_eval_structure (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function allows for energy evaluation of a given pair of structure and sequence (alignment). Model details, energy parameters, and possibly soft constraints are used as provided via the parameter 'fc'. The `vrna_fold_compound_t` does not need to contain any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_EVAL_ONLY);
```

#### Note

Accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE` and `VRNA_FC_TYPE_COMPARATIVE`

#### See also

`vrna_eval_structure_pt()`, `vrna_eval_structure_verbose()`, `vrna_eval_structure_pt_verbose()`, `vrna_fold_compound()`, `vrna_fold_compound_comparative()`, `vrna_eval_covar_structure()`

#### Parameters

|                  |                                                                                        |
|------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>        | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>structure</i> | Secondary structure in dot-bracket notation                                            |

#### Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_structure()` to objects of type `fold_compound`

### 16.1.2.2 `vrna_eval_covar_structure()`

```
float vrna_eval_covar_structure (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Calculate the pseudo energy derived by the covariance scores of a set of aligned sequences.

Consensus structure prediction is driven by covariance scores of base pairs in rows of the provided alignment. This function allows one to retrieve the total amount of this covariance pseudo energy scores. The `vrna_fold_compound_t` does not need to contain any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound_comparative(alignment, NULL, VRNA_OPTION_EVAL_ONLY);
```

#### Note

Accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_COMPARATIVE` only!

#### See also

`vrna_fold_compound_comparative()`, `vrna_eval_structure()`



## Parameters

|                  |                                                                                        |
|------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>        | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>structure</i> | Secondary (consensus) structure in dot-bracket notation                                |

## Returns

The covariance pseudo energy score of the input structure given the input sequence alignment in kcal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_covar_structure()` to objects of type `fold_compound`

16.1.2.3 `vrna_eval_structure_verbose()`

```
float vrna_eval_structure_verbose (
    vrna_fold_compound_t * fc,
    const char * structure,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA and print contributions on a per-loop base.

This function is a simplified version of `vrna_eval_structure_v()` that uses the *default* verbosity level.

## See also

`vrna_eval_structure_pt()`, `vrna_eval_structure_verbose()`, `vrna_eval_structure_pt_verbose()`,

## Parameters

|                  |                                                                                        |
|------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>        | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>structure</i> | Secondary structure in dot-bracket notation                                            |
| <i>file</i>      | A file handle where this function should print to (may be NULL).                       |

## Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_structure_verbose()` to objects of type `fold_compound`

16.1.2.4 `vrna_eval_structure_v()`

```
float vrna_eval_structure_v (
    vrna_fold_compound_t * fc,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA and print contributions on a per-loop base.

This function allows for detailed energy evaluation of a given sequence/structure pair. In contrast to `vrna_eval_structure()` this function prints detailed energy contributions based on individual loops to a file handle. If NULL is passed as file handle, this function defaults to print to stdout. Any positive `verbosity_level` activates potential warning message of the energy evaluating functions, while values  $\geq 1$  allow for detailed control of what data is printed. A negative parameter `verbosity_level` turns off printing all together.

Model details, energy parameters, and possibly soft constraints are used as provided via the parameter 'fc'. The `fold_compound` does not need to contain any DP matrices, but all the most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_EVAL_ONLY);
```

See also

[vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#),

#### Parameters

|                        |                                                                                        |
|------------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>              | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>structure</i>       | Secondary structure in dot-bracket notation                                            |
| <i>verbosity_level</i> | The level of verbosity of this function                                                |
| <i>file</i>            | A file handle where this function should print to (may be NULL).                       |

#### Returns

The free energy of the input structure given the input sequence in kcal/mol

#### 16.1.2.5 vrna\_eval\_structure\_pt()

```
int vrna_eval_structure_pt (
    vrna_fold_compound_t * fc,
    const short * pt )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function allows for energy evaluation of a given sequence/structure pair where the structure is provided in `pair_table` format as obtained from [vrna\\_ptable\(\)](#). Model details, energy parameters, and possibly soft constraints are used as provided via the parameter 'fc'. The `fold_compound` does not need to contain any DP matrices, but all the most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_EVAL_ONLY);
```

See also

[vrna\\_ptable\(\)](#), [vrna\\_eval\\_structure\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#)

#### Parameters

|           |                                                                                        |
|-----------|----------------------------------------------------------------------------------------|
| <i>fc</i> | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>pt</i> | Secondary structure as <code>pair_table</code>                                         |

#### Returns

The free energy of the input structure given the input sequence in 10cal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_structure_pt()` to objects of type `fold_compound`

#### 16.1.2.6 vrna\_eval\_structure\_pt\_verbose()

```
int vrna_eval_structure_pt_verbose (
    vrna_fold_compound_t * fc,
    const short * pt,
    FILE * file )
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function is a simplified version of `vrna_eval_structure_simple_v()` that uses the *default* verbosity level.

See also

`vrna_eval_structure_pt_v()`, `vrna_ptable()`, `vrna_eval_structure_pt()`, `vrna_eval_structure_verbose()`

#### Parameters

|             |                                                                                        |
|-------------|----------------------------------------------------------------------------------------|
| <i>fc</i>   | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>pt</i>   | Secondary structure as <code>pair_table</code>                                         |
| <i>file</i> | A file handle where this function should print to (may be NULL).                       |

#### Returns

The free energy of the input structure given the input sequence in 10cal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_structure_pt_verbose()` to objects of type `fold_compound`

#### 16.1.2.7 vrna\_eval\_structure\_pt\_v()

```
int vrna_eval_structure_pt_v (
    vrna_fold_compound_t * fc,
    const short * pt,
    int verbosity_level,
    FILE * file )
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function allows for energy evaluation of a given sequence/structure pair where the structure is provided in `pair_table` format as obtained from `vrna_ptable()`. Model details, energy parameters, and possibly soft constraints are used as provided via the parameter 'fc'. The `fold_compound` does not need to contain any DP matrices, but all the most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_EVAL_ONLY);
```

In contrast to `vrna_eval_structure_pt()` this function prints detailed energy contributions based on individual loops to a file handle. If NULL is passed as file handle, this function defaults to print to stdout. Any positive `verbosity_level` activates potential warning message of the energy evaluating functions, while values  $\geq 1$  allow for detailed control of what data is printed. A negative parameter `verbosity_level` turns off printing all together.

See also

`vrna_ptable()`, `vrna_eval_structure_pt()`, `vrna_eval_structure_verbose()`

#### Parameters

|                        |                                                                                        |
|------------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>              | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>pt</i>              | Secondary structure as <code>pair_table</code>                                         |
| <i>verbosity_level</i> | The level of verbosity of this function                                                |
| <i>file</i>            | A file handle where this function should print to (may be NULL).                       |

#### Returns

The free energy of the input structure given the input sequence in 10cal/mol

### 16.1.2.8 `vrna_eval_structure_simple()`

```
int vrna_eval_structure_simple (
    const char * string,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function allows for energy evaluation of a given sequence/structure pair. In contrast to `vrna_eval_structure()` this function assumes default model details and default energy parameters in order to evaluate the free energy of the secondary structure. Therefore, it serves as a simple interface function for energy evaluation for situations where no changes on the energy model are required.

See also

[vrna\\_eval\\_structure\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#),

#### Parameters

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence in uppercase letters           |
| <i>structure</i> | Secondary structure in dot-bracket notation |

#### Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** In the target scripting language, this function serves as a wrapper for `vrna_eval_structure_simple_v()` and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

### 16.1.2.9 `vrna_eval_circ_structure()`

```
int vrna_eval_circ_structure (
    const char * string,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a sequence/structure pair where the sequence is circular.

See also

[vrna\\_eval\\_structure\\_simple\(\)](#), [vrna\\_eval\\_gquad\\_structure\(\)](#), [vrna\\_eval\\_circ\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_circ\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

#### Parameters

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence in uppercase letters           |
| <i>structure</i> | Secondary structure in dot-bracket notation |

#### Returns

The free energy of the structure given the circular input sequence in kcal/mol

**SWIG Wrapper Notes** In the target scripting language, this function serves as a wrapper for `vrna_eval_circ_structure_v()` and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to `VRNA_VERBOSITY_QUIET` and `NULL`, respectively.

**16.1.2.10 vrna\_eval\_gquad\_structure()**

```
int vrna_eval_gquad_structure (
    const char * string,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a sequence/structure pair where the structure may contain G-Quadruplexes.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots ('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++...++..++
```

See also

[vrna\\_eval\\_structure\\_simple\(\)](#), [vrna\\_eval\\_circ\\_structure\(\)](#), [vrna\\_eval\\_gquad\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_gquad\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence in uppercase letters           |
| <i>structure</i> | Secondary structure in dot-bracket notation |

**Returns**

The free energy of the structure including contributions of G-quadruplexes in kcal/mol

**SWIG Wrapper Notes** In the target scripting language, this function serves as a wrapper for [vrna\\_eval\\_gquad\\_structure\\_v\(\)](#) and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

**16.1.2.11 vrna\_eval\_circ\_gquad\_structure()**

```
int vrna_eval_circ_gquad_structure (
    const char * string,
    const char * structure )
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a sequence/structure pair where the sequence is circular and the structure may contain G-Quadruplexes.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots ('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++...++..++
```

See also

[vrna\\_eval\\_structure\\_simple\(\)](#), [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_circ\\_gquad\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence in uppercase letters           |
| <i>structure</i> | Secondary structure in dot-bracket notation |

**Returns**

The free energy of the structure including contributions of G-quadruplexes in kcal/mol

**SWIG Wrapper Notes** In the target scripting language, this function serves as a wrapper for [vrna\\_eval\\_circ\\_gquad\\_structure\\_v\(\)](#) and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

**16.1.2.12 vrna\_eval\_structure\_simple\_verbose()**

```
int vrna_eval_structure_simple_verbose (
    const char * string,
    const char * structure,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA and print contributions per loop.

This function is a simplified version of [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) that uses the *default* verbosity level.

**See also**

[vrna\\_eval\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_verbose\\_pt\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#)

**Parameters**

|                  |                                                                  |
|------------------|------------------------------------------------------------------|
| <i>string</i>    | RNA sequence in uppercase letters                                |
| <i>structure</i> | Secondary structure in dot-bracket notation                      |
| <i>file</i>      | A file handle where this function should print to (may be NULL). |

**Returns**

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is not available. Use [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) instead!

**16.1.2.13 vrna\_eval\_structure\_simple\_v()**

```
int vrna_eval_structure_simple_v (
    const char * string,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA and print contributions per loop.

This function allows for detailed energy evaluation of a given sequence/structure pair. In contrast to [vrna\\_eval\\_structure\(\)](#) this function prints detailed energy contributions based on individual loops to a file handle. If NULL is passed as file handle, this function defaults to print to stdout. Any positive `verbosity_level` activates potential warning message of the energy evaluating functions, while values  $\geq 1$  allow for detailed control of what data is printed. A negative parameter `verbosity_level` turns off printing all together.

In contrast to [vrna\\_eval\\_structure\\_verbose\(\)](#) this function assumes default model details and default energy parameters in order to evaluate the free energy of the secondary structure. Therefore, it serves as a simple interface function for energy evaluation for situations where no changes on the energy model are required.

**See also**

[vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#),

## Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                |
| <i>structure</i>       | Secondary structure in dot-bracket notation                      |
| <i>verbosity_level</i> | The level of verbosity of this function                          |
| <i>file</i>            | A file handle where this function should print to (may be NULL). |

## Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_structure\\_simple\(\)](#). The last two arguments for this function are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and `NULL`, respectively.

**16.1.2.14 vrna\_eval\_circ\_structure\_v()**

```
int vrna_eval_circ_structure_v (  
    const char * string,  
    const char * structure,  
    int verbosity_level,  
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate free energy of a sequence/structure pair, assume sequence to be circular and print contributions per loop. This function is the same as [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) but assumes the input sequence to be circularized.

## See also

[vrna\\_eval\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_circ\\_structure\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#)

## Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                |
| <i>structure</i>       | Secondary structure in dot-bracket notation                      |
| <i>verbosity_level</i> | The level of verbosity of this function                          |
| <i>file</i>            | A file handle where this function should print to (may be NULL). |

## Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_structure\(\)](#). The last two arguments for this function are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and `NULL`, respectively.

**16.1.2.15 vrna\_eval\_gquad\_structure\_v()**

```
int vrna_eval_gquad_structure_v (  
    const char * string,  
    const char * structure,  
    int verbosity_level,  
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate free energy of a sequence/structure pair, allow for G-Quadruplexes in the structure and print contributions per loop.

This function is the same as [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) but allows for annotated G-Quadruplexes in the dot-bracket structure input.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++..++..++
```

See also

[vrna\\_eval\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_gquad\\_structure\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#)

#### Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                |
| <i>structure</i>       | Secondary structure in dot-bracket notation                      |
| <i>verbosity_level</i> | The level of verbosity of this function                          |
| <i>file</i>            | A file handle where this function should print to (may be NULL). |

#### Returns

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_gquad\\_structure\(\)](#). The last two arguments for this function are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

#### 16.1.2.16 vrna\_eval\_circ\_gquad\_structure\_v()

```
int vrna_eval_circ_gquad_structure_v (
    const char * string,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate free energy of a sequence/structure pair, assume sequence to be circular, allow for G-Quadruplexes in the structure, and print contributions per loop.

This function is the same as [vrna\\_eval\\_structure\\_simple\\_v\(\)](#) but assumes the input sequence to be circular and allows for annotated G-Quadruplexes in the dot-bracket structure input.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++..++..++
```

#### Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                |
| <i>structure</i>       | Secondary structure in dot-bracket notation                      |
| <i>verbosity_level</i> | The level of verbosity of this function                          |
| <i>file</i>            | A file handle where this function should print to (may be NULL). |



**Returns**

The free energy of the input structure given the input sequence in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_gquad\\_structure\(\)](#). The last two arguments for this function are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and `NULL`, respectively.

**16.1.2.17 vrna\_eval\_consensus\_structure\_simple()**

```
int vrna_eval_consensus_structure_simple (
    const char ** alignment,
    const char * structure )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA sequence alignment.

This function allows for energy evaluation for a given multiple sequence alignment and consensus structure pair. In contrast to [vrna\\_eval\\_structure\(\)](#) this function assumes default model details and default energy parameters in order to evaluate the free energy of the secondary structure. Therefore, it serves as a simple interface function for energy evaluation for situations where no changes on the energy model are required.

**Note**

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

**See also**

[vrna\\_eval\\_covar\\_structure\(\)](#), [vrna\\_eval\\_structure\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#)

**Parameters**

|                  |                                                                             |
|------------------|-----------------------------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters and hyphen ('-') to denote gaps |
| <i>structure</i> | Consensus Secondary structure in dot-bracket notation                       |

**Returns**

The free energy of the consensus structure given the input alignment in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_structure\\_simple\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**16.1.2.18 vrna\_eval\_circ\_consensus\_structure()**

```
int vrna_eval_circ_consensus_structure (
    const char ** alignment,
    const char * structure )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequences are circular.

**Note**

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

**See also**

[vrna\\_eval\\_covar\\_structure\(\)](#), [vrna\\_eval\\_consensus\\_structure\\_simple\(\)](#), [vrna\\_eval\\_gquad\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_circ\\_structure\(\)](#), [vrna\\_eval\\_circ\\_consensus\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                  |                                                       |
|------------------|-------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters           |
| <i>structure</i> | Consensus secondary structure in dot-bracket notation |

**Returns**

The free energy of the consensus structure given the circular input sequence in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**16.1.2.19 vrna\_eval\_gquad\_consensus\_structure()**

```
int vrna_eval_gquad_consensus_structure (
    const char ** alignment,
    const char * structure )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the structure may contain G-Quadruplexes.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++...++..++
```

**Note**

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

**See also**

[vrna\\_eval\\_covar\\_structure\(\)](#), [vrna\\_eval\\_consensus\\_structure\\_simple\(\)](#), [vrna\\_eval\\_circ\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_gquad\\_structure\(\)](#), [vrna\\_eval\\_gquad\\_consensus\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                  |                                                       |
|------------------|-------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters           |
| <i>structure</i> | Consensus secondary structure in dot-bracket notation |

**Returns**

The free energy of the consensus structure including contributions of G-quadruplexes in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_gquad\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**16.1.2.20 vrna\_eval\_circ\_gquad\_consensus\_structure()**

```
int vrna_eval_circ_gquad_consensus_structure (
```

```

    const char ** alignment,
    const char * structure )
#include <ViennaRNA/eval.h>

```

Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequence is circular and the structure may contain G-Quadruplexes.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```

GGAAGGAAAGGAGG
++..++.....++..++

```

#### Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

#### See also

[vrna\\_eval\\_covar\\_structure\(\)](#), [vrna\\_eval\\_consensus\\_structure\\_simple\(\)](#), [vrna\\_eval\\_circ\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_gquad\\_structure\(\)](#), [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure\\_v\(\)](#), [vrna\\_eval\\_structure\(\)](#)

#### Parameters

|                  |                                                       |
|------------------|-------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters           |
| <i>structure</i> | Consensus secondary structure in dot-bracket notation |

#### Returns

The free energy of the consensus structure including contributions of G-quadruplexes in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_gquad\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

#### 16.1.2.21 vrna\_eval\_consensus\_structure\_simple\_verbose()

```

int vrna_eval_consensus_structure_simple_verbose (
    const char ** alignment,
    const char * structure,
    FILE * file )

```

```

#include <ViennaRNA/eval.h>

```

Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop. This function is a simplified version of [vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#) that uses the *default* verbosity level.

#### Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

#### See also

[vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_structure\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#)

#### Parameters

|                  |                                                                                |
|------------------|--------------------------------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>structure</i> | Consensus secondary structure in dot-bracket notation                          |
| <i>file</i>      | A file handle where this function should print to (may be NULL).               |

**Returns**

The free energy of the consensus structure given the aligned input sequences in kcal/mol

**SWIG Wrapper Notes** This function is not available. Use [vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#) instead!

**16.1.2.22 vrna\_eval\_consensus\_structure\_simple\_v()**

```
int vrna_eval_consensus_structure_simple_v (
    const char ** alignment,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop. This function allows for detailed energy evaluation of a given sequence alignment/consensus structure pair. In contrast to [vrna\\_eval\\_consensus\\_structure\\_simple\(\)](#) this function prints detailed energy contributions based on individual loops to a file handle. If NULL is passed as file handle, this function defaults to print to stdout. Any positive `verbosity_level` activates potential warning message of the energy evaluating functions, while values  $\geq 1$  allow for detailed control of what data is printed. A negative parameter `verbosity_level` turns off printing all together.

**Note**

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

**See also**

[vrna\\_eval\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                        |                                                                                |
|------------------------|--------------------------------------------------------------------------------|
| <i>alignment</i>       | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>structure</i>       | Consensus secondary structure in dot-bracket notation                          |
| <i>verbosity_level</i> | The level of verbosity of this function                                        |
| <i>file</i>            | A file handle where this function should print to (may be NULL).               |

**Returns**

The free energy of the consensus structure given the sequence alignment in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_structure\\_simple\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

**16.1.2.23 vrna\_eval\_circ\_consensus\_structure\_v()**

```
int vrna_eval_circ_consensus_structure_v (
    const char ** alignment,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences and print contributions per loop.

This function is identical with [vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#) but assumed the aligned sequences to be circular.

#### Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

#### See also

[vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_circ\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_structure\(\)](#)

#### Parameters

|                        |                                                                                |
|------------------------|--------------------------------------------------------------------------------|
| <i>alignment</i>       | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>structure</i>       | Consensus secondary structure in dot-bracket notation                          |
| <i>verbosity_level</i> | The level of verbosity of this function                                        |
| <i>file</i>            | A file handle where this function should print to (may be NULL).               |

#### Returns

The free energy of the consensus structure given the sequence alignment in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to [VRNA\\_VERBOSE\\_QUIET](#) and NULL, respectively.

#### 16.1.2.24 vrna\_eval\_gquad\_consensus\_structure\_v()

```
int vrna_eval_gquad_consensus_structure_v (
    const char ** alignment,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a consensus structure for an RNA sequence alignment, allow for annotated G- $\leftrightarrow$  Quadruplexes in the structure and print contributions per loop.

This function is identical with [vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#) but allows for annotated G-Quadruplexes in the consensus structure.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++...++..++
```

#### Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

#### See also

[vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_gquad\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_structure\(\)](#)

## Parameters

|                        |                                                                                |
|------------------------|--------------------------------------------------------------------------------|
| <i>alignment</i>       | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>structure</i>       | Consensus secondary structure in dot-bracket notation                          |
| <i>verbosity_level</i> | The level of verbosity of this function                                        |
| <i>file</i>            | A file handle where this function should print to (may be NULL).               |

## Returns

The free energy of the consensus structure given the sequence alignment in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_gquad\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

### 16.1.2.25 vrna\_eval\_circ\_gquad\_consensus\_structure\_v()

```
int vrna_eval_circ_gquad_consensus_structure_v (
    const char ** alignment,
    const char * structure,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences, allow for annotated G-Quadruplexes in the structure and print contributions per loop.

This function is identical with [vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#) but assumes the sequences in the alignment to be circular and allows for annotated G-Quadruplexes in the consensus structure.

G-Quadruplexes are annotated as plus signs ('+') for each G involved in the motif. Linker sequences must be denoted by dots('.') as they are considered unpaired. Below is an example of a 2-layer G-quadruplex:

```
GGAAGGAAAGGAGG
++..++..++..++
```

## Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

## See also

[vrna\\_eval\\_consensus\\_structure\\_simple\\_v\(\)](#), [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure\(\)](#), [vrna\\_eval\\_structure\(\)](#)

## Parameters

|                        |                                                                                |
|------------------------|--------------------------------------------------------------------------------|
| <i>alignment</i>       | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>structure</i>       | Consensus secondary structure in dot-bracket notation                          |
| <i>verbosity_level</i> | The level of verbosity of this function                                        |
| <i>file</i>            | A file handle where this function should print to (may be NULL).               |

## Returns

The free energy of the consensus structure given the sequence alignment in kcal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_circ\\_gquad\\_structure\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

**16.1.2.26 vrna\_eval\_structure\_pt\_simple()**

```
int vrna_eval_structure_pt_simple (
    const char * string,
    const short * pt )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

In contrast to [vrna\\_eval\\_structure\\_pt\(\)](#) this function assumes default model details and default energy parameters in order to evaluate the free energy of the secondary structure. Therefore, it serves as a simple interface function for energy evaluation for situations where no changes on the energy model are required.

See also

[vrna\\_ptable\(\)](#), [vrna\\_eval\\_structure\\_simple\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#)

**Parameters**

|               |                                   |
|---------------|-----------------------------------|
| <i>string</i> | RNA sequence in uppercase letters |
| <i>pt</i>     | Secondary structure as pair_table |

**Returns**

The free energy of the input structure given the input sequence in 10cal/mol

**SWIG Wrapper Notes** In the target scripting language, this function serves as a wrapper for [vrna\\_eval\\_structure\\_pt\\_v\(\)](#) and, thus, allows for two additional, optional arguments, the verbosity level and a file handle which default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

**16.1.2.27 vrna\_eval\_structure\_pt\_simple\_verbose()**

```
int vrna_eval_structure_pt_simple_verbose (
    const char * string,
    const short * pt,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function is a simplified version of [vrna\\_eval\\_structure\\_pt\\_simple\\_v\(\)](#) that uses the *default* verbosity level.

See also

[vrna\\_eval\\_structure\\_pt\\_simple\\_v\(\)](#), [vrna\\_ptable\(\)](#), [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#), [vrna\\_eval\\_structure\\_simple\(\)](#)

**Parameters**

|               |                                                                  |
|---------------|------------------------------------------------------------------|
| <i>string</i> | RNA sequence in uppercase letters                                |
| <i>pt</i>     | Secondary structure as pair_table                                |
| <i>file</i>   | A file handle where this function should print to (may be NULL). |

**Returns**

The free energy of the input structure given the input sequence in 10cal/mol

### 16.1.2.28 vrna\_eval\_structure\_pt\_simple\_v()

```
int vrna_eval_structure_pt_simple_v (
    const char * string,
    const short * pt,
    int verbosity_level,
    FILE * file )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

This function allows for energy evaluation of a given sequence/structure pair where the structure is provided in pair\_table format as obtained from [vrna\\_ptable\(\)](#). Model details, energy parameters, and possibly soft constraints are used as provided via the parameter 'fc'. The fold\_compound does not need to contain any DP matrices, but all the most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_EVAL_ONLY);
```

In contrast to [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#) this function assumes default model details and default energy parameters in order to evaluate the free energy of the secondary structure. Therefore, it serves as a simple interface function for energy evaluation for situations where no changes on the energy model are required.

See also

[vrna\\_ptable\(\)](#), [vrna\\_eval\\_structure\\_pt\\_v\(\)](#), [vrna\\_eval\\_structure\\_simple\(\)](#)

#### Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                |
| <i>pt</i>              | Secondary structure as pair_table                                |
| <i>verbosity_level</i> | The level of verbosity of this function                          |
| <i>file</i>            | A file handle where this function should print to (may be NULL). |

#### Returns

The free energy of the input structure given the input sequence in 10cal/mol

### 16.1.2.29 vrna\_eval\_consensus\_structure\_pt\_simple()

```
int vrna_eval_consensus_structure_pt_simple (
    const char ** alignment,
    const short * pt )
```

```
#include <ViennaRNA/eval.h>
```

Evaluate the Free Energy of a Consensus Secondary Structure given a Sequence Alignment.

#### Note

The free energy returned from this function already includes the covariation pseudo energies that is used for comparative structure prediction within this library.

See also

[vrna\\_eval\\_consensus\\_structure\\_simple\(\)](#), [vrna\\_eval\\_structure\\_pt\(\)](#), [vrna\\_eval\\_structure\(\)](#), [vrna\\_eval\\_covar\\_structure\(\)](#)

#### Parameters

|                  |                                                                                |
|------------------|--------------------------------------------------------------------------------|
| <i>alignment</i> | RNA sequence alignment in uppercase letters. Gaps are denoted by hyphens ('-') |
| <i>pt</i>        | Secondary structure in pair table format                                       |



**Returns**

Free energy of the consensus structure in 10cal/mol

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_structure\\_pt\\_simple\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument

**16.1.2.30 vrna\_eval\_consensus\_structure\_pt\_simple\_verbose()**

```
int vrna_eval_consensus_structure_pt_simple_verbose (
    const char ** alignment,
    const short * pt,
    FILE * file )
#include <ViennaRNA/eval.h>
```

**SWIG Wrapper Notes** This function is not available. Use [vrna\\_eval\\_consensus\\_structure\\_pt\\_v\(\)](#) instead!

**16.1.2.31 vrna\_eval\_consensus\_structure\_pt\_simple\_v()**

```
int vrna_eval_consensus_structure_pt_simple_v (
    const char ** alignment,
    const short * pt,
    int verbosity_level,
    FILE * file )
#include <ViennaRNA/eval.h>
```

**SWIG Wrapper Notes** This function is available through an overloaded version of [vrna\\_eval\\_structure\\_pt\\_simple\(\)](#). Simply pass a sequence alignment as list of strings (including gaps) as first, and the consensus structure as second argument. The last two arguments are optional and default to [VRNA\\_VERBOSITY\\_QUIET](#) and NULL, respectively.

## 16.2 Energy Evaluation for Individual Loops

Functions to evaluate the free energy of particular types of loops.

### 16.2.1 Detailed Description

Functions to evaluate the free energy of particular types of loops.

To assess the free energy contribution of a particular loop within a secondary structure, two variants are provided:

- The bare free energy  $E$  (usually in deka-calories, i.e. multiples of 10cal/mol), and
- The Boltzmann weight  $q = \exp(-\beta E)$  of the free energy  $E$  (with  $\beta = \frac{1}{RT}$ , gas constant  $R$  and temperature  $T$ )

The latter is usually required for partition function computations. Collaboration diagram for Energy Evaluation for Individual Loops:

### Modules

- [Exterior Loops](#)  
*Functions to evaluate the free energy contributions for exterior loops.*
- [Hairpin Loops](#)  
*Functions to evaluate the free energy contributions for hairpin loops.*
- [Internal Loops](#)  
*Functions to evaluate the free energy contributions for internal loops.*
- [Multibranch Loops](#)  
*Functions to evaluate the free energy contributions for multibranch loops.*

## Files

- file [all.h](#)  
*Energy evaluation for MFE and partition function calculations.*
- file [external.h](#)  
*Energy evaluation of exterior loops for MFE and partition function calculations.*
- file [hairpin.h](#)  
*Energy evaluation of hairpin loops for MFE and partition function calculations.*
- file [internal.h](#)  
*Energy evaluation of interior loops for MFE and partition function calculations.*
- file [multibranch.h](#)  
*Energy evaluation of multibranch loops for MFE and partition function calculations.*

## Functions

- int [vrna\\_eval\\_loop\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, const short \*pt)  
*Calculate energy of a loop.*
- int [vrna\\_eval\\_loop\\_pt\\_v](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, const short \*pt, int verbosity\_level)  
*Calculate energy of a loop.*

### 16.2.2 Function Documentation

#### 16.2.2.1 vrna\_eval\_loop\_pt()

```
int vrna_eval_loop_pt (
    vrna_fold_compound_t * fc,
    int i,
    const short * pt )
#include <ViennaRNA/eval.h>
Calculate energy of a loop.
```

##### Parameters

|           |                                                                                           |
|-----------|-------------------------------------------------------------------------------------------|
| <i>fc</i> | A <a href="#">vrna_fold_compound_t</a> containing the energy parameters and model details |
| <i>i</i>  | position of covering base pair                                                            |
| <i>pt</i> | the pair table of the secondary structure                                                 |

##### Returns

free energy of the loop in 10cal/mol

**SWIG Wrapper Notes** This function is attached as method [eval\\_loop\\_pt\(\)](#) to objects of type *fold\_compound*

#### 16.2.2.2 vrna\_eval\_loop\_pt\_v()

```
int vrna_eval_loop_pt_v (
    vrna_fold_compound_t * fc,
    int i,
    const short * pt,
    int verbosity_level )
#include <ViennaRNA/eval.h>
Calculate energy of a loop.
```

## Parameters

|                        |                                                                                        |
|------------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>              | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>i</i>               | position of covering base pair                                                         |
| <i>pt</i>              | the pair table of the secondary structure                                              |
| <i>verbosity_level</i> | The level of verbosity of this function                                                |

## Returns

free energy of the loop in 10cal/mol

## 16.3 Energy Evaluation for Atomic Moves

Functions to evaluate the free energy change of a structure after application of (a set of) atomic moves.

### 16.3.1 Detailed Description

Functions to evaluate the free energy change of a structure after application of (a set of) atomic moves.

Here, atomic moves are not to be confused with moves of actual physical atoms. Instead, an atomic move is considered the smallest conformational change a secondary structure can undergo to form another, distinguishable structure. We currently support the following moves

## Atomic Moves:

- Opening (dissociation) of a single base pair
- Closing (formation) of a single base pair
- Shifting one pairing partner of an existing pair to a different location

Collaboration diagram for Energy Evaluation for Atomic Moves:

## Functions

- float [vrna\\_eval\\_move](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, int m1, int m2)  
*Calculate energy of a move (closing or opening of a base pair)*
- int [vrna\\_eval\\_move\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, short \*pt, int m1, int m2)  
*Calculate energy of a move (closing or opening of a base pair)*

### 16.3.2 Function Documentation

#### 16.3.2.1 vrna\_eval\_move()

```
float vrna_eval_move (
    vrna_fold_compound_t * fc,
    const char * structure,
    int m1,
    int m2 )
```

```
#include <ViennaRNA/eval.h>
```

Calculate energy of a move (closing or opening of a base pair)

If the parameters m1 and m2 are negative, it is deletion (opening) of a base pair, otherwise it is insertion (opening).

## See also

[vrna\\_eval\\_move\\_pt\(\)](#)

## Parameters

|                  |                                                                                        |
|------------------|----------------------------------------------------------------------------------------|
| <i>fc</i>        | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>structure</i> | secondary structure in dot-bracket notation                                            |
| <i>m1</i>        | first coordinate of base pair                                                          |
| <i>m2</i>        | second coordinate of base pair                                                         |

## Returns

energy change of the move in kcal/mol ([INF](#) / 100. upon any error)

**SWIG Wrapper Notes** This function is attached as method `eval_move()` to objects of type `fold_compound`

**16.3.2.2 vrna\_eval\_move\_pt()**

```
int vrna_eval_move_pt (
    vrna_fold_compound_t * fc,
    short * pt,
    int m1,
    int m2 )
```

```
#include <ViennaRNA/eval.h>
```

Calculate energy of a move (closing or opening of a base pair)

If the parameters `m1` and `m2` are negative, it is deletion (opening) of a base pair, otherwise it is insertion (opening).

## See also

[vrna\\_eval\\_move\(\)](#)

## Parameters

|           |                                                                                        |
|-----------|----------------------------------------------------------------------------------------|
| <i>fc</i> | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| <i>pt</i> | the pair table of the secondary structure                                              |
| <i>m1</i> | first coordinate of base pair                                                          |
| <i>m2</i> | second coordinate of base pair                                                         |

## Returns

energy change of the move in 10cal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_move_pt()` to objects of type `fold_compound`

**16.4 Deprecated Interface for Free Energy Evaluation**

Deprecated Energy Evaluation functions.

**16.4.1 Detailed Description**

Deprecated Energy Evaluation functions.

Using the functions below is discouraged as they have been marked deprecated and will be removed from the library in the (near) future! Collaboration diagram for Deprecated Interface for Free Energy Evaluation:

**Functions**

- float [energy\\_of\\_structure](#) (const char \*string, const char \*structure, int verbosity\_level)

*Calculate the free energy of an already folded RNA using global model detail settings.*

- float `energy_of_struct_par` (const char \*string, const char \*structure, `vrna_param_t` \*parameters, int verbosity\_level)

*Calculate the free energy of an already folded RNA.*

- float `energy_of_circ_structure` (const char \*string, const char \*structure, int verbosity\_level)

*Calculate the free energy of an already folded circular RNA.*

- float `energy_of_circ_struct_par` (const char \*string, const char \*structure, `vrna_param_t` \*parameters, int verbosity\_level)

*Calculate the free energy of an already folded circular RNA.*

- int `energy_of_structure_pt` (const char \*string, short \*ptable, short \*s, short \*s1, int verbosity\_level)

*Calculate the free energy of an already folded RNA.*

- int `energy_of_struct_pt_par` (const char \*string, short \*ptable, short \*s, short \*s1, `vrna_param_t` \*parameters, int verbosity\_level)

*Calculate the free energy of an already folded RNA.*

- float `energy_of_move` (const char \*string, const char \*structure, int m1, int m2)

*Calculate energy of a move (closing or opening of a base pair)*

- int `energy_of_move_pt` (short \*pt, short \*s, short \*s1, int m1, int m2)

*Calculate energy of a move (closing or opening of a base pair)*

- int `loop_energy` (short \*ptable, short \*s, short \*s1, int i)

*Calculate energy of a loop.*

- float `energy_of_struct` (const char \*string, const char \*structure)
- int `energy_of_struct_pt` (const char \*string, short \*ptable, short \*s, short \*s1)
- float `energy_of_circ_struct` (const char \*string, const char \*structure)
- int `E_Stem` (int type, int si1, int sj1, int extLoop, `vrna_param_t` \*P)

*Compute the energy contribution of a stem branching off a loop-region.*

- `FLT_OR_DBL exp_E_ExtLoop` (int type, int si1, int sj1, `vrna_exp_param_t` \*P)
- `FLT_OR_DBL exp_E_Stem` (int type, int si1, int sj1, int extLoop, `vrna_exp_param_t` \*P)
- PRIVATE int `E_IntLoop` (int n1, int n2, int type, int type\_2, int si1, int sj1, int sp1, int sq1, `vrna_param_t` \*P)
- PRIVATE `FLT_OR_DBL exp_E_IntLoop` (int u1, int u2, int type, int type2, short si1, short sj1, short sp1, short sq1, `vrna_exp_param_t` \*P)

## Variables

- int `cut_point`  
*first pos of second seq for cofolding*
- int `eos_debug`  
*verbose info from energy\_of\_struct*

## 16.4.2 Function Documentation

### 16.4.2.1 energy\_of\_structure()

```
float energy_of_structure (
    const char * string,
    const char * structure,
    int verbosity_level )
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA using global model detail settings.

If verbosity level is set to a value >0, energies of structure elements are printed to stdout

**Note**

OpenMP: This function relies on several global model settings variables and thus is not to be considered threadsafe. See [energy\\_of\\_struct\\_par\(\)](#) for a completely threadsafe implementation.

**Deprecated** Use [vrna\\_eval\\_structure\(\)](#) or [vrna\\_eval\\_structure\\_verbose\(\)](#) instead!

**See also**

[vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                        |                                             |
|------------------------|---------------------------------------------|
| <i>string</i>          | RNA sequence                                |
| <i>structure</i>       | secondary structure in dot-bracket notation |
| <i>verbosity_level</i> | a flag to turn verbose output on/off        |

**Returns**

the free energy of the input structure given the input sequence in kcal/mol

**16.4.2.2 energy\_of\_struct\_par()**

```
float energy_of_struct_par (
    const char * string,
    const char * structure,
    vrna_param_t * parameters,
    int verbosity_level )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

If verbosity level is set to a value >0, energies of structure elements are printed to stdout

**Deprecated** Use [vrna\\_eval\\_structure\(\)](#) or [vrna\\_eval\\_structure\\_verbose\(\)](#) instead!

**See also**

[vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                        |                                                                                       |
|------------------------|---------------------------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                                     |
| <i>structure</i>       | Secondary structure in dot-bracket notation                                           |
| <i>parameters</i>      | A data structure containing the prescaled energy contributions and the model details. |
| <i>verbosity_level</i> | A flag to turn verbose output on/off                                                  |

**Returns**

The free energy of the input structure given the input sequence in kcal/mol

**16.4.2.3 energy\_of\_circ\_structure()**

```
float energy_of_circ_structure (
    const char * string,
```

```

    const char * structure,
    int verbosity_level )
#include <ViennaRNA/eval.h>
Calculate the free energy of an already folded circular RNA.

```

**Note**

OpenMP: This function relies on several global model settings variables and thus is not to be considered threadsafe. See [energy\\_of\\_circ\\_struct\\_par\(\)](#) for a completely threadsafe implementation.

If verbosity level is set to a value >0, energies of structure elements are printed to stdout

**Deprecated** Use [vrna\\_eval\\_structure\(\)](#) or [vrna\\_eval\\_structure\\_verbose\(\)](#) instead!

**See also**

[vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                        |                                             |
|------------------------|---------------------------------------------|
| <i>string</i>          | RNA sequence                                |
| <i>structure</i>       | Secondary structure in dot-bracket notation |
| <i>verbosity_level</i> | A flag to turn verbose output on/off        |

**Returns**

The free energy of the input structure given the input sequence in kcal/mol

**16.4.2.4 energy\_of\_circ\_struct\_par()**

```

float energy_of_circ_struct_par (
    const char * string,
    const char * structure,
    vrna_param_t * parameters,
    int verbosity_level )
#include <ViennaRNA/eval.h>
Calculate the free energy of an already folded circular RNA.
If verbosity level is set to a value >0, energies of structure elements are printed to stdout

```

**Deprecated** Use [vrna\\_eval\\_structure\(\)](#) or [vrna\\_eval\\_structure\\_verbose\(\)](#) instead!

**See also**

[vrna\\_eval\\_structure\(\)](#)

**Parameters**

|                        |                                                                                       |
|------------------------|---------------------------------------------------------------------------------------|
| <i>string</i>          | RNA sequence                                                                          |
| <i>structure</i>       | Secondary structure in dot-bracket notation                                           |
| <i>parameters</i>      | A data structure containing the prescaled energy contributions and the model details. |
| <i>verbosity_level</i> | A flag to turn verbose output on/off                                                  |

**Returns**

The free energy of the input structure given the input sequence in kcal/mol

**16.4.2.5 energy\_of\_structure\_pt()**

```
int energy_of_structure_pt (
    const char * string,
    short * ptable,
    short * s,
    short * s1,
    int verbosity_level )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

If verbosity level is set to a value >0, energies of structure elements are printed to stdout

**Note**

OpenMP: This function relies on several global model settings variables and thus is not to be considered threadsafe. See [energy\\_of\\_struct\\_pt\\_par\(\)](#) for a completely threadsafe implementation.

**Deprecated** Use [vrna\\_eval\\_structure\\_pt\(\)](#) or [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#) instead!

**See also**

[vrna\\_eval\\_structure\\_pt\(\)](#)

**Parameters**

|                        |                                           |
|------------------------|-------------------------------------------|
| <i>string</i>          | RNA sequence                              |
| <i>ptable</i>          | the pair table of the secondary structure |
| <i>s</i>               | encoded RNA sequence                      |
| <i>s1</i>              | encoded RNA sequence                      |
| <i>verbosity_level</i> | a flag to turn verbose output on/off      |

**Returns**

the free energy of the input structure given the input sequence in 10kcal/mol

**16.4.2.6 energy\_of\_struct\_pt\_par()**

```
int energy_of_struct_pt_par (
    const char * string,
    short * ptable,
    short * s,
    short * s1,
    vrna_param_t * parameters,
    int verbosity_level )
```

```
#include <ViennaRNA/eval.h>
```

Calculate the free energy of an already folded RNA.

If verbosity level is set to a value >0, energies of structure elements are printed to stdout

**Deprecated** Use [vrna\\_eval\\_structure\\_pt\(\)](#) or [vrna\\_eval\\_structure\\_pt\\_verbose\(\)](#) instead!



See also

[vrna\\_eval\\_structure\\_pt\(\)](#)

#### Parameters

|                        |                                                                                       |
|------------------------|---------------------------------------------------------------------------------------|
| <i>string</i>          | RNA sequence in uppercase letters                                                     |
| <i>ptable</i>          | The pair table of the secondary structure                                             |
| <i>s</i>               | Encoded RNA sequence                                                                  |
| <i>s1</i>              | Encoded RNA sequence                                                                  |
| <i>parameters</i>      | A data structure containing the prescaled energy contributions and the model details. |
| <i>verbosity_level</i> | A flag to turn verbose output on/off                                                  |

#### Returns

The free energy of the input structure given the input sequence in 10kcal/mol

#### 16.4.2.7 energy\_of\_move()

```
float energy_of_move (
    const char * string,
    const char * structure,
    int m1,
    int m2 )
```

#include <[ViennaRNA/eval.h](#)>

Calculate energy of a move (closing or opening of a base pair)

If the parameters m1 and m2 are negative, it is deletion (opening) of a base pair, otherwise it is insertion (opening).

**Deprecated** Use [vrna\\_eval\\_move\(\)](#) instead!

See also

[vrna\\_eval\\_move\(\)](#)

#### Parameters

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence                                |
| <i>structure</i> | secondary structure in dot-bracket notation |
| <i>m1</i>        | first coordinate of base pair               |
| <i>m2</i>        | second coordinate of base pair              |

#### Returns

energy change of the move in kcal/mol

#### 16.4.2.8 energy\_of\_move\_pt()

```
int energy_of_move_pt (
    short * pt,
    short * s,
    short * s1,
    int m1,
    int m2 )
```

```
#include <ViennaRNA/eval.h>
```

Calculate energy of a move (closing or opening of a base pair)

If the parameters *m1* and *m2* are negative, it is deletion (opening) of a base pair, otherwise it is insertion (opening).

**Deprecated** Use `vrna_eval_move_pt()` instead!

See also

`vrna_eval_move_pt()`

Parameters

|           |                                           |
|-----------|-------------------------------------------|
| <i>pt</i> | the pair table of the secondary structure |
| <i>s</i>  | encoded RNA sequence                      |
| <i>s1</i> | encoded RNA sequence                      |
| <i>m1</i> | first coordinate of base pair             |
| <i>m2</i> | second coordinate of base pair            |

Returns

energy change of the move in 10cal/mol

#### 16.4.2.9 loop\_energy()

```
int loop_energy (
    short * ptable,
    short * s,
    short * s1,
    int i )
```

```
#include <ViennaRNA/eval.h>
```

Calculate energy of a loop.

**Deprecated** Use `vrna_eval_loop_pt()` instead!

See also

`vrna_eval_loop_pt()`

Parameters

|               |                                           |
|---------------|-------------------------------------------|
| <i>ptable</i> | the pair table of the secondary structure |
| <i>s</i>      | encoded RNA sequence                      |
| <i>s1</i>     | encoded RNA sequence                      |
| <i>i</i>      | position of covering base pair            |

Returns

free energy of the loop in 10cal/mol

#### 16.4.2.10 energy\_of\_struct()

```
float energy_of_struct (
```

```
const char * string,  
const char * structure )  
#include <ViennaRNA/eval.h>  
Calculate the free energy of an already folded RNA
```

**Note**

This function is not entirely threadsafe! Depending on the state of the global variable `eos_debug` it prints energy information to stdout or not...

**Deprecated** This function is deprecated and should not be used in future programs! Use `energy_of_structure()` instead!

**See also**

[energy\\_of\\_structure](#), [energy\\_of\\_circ\\_struct\(\)](#), [energy\\_of\\_struct\\_pt\(\)](#)

**Parameters**

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence                                |
| <i>structure</i> | secondary structure in dot-bracket notation |

**Returns**

the free energy of the input structure given the input sequence in kcal/mol

**16.4.2.11 energy\_of\_struct\_pt()**

```
int energy_of_struct_pt (  
const char * string,  
short * ptable,  
short * s,  
short * s1 )  
#include <ViennaRNA/eval.h>  
Calculate the free energy of an already folded RNA
```

**Note**

This function is not entirely threadsafe! Depending on the state of the global variable `eos_debug` it prints energy information to stdout or not...

**Deprecated** This function is deprecated and should not be used in future programs! Use `energy_of_structure_pt()` instead!

**See also**

[make\\_pair\\_table\(\)](#), [energy\\_of\\_structure\(\)](#)

**Parameters**

|               |                                           |
|---------------|-------------------------------------------|
| <i>string</i> | RNA sequence                              |
| <i>ptable</i> | the pair table of the secondary structure |
| <i>s</i>      | encoded RNA sequence                      |
| <i>s1</i>     | encoded RNA sequence                      |

**Returns**

the free energy of the input structure given the input sequence in 10kcal/mol

**16.4.2.12 energy\_of\_circ\_struct()**

```
float energy_of_circ_struct (
    const char * string,
    const char * structure )
#include <ViennaRNA/eval.h>
Calculate the free energy of an already folded circular RNA
```

**Note**

This function is not entirely threadsafe! Depending on the state of the global variable `eos_debug` it prints energy information to stdout or not...

**Deprecated** This function is deprecated and should not be used in future programs Use `energy_of_circ_structure()` instead!

**See also**

[energy\\_of\\_circ\\_structure\(\)](#), [energy\\_of\\_struct\(\)](#), [energy\\_of\\_struct\\_pt\(\)](#)

**Parameters**

|                  |                                             |
|------------------|---------------------------------------------|
| <i>string</i>    | RNA sequence                                |
| <i>structure</i> | secondary structure in dot-bracket notation |

**Returns**

the free energy of the input structure given the input sequence in kcal/mol

**16.4.2.13 E\_Stem()**

```
int E_Stem (
    int type,
    int si1,
    int sj1,
    int extLoop,
    vrna_param_t * P )
#include <ViennaRNA/loops/external.h>
Compute the energy contribution of a stem branching off a loop-region.
```

This function computes the energy contribution of a stem that branches off a loop region. This can be the case in multiloops, when a stem branching off increases the degree of the loop but also *immediately interior base pairs* of an exterior loop contribute free energy. To switch the behavior of the function according to the evaluation of a multiloop- or exterior-loop-stem, you pass the flag 'extLoop'. The returned energy contribution consists of a TerminalAU penalty if the pair type is greater than 2, dangling end contributions of mismatching nucleotides adjacent to the stem if only one of the si1, sj1 parameters is greater than 0 and mismatch energies if both mismatching nucleotides are positive values. Thus, to avoid incorporating dangling end or mismatch energies just pass a negative number, e.g. -1 to the mismatch argument.

This is an illustration of how the energy contribution is assembled:

```

      3'   5'
      |   |
      X - Y
5'-si1      sj1-3'
```

Here, (X,Y) is the base pair that closes the stem that branches off a loop region. The nucleotides *si1* and *sj1* are the 5'- and 3'- mismatches, respectively. If the base pair type of (X,Y) is greater than 2 (i.e. an A-U or G-U pair, the TerminalAU penalty will be included in the energy contribution returned. If *si1* and *sj1* are both nonnegative numbers, mismatch energies will also be included. If one of *si1* or *sj1* is a negative value, only 5' or 3' dangling end contributions are taken into account. To prohibit any of these mismatch contributions to be incorporated, just pass a negative number to both, *si1* and *sj1*. In case the argument *extLoop* is 0, the returned energy contribution also includes the *internal-loop-penalty* of a multiloop stem with closing pair type.

See also

`E_MLstem()`  
`E_ExtLoop()`

Note

This function is threadsafe

**Deprecated** Please use one of the functions `vrna_E_ext_stem()` and `E_MLstem()` instead! Use the former for cases where *extLoop* != 0 and the latter otherwise.

Parameters

|                |                                                                                            |
|----------------|--------------------------------------------------------------------------------------------|
| <i>type</i>    | The pair type of the first base pair un the stem                                           |
| <i>si1</i>     | The 5'-mismatching nucleotide                                                              |
| <i>sj1</i>     | The 3'-mismatching nucleotide                                                              |
| <i>extLoop</i> | A flag that indicates whether the contribution reflects the one of an exterior loop or not |
| <i>P</i>       | The data structure containing scaled energy parameters                                     |

Returns

The Free energy of the branch off the loop in dcal/mol

#### 16.4.2.14 exp\_E\_ExtLoop()

```
FLT_OR_DBL exp_E_ExtLoop (
    int type,
    int si1,
    int sj1,
    vrna_exp_param_t * P )
```

```
#include <ViennaRNA/loops/external.h>
```

This is the partition function variant of `E_ExtLoop()`

**Deprecated** Use `vrna_exp_E_ext_stem()` instead!

See also

`E_ExtLoop()`

Returns

The Boltzmann weighted energy contribution of the introduced exterior-loop stem

### 16.4.2.15 exp\_E\_Stem()

```
FLT_OR_DBL exp_E_Stem (
    int type,
    int sil,
    int sjl,
    int extLoop,
    vrna_exp_param_t * P )
#include <ViennaRNA/loops/external.h>
```

**Compute the Boltzmann weighted energy contribution of a stem branching off a loop-region**

This is the partition function variant of [E\\_Stem\(\)](#)

See also

[E\\_Stem\(\)](#)

**Note**

This function is threadsafe

**Returns**

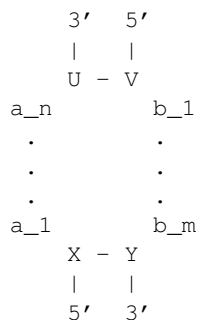
The Boltzmann weighted energy contribution of the branch off the loop

### 16.4.2.16 E\_IntLoop()

```
PRIVATE int E_IntLoop (
    int n1,
    int n2,
    int type,
    int type_2,
    int sil,
    int sjl,
    int spl,
    int sql,
    vrna_param_t * P )
#include <ViennaRNA/loops/internal.h>
```

**Compute the Energy of an interior-loop**

This function computes the free energy  $\Delta G$  of an interior-loop with the following structure:



This general structure depicts an interior-loop that is closed by the base pair (X,Y). The enclosed base pair is (V,U) which leaves the unpaired bases a\_1-a\_n and b\_1-b\_n that constitute the loop. In this example, the length of the interior-loop is  $(n + m)$  where n or m may be 0 resulting in a bulge-loop or base pair stack. The mismatching

nucleotides for the closing pair (X,Y) are:

5'-mismatch: a\_1

3'-mismatch: b\_m

and for the enclosed base pair (V,U):

5'-mismatch: b\_1

3'-mismatch: a\_n

#### Note

Base pairs are always denoted in 5'->3' direction. Thus the enclosed base pair must be 'turned around' when evaluating the free energy of the interior-loop

#### See also

[scale\\_parameters\(\)](#)

[vrna\\_param\\_t](#)

#### Note

This function is threadsafe

#### Parameters

|                                       |                                                               |
|---------------------------------------|---------------------------------------------------------------|
| <i>n1</i>                             | The size of the 'left'-loop (number of unpaired nucleotides)  |
| <i>n2</i>                             | The size of the 'right'-loop (number of unpaired nucleotides) |
| <i>type</i>                           | The pair type of the base pair closing the interior loop      |
| <i>type</i> <sub>↔</sub><br><i>_2</i> | The pair type of the enclosed base pair                       |
| <i>si1</i>                            | The 5'-mismatching nucleotide of the closing pair             |
| <i>sj1</i>                            | The 3'-mismatching nucleotide of the closing pair             |
| <i>sp1</i>                            | The 3'-mismatching nucleotide of the enclosed pair            |
| <i>sq1</i>                            | The 5'-mismatching nucleotide of the enclosed pair            |
| <i>P</i>                              | The datastructure containing scaled energy parameters         |

#### Returns

The Free energy of the Interior-loop in dcal/mol

#### 16.4.2.17 exp\_E\_IntLoop()

```
PRIVATE FLT_OR_DBL exp_E_IntLoop (
    int u1,
    int u2,
    int type,
    int type2,
    short si1,
    short sj1,
    short sp1,
    short sq1,
    vrna_exp_param_t * P )
#include <ViennaRNA/loops/internal.h>
```

**Compute Boltzmann weight  $e^{-\Delta G/kT}$  of interior loop**

multiply by scale[u1+u2+2] for scaling

## See also

[get\\_scaled\\_pf\\_parameters\(\)](#)  
[vrna\\_exp\\_param\\_t](#)  
[E\\_IntLoop\(\)](#)

## Note

This function is threadsafe

## Parameters

|              |                                                                                |
|--------------|--------------------------------------------------------------------------------|
| <i>u1</i>    | The size of the 'left'-loop (number of unpaired nucleotides)                   |
| <i>u2</i>    | The size of the 'right'-loop (number of unpaired nucleotides)                  |
| <i>type</i>  | The pair type of the base pair closing the interior loop                       |
| <i>type2</i> | The pair type of the enclosed base pair                                        |
| <i>si1</i>   | The 5'-mismatching nucleotide of the closing pair                              |
| <i>sj1</i>   | The 3'-mismatching nucleotide of the closing pair                              |
| <i>sp1</i>   | The 3'-mismatching nucleotide of the enclosed pair                             |
| <i>sq1</i>   | The 5'-mismatching nucleotide of the enclosed pair                             |
| <i>P</i>     | The datastructure containing scaled Boltzmann weights of the energy parameters |

## Returns

The Boltzmann weight of the Interior-loop

## 16.5 The RNA Folding Grammar

The RNA folding grammar as implemented in RNAlib.

### 16.5.1 Detailed Description

The RNA folding grammar as implemented in RNAlib.

Collaboration diagram for The RNA Folding Grammar:

## Modules

- [Fine-tuning of the Implemented Models](#)

*Functions and data structures to fine-tune the implemented secondary structure evaluation model.*

- [Energy Parameters](#)

*All relevant functions to retrieve and copy pre-calculated energy parameter sets as well as reading/writing the energy parameter set from/to file(s).*

- [Extending the Folding Grammar with Additional Domains](#)

*This module covers simple and straight-forward extensions to the RNA folding grammar.*

- [Constraining the RNA Folding Grammar](#)

*This module provides general functions that allow for an easy control of constrained secondary structure prediction and evaluation.*

## Files

- file [grammar.h](#)

*Implementations for the RNA folding grammar.*



## Data Structures

- struct [vrna\\_gr\\_aux\\_s](#)

### 16.5.2 Data Structure Documentation

#### 16.5.2.1 struct vrna\_gr\_aux\_s

##### Data Fields

- vrna\_callback\_gr\_cond \* **cb\_proc**  
*A callback for pre- and post-processing of auxiliary grammar rules.*

## 16.6 Fine-tuning of the Implemented Models

Functions and data structures to fine-tune the implemented secondary structure evaluation model.

### 16.6.1 Detailed Description

Functions and data structures to fine-tune the implemented secondary structure evaluation model.

Collaboration diagram for Fine-tuning of the Implemented Models:

#### Files

- file [model.h](#)  
*The model details data structure and its corresponding modifiers.*

#### Data Structures

- struct [vrna\\_md\\_s](#)  
*The data structure that contains the complete model details used throughout the calculations. [More...](#)*

#### Macros

- `#define VRNA_MODEL_DEFAULT_TEMPERATURE 37.0`  
*Default temperature for structure prediction and free energy evaluation in °C*
- `#define VRNA_MODEL_DEFAULT_PF_SCALE -1`  
*Default scaling factor for partition function computations.*
- `#define VRNA_MODEL_DEFAULT_BETA_SCALE 1.`  
*Default scaling factor for absolute thermodynamic temperature in Boltzmann factors.*
- `#define VRNA_MODEL_DEFAULT_DANGLES 2`  
*Default dangling end model.*
- `#define VRNA_MODEL_DEFAULT_SPECIAL_HP 1`  
*Default model behavior for lookup of special tri-, tetra-, and hexa-loops.*
- `#define VRNA_MODEL_DEFAULT_NO_LP 0`  
*Default model behavior for so-called 'lonely pairs'.*
- `#define VRNA_MODEL_DEFAULT_NO_GU 0`  
*Default model behavior for G-U base pairs.*
- `#define VRNA_MODEL_DEFAULT_NO_GU_CLOSURE 0`  
*Default model behavior for G-U base pairs closing a loop.*
- `#define VRNA_MODEL_DEFAULT_CIRC 0`  
*Default model behavior to treat a molecule as a circular RNA (DNA)*
- `#define VRNA_MODEL_DEFAULT_GQUAD 0`  
*Default model behavior regarding the treatment of G-Quadruplexes.*
- `#define VRNA_MODEL_DEFAULT_UNIQ_ML 0`

- Default behavior of the model regarding unique multi-branch loop decomposition.*

  - `#define VRNA_MODEL_DEFAULT_ENERGY_SET 0`

*Default model behavior on which energy set to use.*
- `#define VRNA_MODEL_DEFAULT_BACKTRACK 1`

*Default model behavior with regards to backtracking of structures.*
- `#define VRNA_MODEL_DEFAULT_BACKTRACK_TYPE 'F'`

*Default model behavior on what type of backtracking to perform.*
- `#define VRNA_MODEL_DEFAULT_COMPUTE_BPP 1`

*Default model behavior with regards to computing base pair probabilities.*
- `#define VRNA_MODEL_DEFAULT_MAX_BP_SPAN -1`

*Default model behavior for the allowed maximum base pair span.*
- `#define VRNA_MODEL_DEFAULT_WINDOW_SIZE -1`

*Default model behavior for the sliding window approach.*
- `#define VRNA_MODEL_DEFAULT_LOG_ML 0`

*Default model behavior on how to evaluate the energy contribution of multi-branch loops.*
- `#define VRNA_MODEL_DEFAULT_ALI_OLD_EN 0`

*Default model behavior for consensus structure energy evaluation.*
- `#define VRNA_MODEL_DEFAULT_ALI_RIBO 0`

*Default model behavior for consensus structure co-variance contribution assessment.*
- `#define VRNA_MODEL_DEFAULT_ALI_CV_FACT 1.`

*Default model behavior for weighting the co-variance score in consensus structure prediction.*
- `#define VRNA_MODEL_DEFAULT_ALI_NC_FACT 1.`

*Default model behavior for weighting the nucleotide conservation? in consensus structure prediction.*
- `#define MAXALPHA 20`

*Maximal length of alphabet.*

## Typedefs

- `typedef struct vrna_md_s vrna_md_t`  
*Typename for the model details data structure [vrna\\_md\\_s](#).*

## Functions

- `void vrna_md_set_default (vrna_md_t *md)`  
*Apply default model details to a provided [vrna\\_md\\_t](#) data structure.*
- `void vrna_md_update (vrna_md_t *md)`  
*Update the model details data structure.*
- `vrna_md_t * vrna_md_copy (vrna_md_t *md_to, const vrna_md_t *md_from)`  
*Copy/Clone a [vrna\\_md\\_t](#) model.*
- `char * vrna_md_option_string (vrna_md_t *md)`  
*Get a corresponding commandline parameter string of the options in a [vrna\\_md\\_t](#).*
- `void vrna_md_defaults_reset (vrna_md_t *md_p)`  
*Reset the global default model details to a specific set of parameters, or their initial values.*
- `void vrna_md_defaults_temperature (double T)`  
*Set default temperature for energy evaluation of loops.*
- `double vrna_md_defaults_temperature_get (void)`  
*Get default temperature for energy evaluation of loops.*
- `void vrna_md_defaults_betaScale (double b)`  
*Set default scaling factor of thermodynamic temperature in Boltzmann factors.*
- `double vrna_md_defaults_betaScale_get (void)`  
*Get default scaling factor of thermodynamic temperature in Boltzmann factors.*
- `void vrna_md_defaults_dangles (int d)`

- Set default dangle model for structure prediction.*

  - int [vrna\\_md\\_defaults\\_dangles\\_get](#) (void)

*Get default dangle model for structure prediction.*
- void [vrna\\_md\\_defaults\\_special\\_hp](#) (int flag)

*Set default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.*

  - int [vrna\\_md\\_defaults\\_special\\_hp\\_get](#) (void)

*Get default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.*
- void [vrna\\_md\\_defaults\\_noLP](#) (int flag)

*Set default behavior for prediction of canonical secondary structures.*

  - int [vrna\\_md\\_defaults\\_noLP\\_get](#) (void)

*Get default behavior for prediction of canonical secondary structures.*
- void [vrna\\_md\\_defaults\\_noGU](#) (int flag)

*Set default behavior for treatment of G-U wobble pairs.*

  - int [vrna\\_md\\_defaults\\_noGU\\_get](#) (void)

*Get default behavior for treatment of G-U wobble pairs.*
- void [vrna\\_md\\_defaults\\_noGUclosure](#) (int flag)

*Set default behavior for G-U pairs as closing pair for loops.*

  - int [vrna\\_md\\_defaults\\_noGUclosure\\_get](#) (void)

*Get default behavior for G-U pairs as closing pair for loops.*
- void [vrna\\_md\\_defaults\\_logML](#) (int flag)

*Set default behavior recomputing free energies of multi-branch loops using a logarithmic model.*

  - int [vrna\\_md\\_defaults\\_logML\\_get](#) (void)

*Get default behavior recomputing free energies of multi-branch loops using a logarithmic model.*
- void [vrna\\_md\\_defaults\\_circ](#) (int flag)

*Set default behavior whether input sequences are circularized.*

  - int [vrna\\_md\\_defaults\\_circ\\_get](#) (void)

*Get default behavior whether input sequences are circularized.*
- void [vrna\\_md\\_defaults\\_gquad](#) (int flag)

*Set default behavior for treatment of G-Quadruplexes.*

  - int [vrna\\_md\\_defaults\\_gquad\\_get](#) (void)

*Get default behavior for treatment of G-Quadruplexes.*
- void [vrna\\_md\\_defaults\\_uniq\\_ML](#) (int flag)

*Set default behavior for creating additional matrix for unique multi-branch loop prediction.*

  - int [vrna\\_md\\_defaults\\_uniq\\_ML\\_get](#) (void)

*Get default behavior for creating additional matrix for unique multi-branch loop prediction.*
- void [vrna\\_md\\_defaults\\_energy\\_set](#) (int e)

*Set default energy set.*

  - int [vrna\\_md\\_defaults\\_energy\\_set\\_get](#) (void)

*Get default energy set.*
- void [vrna\\_md\\_defaults\\_backtrack](#) (int flag)

*Set default behavior for whether to backtrack secondary structures.*

  - int [vrna\\_md\\_defaults\\_backtrack\\_get](#) (void)

*Get default behavior for whether to backtrack secondary structures.*
- void [vrna\\_md\\_defaults\\_backtrack\\_type](#) (char t)

*Set default backtrack type, i.e. which DP matrix is used.*

  - char [vrna\\_md\\_defaults\\_backtrack\\_type\\_get](#) (void)

*Get default backtrack type, i.e. which DP matrix is used.*
- void [vrna\\_md\\_defaults\\_compute\\_bpp](#) (int flag)

*Set the default behavior for whether to compute base pair probabilities after partition function computation.*

  - int [vrna\\_md\\_defaults\\_compute\\_bpp\\_get](#) (void)

*Get the default behavior for whether to compute base pair probabilities after partition function computation.*

- void [vrna\\_md\\_defaults\\_max\\_bp\\_span](#) (int span)  
*Set default maximal base pair span.*
- int [vrna\\_md\\_defaults\\_max\\_bp\\_span\\_get](#) (void)  
*Get default maximal base pair span.*
- void [vrna\\_md\\_defaults\\_min\\_loop\\_size](#) (int size)  
*Set default minimal loop size.*
- int [vrna\\_md\\_defaults\\_min\\_loop\\_size\\_get](#) (void)  
*Get default minimal loop size.*
- void [vrna\\_md\\_defaults\\_window\\_size](#) (int size)  
*Set default window size for sliding window structure prediction approaches.*
- int [vrna\\_md\\_defaults\\_window\\_size\\_get](#) (void)  
*Get default window size for sliding window structure prediction approaches.*
- void [vrna\\_md\\_defaults\\_oldAliEn](#) (int flag)  
*Set default behavior for whether to use old energy model for comparative structure prediction.*
- int [vrna\\_md\\_defaults\\_oldAliEn\\_get](#) (void)  
*Get default behavior for whether to use old energy model for comparative structure prediction.*
- void [vrna\\_md\\_defaults\\_ribo](#) (int flag)  
*Set default behavior for whether to use Ribosum Scoring in comparative structure prediction.*
- int [vrna\\_md\\_defaults\\_ribo\\_get](#) (void)  
*Get default behavior for whether to use Ribosum Scoring in comparative structure prediction.*
- void [vrna\\_md\\_defaults\\_cv\\_fact](#) (double factor)  
*Set the default co-variance scaling factor used in comparative structure prediction.*
- double [vrna\\_md\\_defaults\\_cv\\_fact\\_get](#) (void)  
*Get the default co-variance scaling factor used in comparative structure prediction.*
- void [vrna\\_md\\_defaults\\_nc\\_fact](#) (double factor)
- double [vrna\\_md\\_defaults\\_nc\\_fact\\_get](#) (void)
- void [vrna\\_md\\_defaults\\_sfact](#) (double factor)  
*Set the default scaling factor used to avoid under-/overflows in partition function computation.*
- double [vrna\\_md\\_defaults\\_sfact\\_get](#) (void)  
*Get the default scaling factor used to avoid under-/overflows in partition function computation.*
- void [set\\_model\\_details](#) ([vrna\\_md\\_t](#) \*md)  
*Set default model details.*

## Variables

- double [temperature](#)  
*Rescale energy parameters to a temperature in degC.*
- double [pf\\_scale](#)  
*A scaling factor used by [pf\\_fold\(\)](#) to avoid overflows.*
- int [dangles](#)  
*Switch the energy model for dangling end contributions (0, 1, 2, 3)*
- int [tetra\\_loop](#)  
*Include special stabilizing energies for some tri-, tetra- and hexa-loops;.*
- int [noLonelyPairs](#)  
*Global switch to avoid/allow helices of length 1.*
- int [noGU](#)  
*Global switch to forbid/allow GU base pairs at all.*
- int [no\\_closingGU](#)  
*GU allowed only inside stacks if set to 1.*
- int [circ](#)  
*backward compatibility variable.. this does not effect anything*

- int **gquad**  
*Allow G-quadruplex formation.*
- int **uniq\_ML**  
*do ML decomposition uniquely (for subopt)*
- int **energy\_set**  
*0 = BP; 1=any with GC; 2=any with AU-parameter*
- int **do\_backtrack**  
*do backtracking, i.e. compute secondary structures or base pair probabilities*
- char **backtrack\_type**  
*A backtrack array marker for [inverse\\_fold\(\)](#)*
- char \* **nonstandards**  
*contains allowed non standard base pairs*
- int **max\_bp\_span**  
*Maximum allowed base pair span.*
- int **oldAliEn**  
*use old alifold energies (with gaps)*
- int **ribo**  
*use ribosum matrices*
- int **logML**  
*if nonzero use logarithmic ML energy in [energy\\_of\\_struct](#)*

## 16.6.2 Data Structure Documentation

### 16.6.2.1 struct vrna\_md\_s

The data structure that contains the complete model details used throughout the calculations.

For convenience reasons, we provide the type name [vrna\\_md\\_t](#) to address this data structure without the use of the struct keyword

See also

[vrna\\_md\\_set\\_default\(\)](#), [set\\_model\\_details\(\)](#), [vrna\\_md\\_update\(\)](#), [vrna\\_md\\_t](#)

**SWIG Wrapper Notes** This data structure is wrapped as an object **md** with multiple related functions attached as methods.

A new set of default parameters can be obtained by calling the constructor of **md**:

- `md()` – Initialize with default settings

The resulting object has a list of attached methods which directly correspond to functions that mainly operate on the corresponding C data structure:

- `reset()` – [vrna\\_md\\_set\\_default\(\)](#)
- `set_from_globals()` – [set\\_model\\_details\(\)](#)
- `option_string()` – [vrna\\_md\\_option\\_string\(\)](#)

Note, that default parameters can be modified by directly setting any of the following global variables. Internally, getting/setting default parameters using their global variable representative translates into calls of the following functions, therefore these wrappers for these functions do not exist in the scripting language interface(s):

---

| global variable | C getter | C setter |
|-----------------|----------|----------|
|-----------------|----------|----------|

| global variable | C getter                                              | C setter                                          |
|-----------------|-------------------------------------------------------|---------------------------------------------------|
| temperature     | <a href="#">vrna_md_defaults_temperature_get()</a>    | <a href="#">vrna_md_defaults_temperature()</a>    |
| dangles         | <a href="#">vrna_md_defaults_dangles_get()</a>        | <a href="#">vrna_md_defaults_dangles()</a>        |
| betaScale       | <a href="#">vrna_md_defaults_betaScale_get()</a>      | <a href="#">vrna_md_defaults_betaScale()</a>      |
| tetra_loop      | this is an alias of <i>special_hp</i>                 |                                                   |
| special_hp      | <a href="#">vrna_md_defaults_special_hp_get()</a>     | <a href="#">vrna_md_defaults_special_hp()</a>     |
| noLonelyPairs   | this is an alias of <i>noLP</i>                       |                                                   |
| noLP            | <a href="#">vrna_md_defaults_noLP_get()</a>           | <a href="#">vrna_md_defaults_noLP()</a>           |
| noGU            | <a href="#">vrna_md_defaults_noGU_get()</a>           | <a href="#">vrna_md_defaults_noGU()</a>           |
| no_closingGU    | this is an alias of <i>noGUclosure</i>                |                                                   |
| noGUclosure     | <a href="#">vrna_md_defaults_noGUclosure_get()</a>    | <a href="#">vrna_md_defaults_noGUclosure()</a>    |
| logML           | <a href="#">vrna_md_defaults_logML_get()</a>          | <a href="#">vrna_md_defaults_logML()</a>          |
| circ            | <a href="#">vrna_md_defaults_circ_get()</a>           | <a href="#">vrna_md_defaults_circ()</a>           |
| gquad           | <a href="#">vrna_md_defaults_gquad_get()</a>          | <a href="#">vrna_md_defaults_gquad()</a>          |
| uniq_ML         | <a href="#">vrna_md_defaults_uniq_ML_get()</a>        | <a href="#">vrna_md_defaults_uniq_ML()</a>        |
| energy_set      | <a href="#">vrna_md_defaults_energy_set_get()</a>     | <a href="#">vrna_md_defaults_energy_set()</a>     |
| backtrack       | <a href="#">vrna_md_defaults_backtrack_get()</a>      | <a href="#">vrna_md_defaults_backtrack()</a>      |
| backtrack_type  | <a href="#">vrna_md_defaults_backtrack_type_get()</a> | <a href="#">vrna_md_defaults_backtrack_type()</a> |
| do_backtrack    | this is an alias of <i>compute_bpp</i>                |                                                   |
| compute_bpp     | <a href="#">vrna_md_defaults_compute_bpp_get()</a>    | <a href="#">vrna_md_defaults_compute_bpp()</a>    |
| max_bp_span     | <a href="#">vrna_md_defaults_max_bp_span_get()</a>    | <a href="#">vrna_md_defaults_max_bp_span()</a>    |
| min_loop_size   | <a href="#">vrna_md_defaults_min_loop_size_get()</a>  | <a href="#">vrna_md_defaults_min_loop_size()</a>  |
| window_size     | <a href="#">vrna_md_defaults_window_size_get()</a>    | <a href="#">vrna_md_defaults_window_size()</a>    |
| oldAliEn        | <a href="#">vrna_md_defaults_oldAliEn_get()</a>       | <a href="#">vrna_md_defaults_oldAliEn()</a>       |
| ribo            | <a href="#">vrna_md_defaults_ribo_get()</a>           | <a href="#">vrna_md_defaults_ribo()</a>           |
| cv_fact         | <a href="#">vrna_md_defaults_cv_fact_get()</a>        | <a href="#">vrna_md_defaults_cv_fact()</a>        |
| nc_fact         | <a href="#">vrna_md_defaults_nc_fact_get()</a>        | <a href="#">vrna_md_defaults_nc_fact()</a>        |
| sfact           | <a href="#">vrna_md_defaults_sfact_get()</a>          | <a href="#">vrna_md_defaults_sfact()</a>          |

## Data Fields

- double **temperature**  
*The temperature used to scale the thermodynamic parameters.*
- double **betaScale**  
*A scaling factor for the thermodynamic temperature of the Boltzmann factors.*
- int **pf\_smooth**  
*A flag specifying whether energies in Boltzmann factors need to be smoothed.*
- int **dangles**  
*Specifies the dangle model used in any energy evaluation (0, 1, 2 or 3)*
- int **special\_hp**  
*Include special hairpin contributions for tri, tetra and hexaloops.*
- int **noLP**  
*Only consider canonical structures, i.e. no 'lonely' base pairs.*
- int **noGU**  
*Do not allow GU pairs.*
- int **noGUclosure**  
*Do not allow loops to be closed by GU pair.*

- int **logML**  
*Use logarithmic scaling for multiloops.*
- int **circ**  
*Assume RNA to be circular instead of linear.*
- int **gquad**  
*Include G-quadruplexes in structure prediction.*
- int **uniq\_ML**  
*Flag to ensure unique multi-branch loop decomposition during folding.*
- int **energy\_set**  
*Specifies the energy set that defines set of compatible base pairs.*
- int **backtrack**  
*Specifies whether or not secondary structures should be backtraced.*
- char **backtrack\_type**  
*Specifies in which matrix to backtrack.*
- int **compute\_bpp**  
*Specifies whether or not backward recursions for base pair probability (bpp) computation will be performed.*
- char **nonstandards** [64]  
*contains allowed non standard bases*
- int **max\_bp\_span**  
*maximum allowed base pair span*
- int **min\_loop\_size**  
*Minimum size of hairpin loops.*
- int **window\_size**  
*Size of the sliding window for locally optimal structure prediction.*
- int **oldAliEn**  
*Use old alifold energy model.*
- int **ribo**  
*Use ribosum scoring table in alifold energy model.*
- double **cv\_fact**  
*Co-variance scaling factor for consensus structure prediction.*
- double **nc\_fact**  
*Scaling factor to weight co-variance contributions of non-canonical pairs.*
- double **sfact**  
*Scaling factor for partition function scaling.*
- int **rtype** [8]  
*Reverse base pair type array.*
- short **alias** [MAXALPHA+1]  
*alias of an integer nucleotide representation*
- int **pair** [MAXALPHA+1][MAXALPHA+1]  
*Integer representation of a base pair.*
- float **pair\_dist** [7][7]  
*Base pair dissimilarity, a.k.a. distance matrix.*

#### 16.6.2.1.1 Field Documentation

#### 16.6.2.1.1.1 **dangles** `int vrna_md_s::dangles`

Specifies the dangle model used in any energy evaluation (0,1,2 or 3)

If set to 0 no stabilizing energies are assigned to bases adjacent to helices in free ends and multiloops (so called dangling ends). Normally (dangles = 1) dangling end energies are assigned only to unpaired bases and a base cannot participate simultaneously in two dangling ends. In the partition function algorithm [vrna\\_pf\(\)](#) these checks are neglected. To provide comparability between free energy minimization and partition function algorithms, the default setting is 2. This treatment of dangling ends gives more favorable energies to helices directly adjacent to one another, which can be beneficial since such helices often do engage in stabilizing interactions through co-axial stacking.

If set to 3 co-axial stacking is explicitly included for adjacent helices in multiloops. The option affects only mfe folding and energy evaluation ([vrna\\_mfe\(\)](#) and [vrna\\_eval\\_structure\(\)](#)), as well as suboptimal folding ([vrna\\_subopt\(\)](#)) via re-evaluation of energies. Co-axial stacking with one intervening mismatch is not considered so far.

##### Note

Some function do not implement all dangle model but only a subset of (0,1,2,3). In particular, partition function algorithms can only handle 0 and 2. Read the documentation of the particular recurrences or energy evaluation function for information about the provided dangle model.

#### 16.6.2.1.1.2 **min\_loop\_size** `int vrna_md_s::min_loop_size`

Minimum size of hairpin loops.

##### Note

The default value for this field is [TURN](#), however, it may be 0 in cofolding context.

### 16.6.3 Macro Definition Documentation

#### 16.6.3.1 **VRNA\_MODEL\_DEFAULT\_TEMPERATURE**

```
#define VRNA_MODEL_DEFAULT_TEMPERATURE 37.0
#include <ViennaRNA/model.h>
```

Default temperature for structure prediction and free energy evaluation in °C

See also

[vrna\\_md\\_t.temperature](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.2 **VRNA\_MODEL\_DEFAULT\_PF\_SCALE**

```
#define VRNA_MODEL_DEFAULT_PF_SCALE -1
#include <ViennaRNA/model.h>
```

Default scaling factor for partition function computations.

See also

[vrna\\_exp\\_param\\_t.pf\\_scale](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.3 **VRNA\_MODEL\_DEFAULT\_BETA\_SCALE**

```
#define VRNA_MODEL_DEFAULT_BETA_SCALE 1.
#include <ViennaRNA/model.h>
```

Default scaling factor for absolute thermodynamic temperature in Boltzmann factors.

See also

[vrna\\_exp\\_param\\_t.alpha](#), [vrna\\_md\\_t.betaScale](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)



#### 16.6.3.4 VRNA\_MODEL\_DEFAULT\_DANGLES

```
#define VRNA_MODEL_DEFAULT_DANGLES 2
#include <ViennaRNA/model.h>
```

Default dangling end model.

See also

[vrna\\_md\\_t.dangles](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.5 VRNA\_MODEL\_DEFAULT\_SPECIAL\_HP

```
#define VRNA_MODEL_DEFAULT_SPECIAL_HP 1
#include <ViennaRNA/model.h>
```

Default model behavior for lookup of special tri-, tetra-, and hexa-loops.

See also

[vrna\\_md\\_t.special\\_hp](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.6 VRNA\_MODEL\_DEFAULT\_NO\_LP

```
#define VRNA_MODEL_DEFAULT_NO_LP 0
#include <ViennaRNA/model.h>
```

Default model behavior for so-called 'lonely pairs'.

See also

[vrna\\_md\\_t.noLP](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.7 VRNA\_MODEL\_DEFAULT\_NO\_GU

```
#define VRNA_MODEL_DEFAULT_NO_GU 0
#include <ViennaRNA/model.h>
```

Default model behavior for G-U base pairs.

See also

[vrna\\_md\\_t.noGU](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.8 VRNA\_MODEL\_DEFAULT\_NO\_GU\_CLOSURE

```
#define VRNA_MODEL_DEFAULT_NO_GU_CLOSURE 0
#include <ViennaRNA/model.h>
```

Default model behavior for G-U base pairs closing a loop.

See also

[vrna\\_md\\_t.noGUclosure](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

#### 16.6.3.9 VRNA\_MODEL\_DEFAULT\_CIRC

```
#define VRNA_MODEL_DEFAULT_CIRC 0
#include <ViennaRNA/model.h>
```

Default model behavior to treat a molecule as a circular RNA (DNA)

See also

[vrna\\_md\\_t.circ](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.10 VRNA\_MODEL\_DEFAULT\_GQUAD

```
#define VRNA_MODEL_DEFAULT_GQUAD 0
#include <ViennaRNA/model.h>
```

Default model behavior regarding the treatment of G-Quadruplexes.

See also

[vrna\\_md\\_t.gquad](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.11 VRNA\_MODEL\_DEFAULT\_UNIQ\_ML

```
#define VRNA_MODEL_DEFAULT_UNIQ_ML 0
#include <ViennaRNA/model.h>
```

Default behavior of the model regarding unique multi-branch loop decomposition.

See also

[vrna\\_md\\_t.uniq\\_ML](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.12 VRNA\_MODEL\_DEFAULT\_ENERGY\_SET

```
#define VRNA_MODEL_DEFAULT_ENERGY_SET 0
#include <ViennaRNA/model.h>
```

Default model behavior on which energy set to use.

See also

[vrna\\_md\\_t.energy\\_set](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.13 VRNA\_MODEL\_DEFAULT\_BACKTRACK

```
#define VRNA_MODEL_DEFAULT_BACKTRACK 1
#include <ViennaRNA/model.h>
```

Default model behavior with regards to backtracking of structures.

See also

[vrna\\_md\\_t.backtrack](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.14 VRNA\_MODEL\_DEFAULT\_BACKTRACK\_TYPE

```
#define VRNA_MODEL_DEFAULT_BACKTRACK_TYPE 'F'
#include <ViennaRNA/model.h>
```

Default model behavior on what type of backtracking to perform.

See also

[vrna\\_md\\_t.backtrack\\_type](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.15 VRNA\_MODEL\_DEFAULT\_COMPUTE\_BPP

```
#define VRNA_MODEL_DEFAULT_COMPUTE_BPP 1
#include <ViennaRNA/model.h>
```

Default model behavior with regards to computing base pair probabilities.

See also

[vrna\\_md\\_t.compute\\_bpp](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.16 VRNA\_MODEL\_DEFAULT\_MAX\_BP\_SPAN**

```
#define VRNA_MODEL_DEFAULT_MAX_BP_SPAN -1
#include <ViennaRNA/model.h>
```

Default model behavior for the allowed maximum base pair span.

See also

[vrna\\_md\\_t.max\\_bp\\_span](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.17 VRNA\_MODEL\_DEFAULT\_WINDOW\_SIZE**

```
#define VRNA_MODEL_DEFAULT_WINDOW_SIZE -1
#include <ViennaRNA/model.h>
```

Default model behavior for the sliding window approach.

See also

[vrna\\_md\\_t.window\\_size](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.18 VRNA\_MODEL\_DEFAULT\_LOG\_ML**

```
#define VRNA_MODEL_DEFAULT_LOG_ML 0
#include <ViennaRNA/model.h>
```

Default model behavior on how to evaluate the energy contribution of multi-branch loops.

See also

[vrna\\_md\\_t.logML](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.19 VRNA\_MODEL\_DEFAULT\_ALI\_OLD\_EN**

```
#define VRNA_MODEL_DEFAULT_ALI_OLD_EN 0
#include <ViennaRNA/model.h>
```

Default model behavior for consensus structure energy evaluation.

See also

[vrna\\_md\\_t.oldAliEn](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.20 VRNA\_MODEL\_DEFAULT\_ALI\_RIBO**

```
#define VRNA_MODEL_DEFAULT_ALI_RIBO 0
#include <ViennaRNA/model.h>
```

Default model behavior for consensus structure co-variance contribution assessment.

See also

[vrna\\_md\\_t.ribo](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

**16.6.3.21 VRNA\_MODEL\_DEFAULT\_ALI\_CV\_FACT**

```
#define VRNA_MODEL_DEFAULT_ALI_CV_FACT 1.
#include <ViennaRNA/model.h>
```

Default model behavior for weighting the co-variance score in consensus structure prediction.

See also

[vrna\\_md\\_t.cv\\_fact](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.3.22 VRNA\_MODEL\_DEFAULT\_ALI\_NC\_FACT

```
#define VRNA_MODEL_DEFAULT_ALI_NC_FACT 1.
#include <ViennaRNA/model.h>
```

Default model behavior for weighting the nucleotide conservation? in consensus structure prediction.

See also

[vrna\\_md\\_t.nc\\_fact](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#)

## 16.6.4 Function Documentation

### 16.6.4.1 vrna\_md\_set\_default()

```
void vrna_md_set_default (
    vrna_md_t * md )
#include <ViennaRNA/model.h>
```

Apply default model details to a provided [vrna\\_md\\_t](#) data structure.

Use this function to initialize a [vrna\\_md\\_t](#) data structure with its default values

Parameters

|           |                                                                 |
|-----------|-----------------------------------------------------------------|
| <i>md</i> | A pointer to the data structure that is about to be initialized |
|-----------|-----------------------------------------------------------------|

### 16.6.4.2 vrna\_md\_update()

```
void vrna_md_update (
    vrna_md_t * md )
#include <ViennaRNA/model.h>
```

Update the model details data structure.

This function should be called after changing the [vrna\\_md\\_t.energy\\_set](#) attribute since it re-initializes base pairing related arrays within the [vrna\\_md\\_t](#) data structure. In particular, [vrna\\_md\\_t.pair](#), [vrna\\_md\\_t.alias](#), and [vrna\\_md\\_t.rtype](#) are set to the values that correspond to the specified [vrna\\_md\\_t.energy\\_set](#) option

See also

[vrna\\_md\\_t](#), [vrna\\_md\\_t.energy\\_set](#), [vrna\\_md\\_t.pair](#), [vrna\\_md\\_t.rtype](#), [vrna\\_md\\_t.alias](#), [vrna\\_md\\_set\\_default\(\)](#)

### 16.6.4.3 vrna\_md\_copy()

```
vrna_md_t * vrna_md_copy (
    vrna_md_t * md_to,
    const vrna_md_t * md_from )
#include <ViennaRNA/model.h>
```

Copy/Clone a [vrna\\_md\\_t](#) model.

Use this function to clone a given model either inplace (target container [md\\_to](#) given) or create a copy by cloning the source model and returning it ([md\\_to](#) == NULL).

Parameters

|                |                                                                                                 |
|----------------|-------------------------------------------------------------------------------------------------|
| <i>md_to</i>   | The model to be overwritten (if non-NULL and <a href="#">md_to</a> != <a href="#">md_from</a> ) |
| <i>md_from</i> | The model to copy (if non-NULL)                                                                 |

**Returns**

A pointer to the copy model (or NULL if `md_from == NULL`)

**16.6.4.4 vrna\_md\_option\_string()**

```
char * vrna_md_option_string (
    vrna_md_t * md )
```

```
#include <ViennaRNA/model.h>
```

Get a corresponding commandline parameter string of the options in a [vrna\\_md\\_t](#).

**Note**

This function is not threadsafe!

**16.6.4.5 vrna\_md\_defaults\_reset()**

```
void vrna_md_defaults_reset (
    vrna_md_t * md_p )
```

```
#include <ViennaRNA/model.h>
```

Reset the global default model details to a specific set of parameters, or their initial values.

This function resets the global default model details to their initial values, i.e. as specified by the ViennaRNA Package release, upon passing NULL as argument. Alternatively it resets them according to a set of provided parameters.

**Note**

The global default parameters affect all function calls of RNAlib where model details are not explicitly provided. Hence, any change of them is not considered threadsafe

**Warning**

This function first resets the global default settings to factory defaults, and only then applies user provided settings (if any). User settings that do not meet specifications are skipped.

**See also**

[vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#)

**Parameters**

|                   |                                                                                                    |
|-------------------|----------------------------------------------------------------------------------------------------|
| <code>md_p</code> | A set of model details to use as global default (if NULL is passed, factory defaults are restored) |
|-------------------|----------------------------------------------------------------------------------------------------|

**16.6.4.6 vrna\_md\_defaults\_temperature()**

```
void vrna_md_defaults_temperature (
    double T )
```

```
#include <ViennaRNA/model.h>
```

Set default temperature for energy evaluation of loops.

**See also**

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_TEMPERATURE](#)

## Parameters

|          |                           |
|----------|---------------------------|
| <i>T</i> | Temperature in centigrade |
|----------|---------------------------|

**16.6.4.7 vrna\_md\_defaults\_temperature\_get()**

```
double vrna_md_defaults_temperature_get (
    void )
#include <ViennaRNA/model.h>
Get default temperature for energy evaluation of loops.
```

## See also

[vrna\\_md\\_defaults\\_temperature\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_TEMPERATURE](#)

## Returns

The global default settings for temperature in centigrade

**16.6.4.8 vrna\_md\_defaults\_betaScale()**

```
void vrna_md_defaults_betaScale (
    double b )
#include <ViennaRNA/model.h>
Set default scaling factor of thermodynamic temperature in Boltzmann factors.
Boltzmann factors are then computed as  $\exp(-E/(b \cdot kT))$ .
```

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BETA\\_SCALE](#)

## Parameters

|          |                                    |
|----------|------------------------------------|
| <i>b</i> | The scaling factor, default is 1.0 |
|----------|------------------------------------|

**16.6.4.9 vrna\_md\_defaults\_betaScale\_get()**

```
double vrna_md_defaults_betaScale_get (
    void )
#include <ViennaRNA/model.h>
Get default scaling factor of thermodynamic temperature in Boltzmann factors.
```

## See also

[vrna\\_md\\_defaults\\_betaScale\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BETA\\_SCALE](#)

## Returns

The global default thermodynamic temperature scaling factor

**16.6.4.10 vrna\_md\_defaults\_dangles()**

```
void vrna_md_defaults_dangles (
    int d )
#include <ViennaRNA/model.h>
Set default dangle model for structure prediction.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_DANGLES](#)

**Parameters**

|          |                  |
|----------|------------------|
| <i>d</i> | The dangle model |
|----------|------------------|

**16.6.4.11 vrna\_md\_defaults\_dangles\_get()**

```
int vrna_md_defaults_dangles_get (
    void )
#include <ViennaRNA/model.h>
Get default dangle model for structure prediction.
```

See also

[vrna\\_md\\_defaults\\_dangles\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_DANGLES](#)

**Returns**

The global default settings for the dangle model

**16.6.4.12 vrna\_md\_defaults\_special\_hp()**

```
void vrna_md_defaults_special_hp (
    int flag )
#include <ViennaRNA/model.h>
Set default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_SPECIAL\\_HP](#)

**Parameters**

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.13 vrna\_md\_defaults\_special\_hp\_get()**

```
int vrna_md_defaults_special_hp_get (
    void )
#include <ViennaRNA/model.h>
Get default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.
```

## See also

[vrna\\_md\\_defaults\\_special\\_hp\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_SPECIAL\\_HP](#)

## Returns

The global default settings for the treatment of special hairpin loops

**16.6.4.14 vrna\_md\_defaults\_noLP()**

```
void vrna_md_defaults_noLP (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set default behavior for prediction of canonical secondary structures.

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_LP](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.15 vrna\_md\_defaults\_noLP\_get()**

```
int vrna_md_defaults_noLP_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default behavior for prediction of canonical secondary structures.

## See also

[vrna\\_md\\_defaults\\_noLP\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_LP](#)

## Returns

The global default settings for predicting canonical secondary structures

**16.6.4.16 vrna\_md\_defaults\_noGU()**

```
void vrna_md_defaults_noGU (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set default behavior for treatment of G-U wobble pairs.

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|



**16.6.4.17 vrna\_md\_defaults\_noGU\_get()**

```
int vrna_md_defaults_noGU_get (
    void )
#include <ViennaRNA/model.h>
Get default behavior for treatment of G-U wobble pairs.
```

See also

[vrna\\_md\\_defaults\\_noGU\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU](#)

Returns

The global default settings for treatment of G-U wobble pairs

**16.6.4.18 vrna\_md\_defaults\_noGUclosure()**

```
void vrna_md_defaults_noGUclosure (
    int flag )
#include <ViennaRNA/model.h>
Set default behavior for G-U pairs as closing pair for loops.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU\\_CLOSURE](#)

Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.19 vrna\_md\_defaults\_noGUclosure\_get()**

```
int vrna_md_defaults_noGUclosure_get (
    void )
#include <ViennaRNA/model.h>
Get default behavior for G-U pairs as closing pair for loops.
```

See also

[vrna\\_md\\_defaults\\_noGUclosure\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU\\_CLOSURE](#)

Returns

The global default settings for treatment of G-U pairs closing a loop

**16.6.4.20 vrna\_md\_defaults\_logML()**

```
void vrna_md_defaults_logML (
    int flag )
#include <ViennaRNA/model.h>
Set default behavior recomputing free energies of multi-branch loops using a logarithmic model.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_LOG\\_ML](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.21 vrna\_md\_defaults\_logML\_get()**

```
int vrna_md_defaults_logML_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default behavior recomputing free energies of multi-branch loops using a logarithmic model.

## See also

[vrna\\_md\\_defaults\\_logML\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_LOG\\_M](#)

## Returns

The global default settings for logarithmic model in multi-branch loop free energy evaluation

**16.6.4.22 vrna\_md\_defaults\_circ()**

```
void vrna_md_defaults_circ (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set default behavior whether input sequences are circularized.

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_CIRC](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.23 vrna\_md\_defaults\_circ\_get()**

```
int vrna_md_defaults_circ_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default behavior whether input sequences are circularized.

## See also

[vrna\\_md\\_defaults\\_circ\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_CIRC](#)

## Returns

The global default settings for treating input sequences as circular

**16.6.4.24 vrna\_md\_defaults\_gquad()**

```
void vrna_md_defaults_gquad (
    int flag )
```

```
#include <ViennaRNA/model.h>
Set default behavior for treatment of G-Quadruplexes.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_GQUAD](#)

Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

#### 16.6.4.25 vrna\_md\_defaults\_gquad\_get()

```
int vrna_md_defaults_gquad_get (
    void )
#include <ViennaRNA/model.h>
Get default behavior for treatment of G-Quadruplexes.
```

See also

[vrna\\_md\\_defaults\\_gquad\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_GQUAD](#)

Returns

The global default settings for treatment of G-Quadruplexes

#### 16.6.4.26 vrna\_md\_defaults\_uniq\_ML()

```
void vrna_md_defaults_uniq_ML (
    int flag )
#include <ViennaRNA/model.h>
Set default behavior for creating additional matrix for unique multi-branch loop prediction.
```

Note

Activating this option usually results in higher memory consumption!

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_UNIQ\\_ML](#)

Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

#### 16.6.4.27 vrna\_md\_defaults\_uniq\_ML\_get()

```
int vrna_md_defaults_uniq_ML_get (
    void )
#include <ViennaRNA/model.h>
Get default behavior for creating additional matrix for unique multi-branch loop prediction.
```

## See also

[vrna\\_md\\_defaults\\_uniq\\_ML\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_UNIQ](#)

## Returns

The global default settings for creating additional matrices for unique multi-branch loop prediction

**16.6.4.28 vrna\_md\_defaults\_energy\_set()**

```
void vrna_md_defaults_energy_set (
    int e )
#include <ViennaRNA/model.h>
Set default energy set.
```

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ENERGY\\_SET](#)

## Parameters

|          |                         |
|----------|-------------------------|
| <i>e</i> | Energy set (0, 1, 2, 3) |
|----------|-------------------------|

**16.6.4.29 vrna\_md\_defaults\_energy\_set\_get()**

```
int vrna_md_defaults_energy_set_get (
    void )
#include <ViennaRNA/model.h>
Get default energy set.
```

## See also

[vrna\\_md\\_defaults\\_energy\\_set\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_EN](#)

## Returns

The global default settings for the energy set

**16.6.4.30 vrna\_md\_defaults\_backtrack()**

```
void vrna_md_defaults_backtrack (
    int flag )
#include <ViennaRNA/model.h>
Set default behavior for whether to backtrack secondary structures.
```

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BACKTRACK](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.31 vrna\_md\_defaults\_backtrack\_get()**

```
int vrna_md_defaults_backtrack_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default behavior for whether to backtrack secondary structures.

See also

[vrna\\_md\\_defaults\\_backtrack\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BACKTRACK](#)

Returns

The global default settings for backtracking structures

**16.6.4.32 vrna\_md\_defaults\_backtrack\_type()**

```
void vrna_md_defaults_backtrack_type (
    char t )
```

```
#include <ViennaRNA/model.h>
```

Set default backtrack type, i.e. which DP matrix is used.

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BACKTRACK\\_TYPE](#)

Parameters

|          |                             |
|----------|-----------------------------|
| <i>t</i> | The type ('F', 'C', or 'M') |
|----------|-----------------------------|

**16.6.4.33 vrna\_md\_defaults\_backtrack\_type\_get()**

```
char vrna_md_defaults_backtrack_type_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default backtrack type, i.e. which DP matrix is used.

See also

[vrna\\_md\\_defaults\\_backtrack\\_type\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_BACKTRACK\\_TYPE](#)

Returns

The global default settings that specify which DP matrix is used for backtracking

**16.6.4.34 vrna\_md\_defaults\_compute\_bpp()**

```
void vrna_md_defaults_compute_bpp (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set the default behavior for whether to compute base pair probabilities after partition function computation.

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_COMPUTE\\_BPP](#)

## Parameters

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.35 vrna\_md\_defaults\_compute\_bpp\_get()**

```
int vrna_md_defaults_compute_bpp_get (
    void )
#include <ViennaRNA/model.h>
```

Get the default behavior for whether to compute base pair probabilities after partition function computation.

## See also

[vrna\\_md\\_defaults\\_compute\\_bpp\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_C](#)

## Returns

The global default settings that specify whether base pair probabilities are computed together with partition function

**16.6.4.36 vrna\_md\_defaults\_max\_bp\_span()**

```
void vrna_md_defaults_max_bp_span (
    int span )
#include <ViennaRNA/model.h>
```

Set default maximal base pair span.

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_MAX\\_BP\\_SPAN](#)

## Parameters

|             |                        |
|-------------|------------------------|
| <i>span</i> | Maximal base pair span |
|-------------|------------------------|

**16.6.4.37 vrna\_md\_defaults\_max\_bp\_span\_get()**

```
int vrna_md_defaults_max_bp_span_get (
    void )
#include <ViennaRNA/model.h>
```

Get default maximal base pair span.

## See also

[vrna\\_md\\_defaults\\_max\\_bp\\_span\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_C](#)

## Returns

The global default settings for maximum base pair span

**16.6.4.38 vrna\_md\_defaults\_min\_loop\_size()**

```
void vrna_md_defaults_min_loop_size (
    int size )
```

```
#include <ViennaRNA/model.h>
Set default minimal loop size.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [TURN](#)

Parameters

|             |                                                                      |
|-------------|----------------------------------------------------------------------|
| <i>size</i> | Minimal size, i.e. number of unpaired nucleotides for a hairpin loop |
|-------------|----------------------------------------------------------------------|

#### 16.6.4.39 vrna\_md\_defaults\_min\_loop\_size\_get()

```
int vrna_md_defaults_min_loop_size_get (
    void )
#include <ViennaRNA/model.h>
Get default minimal loop size.
```

See also

[vrna\\_md\\_defaults\\_min\\_loop\\_size\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [TURN](#)

Returns

The global default settings for minimal size of hairpin loops

#### 16.6.4.40 vrna\_md\_defaults\_window\_size()

```
void vrna_md_defaults_window_size (
    int size )
#include <ViennaRNA/model.h>
Set default window size for sliding window structure prediction approaches.
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_WINDOW\\_SIZE](#)

Parameters

|             |                                |
|-------------|--------------------------------|
| <i>size</i> | The size of the sliding window |
|-------------|--------------------------------|

#### 16.6.4.41 vrna\_md\_defaults\_window\_size\_get()

```
int vrna_md_defaults_window_size_get (
    void )
#include <ViennaRNA/model.h>
Get default window size for sliding window structure prediction approaches.
```

See also

[vrna\\_md\\_defaults\\_window\\_size\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_W](#)

**Returns**

The global default settings for the size of the sliding window

**16.6.4.42 vrna\_md\_defaults\_oldAliEn()**

```
void vrna_md_defaults_oldAliEn (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set default behavior for whether to use old energy model for comparative structure prediction.

**Note**

This option is outdated. Activating the old energy model usually results in worse consensus structure predictions.

**See also**

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_OLD\\_EN](#)

**Parameters**

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|

**16.6.4.43 vrna\_md\_defaults\_oldAliEn\_get()**

```
int vrna_md_defaults_oldAliEn_get (
    void )
```

```
#include <ViennaRNA/model.h>
```

Get default behavior for whether to use old energy model for comparative structure prediction.

**See also**

[vrna\\_md\\_defaults\\_oldAliEn\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_O](#)

**Returns**

The global default settings for using old energy model for comparative structure prediction

**16.6.4.44 vrna\_md\_defaults\_ribo()**

```
void vrna_md_defaults_ribo (
    int flag )
```

```
#include <ViennaRNA/model.h>
```

Set default behavior for whether to use Ribosum Scoring in comparative structure prediction.

**See also**

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_RIBO](#)

**Parameters**

|             |                                    |
|-------------|------------------------------------|
| <i>flag</i> | On/Off switch (0 = OFF, else = ON) |
|-------------|------------------------------------|



**16.6.4.45 vrna\_md\_defaults\_ribo\_get()**

```
int vrna_md_defaults_ribo_get (
    void )
#include <ViennaRNA/model.h>
```

Get default behavior for whether to use Ribosum Scoring in comparative structure prediction.

See also

[vrna\\_md\\_defaults\\_ribo\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_RIBO](#)

Returns

The global default settings for using Ribosum scoring in comparative structure prediction

**16.6.4.46 vrna\_md\_defaults\_cv\_fact()**

```
void vrna_md_defaults_cv_fact (
    double factor )
#include <ViennaRNA/model.h>
```

Set the default co-variance scaling factor used in comparative structure prediction.

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_CV\\_FACT](#)

Parameters

|               |                        |
|---------------|------------------------|
| <i>factor</i> | The co-variance factor |
|---------------|------------------------|

**16.6.4.47 vrna\_md\_defaults\_cv\_fact\_get()**

```
double vrna_md_defaults_cv_fact_get (
    void )
#include <ViennaRNA/model.h>
```

Get the default co-variance scaling factor used in comparative structure prediction.

See also

[vrna\\_md\\_defaults\\_cv\\_fact\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_CV\\_FACT](#)

Returns

The global default settings for the co-variance factor

**16.6.4.48 vrna\_md\_defaults\_nc\_fact()**

```
void vrna_md_defaults_nc_fact (
    double factor )
#include <ViennaRNA/model.h>
```

See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_NC\\_FACT](#)

## Parameters

|               |  |
|---------------|--|
| <i>factor</i> |  |
|---------------|--|

**16.6.4.49 vrna\_md\_defaults\_nc\_fact\_get()**

```
double vrna_md_defaults_nc_fact_get (
    void )
#include <ViennaRNA/model.h>
```

## See also

[vrna\\_md\\_defaults\\_nc\\_fact\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_MODEL\\_DEFAULT\\_ALI\\_NC](#)

## Returns

**16.6.4.50 vrna\_md\_defaults\_sfact()**

```
void vrna_md_defaults_sfact (
    double factor )
#include <ViennaRNA/model.h>
```

Set the default scaling factor used to avoid under-/overflows in partition function computation.

## See also

[vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#)

## Parameters

|               |                                    |
|---------------|------------------------------------|
| <i>factor</i> | The scaling factor (default: 1.07) |
|---------------|------------------------------------|

**16.6.4.51 vrna\_md\_defaults\_sfact\_get()**

```
double vrna_md_defaults_sfact_get (
    void )
#include <ViennaRNA/model.h>
```

Get the default scaling factor used to avoid under-/overflows in partition function computation.

## See also

[vrna\\_md\\_defaults\\_sfact\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_md\\_t](#)

## Returns

The global default settings of the scaling factor

**16.6.4.52 set\_model\_details()**

```
void set_model_details (
    vrna_md_t * md )
#include <ViennaRNA/model.h>
```

Set default model details.

Use this function if you wish to initialize a `vrna_md_t` data structure with its default values, i.e. the global model settings as provided by the deprecated global variables.

**Deprecated** This function will vanish as soon as backward compatibility of RNAlib is dropped (expected in version 3). Use `vrna_md_set_default()` instead!

#### Parameters

|                 |                                                                 |
|-----------------|-----------------------------------------------------------------|
| <code>md</code> | A pointer to the data structure that is about to be initialized |
|-----------------|-----------------------------------------------------------------|

## 16.6.5 Variable Documentation

### 16.6.5.1 temperature

```
double temperature [extern]
```

```
#include <ViennaRNA/model.h>
```

Rescale energy parameters to a temperature in degC.

Default is 37C. You have to call the `update_..._params()` functions after changing this parameter.

**Deprecated** Use `vrna_md_defaults_temperature()`, and `vrna_md_defaults_temperature_get()` to change, and read the global default temperature settings

See also

[vrna\\_md\\_defaults\\_temperature\(\)](#), [vrna\\_md\\_defaults\\_temperature\\_get\(\)](#), [vrna\\_md\\_defaults\\_reset\(\)](#)

### 16.6.5.2 pf\_scale

```
double pf_scale [extern]
```

```
#include <ViennaRNA/model.h>
```

A scaling factor used by `pf_fold()` to avoid overflows.

Should be set to approximately  $\exp((-F/kT)/length)$ , where  $F$  is an estimate for the ensemble free energy, for example the minimum free energy. You must call `update_pf_params()` after changing this parameter.

If `pf_scale` is -1 (the default), an estimate will be provided automatically when computing partition functions, e.g. `pf_fold()`. The automatic estimate is usually insufficient for sequences more than a few hundred bases long.

### 16.6.5.3 dangles

```
int dangles [extern]
```

```
#include <ViennaRNA/model.h>
```

Switch the energy model for dangling end contributions (0, 1, 2, 3)

If set to 0 no stabilizing energies are assigned to bases adjacent to helices in free ends and multiloops (so called dangling ends). Normally (`dangles` = 1) dangling end energies are assigned only to unpaired bases and a base cannot participate simultaneously in two dangling ends. In the partition function algorithm `pf_fold()` these checks are neglected. If `dangles` is set to 2, all folding routines will follow this convention. This treatment of dangling ends gives more favorable energies to helices directly adjacent to one another, which can be beneficial since such helices often do engage in stabilizing interactions through co-axial stacking.

If `dangles` = 3 co-axial stacking is explicitly included for adjacent helices in multiloops. The option affects only mfe folding and energy evaluation (`fold()` and `energy_of_structure()`), as well as suboptimal folding (`subopt()`) via re-evaluation of energies. Co-axial stacking with one intervening mismatch is not considered so far.

Default is 2 in most algorithms, partition function algorithms can only handle 0 and 2

#### 16.6.5.4 tetra\_loop

```
int tetra_loop [extern]
#include <ViennaRNA/model.h>
```

Include special stabilizing energies for some tri-, tetra- and hexa-loops; default is 1.

#### 16.6.5.5 noLonelyPairs

```
int noLonelyPairs [extern]
#include <ViennaRNA/model.h>
```

Global switch to avoid/allow helices of length 1.  
Disallow all pairs which can only occur as lonely pairs (i.e. as helix of length 1). This avoids lonely base pairs in the predicted structures in most cases.

#### 16.6.5.6 energy\_set

```
int energy_set [extern]
#include <ViennaRNA/model.h>
```

0 = BP; 1=any with GC; 2=any with AU-parameter  
If set to 1 or 2: fold sequences from an artificial alphabet ABCD..., where A pairs B, C pairs D, etc. using either GC (1) or AU parameters (2); default is 0, you probably don't want to change it.

#### 16.6.5.7 do\_backtrack

```
int do_backtrack [extern]
#include <ViennaRNA/model.h>
```

do backtracking, i.e. compute secondary structures or base pair probabilities  
If 0, do not calculate pair probabilities in [pf\\_fold\(\)](#); this is about twice as fast. Default is 1.

#### 16.6.5.8 backtrack\_type

```
char backtrack_type [extern]
#include <ViennaRNA/model.h>
```

A backtrack array marker for [inverse\\_fold\(\)](#)  
If set to 'C': force (1,N) to be paired, 'M' fold as if the sequence were inside a multiloop. Otherwise ('F') the usual mfe structure is computed.

#### 16.6.5.9 nonstandards

```
char* nonstandards [extern]
#include <ViennaRNA/model.h>
```

contains allowed non standard base pairs  
Lists additional base pairs that will be allowed to form in addition to GC, CG, AU, UA, GU and UG. Nonstandard base pairs are given a stacking energy of 0.

#### 16.6.5.10 max\_bp\_span

```
int max_bp_span [extern]
#include <ViennaRNA/model.h>
```

Maximum allowed base pair span.  
A value of -1 indicates no restriction for distant base pairs.

## 16.7 Energy Parameters

All relevant functions to retrieve and copy pre-calculated energy parameter sets as well as reading/writing the energy parameter set from/to file(s).

### 16.7.1 Detailed Description

All relevant functions to retrieve and copy pre-calculated energy parameter sets as well as reading/writing the energy parameter set from/to file(s).

This module covers all relevant functions for pre-calculation of the energy parameters necessary for the folding routines provided by RNAlib. Furthermore, the energy parameter set in the RNAlib can be easily exchanged by a user-defined one. It is also possible to write the current energy parameter set into a text file. Collaboration diagram for Energy Parameters:

#### Modules

- [Reading/Writing Energy Parameter Sets from/to File](#)  
*Read and Write energy parameter sets from and to files or strings.*

#### Files

- file [basic.h](#)  
*Functions to deal with sets of energy parameters.*
- file [constants.h](#)  
*Energy parameter constants.*
- file [convert.h](#)  
*Functions and definitions for energy parameter file format conversion.*
- file [io.h](#)  
*Read and write energy parameter files.*

#### Data Structures

- struct [vrna\\_param\\_s](#)  
*The datastructure that contains temperature scaled energy parameters. [More...](#)*
- struct [vrna\\_exp\\_param\\_s](#)  
*The data structure that contains temperature scaled Boltzmann weights of the energy parameters. [More...](#)*

#### Typedefs

- typedef struct [vrna\\_param\\_s](#) **vrna\_param\_t**  
*Typename for the free energy parameter data structure [vrna\\_params](#).*
- typedef struct [vrna\\_exp\\_param\\_s](#) **vrna\_exp\_param\_t**  
*Typename for the Boltzmann factor data structure [vrna\\_exp\\_params](#).*
- typedef struct [vrna\\_param\\_s](#) paramT  
*Old typename of [vrna\\_param\\_s](#).*
- typedef struct [vrna\\_exp\\_param\\_s](#) pf\_paramT  
*Old typename of [vrna\\_exp\\_param\\_s](#).*

#### Functions

- [vrna\\_param\\_t \\* vrna\\_params](#) ([vrna\\_md\\_t](#) \*md)  
*Get a data structure containing prescaled free energy parameters.*
- [vrna\\_param\\_t \\* vrna\\_params\\_copy](#) ([vrna\\_param\\_t](#) \*par)  
*Get a copy of the provided free energy parameters.*
- [vrna\\_exp\\_param\\_t \\* vrna\\_exp\\_params](#) ([vrna\\_md\\_t](#) \*md)  
*Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors.*
- [vrna\\_exp\\_param\\_t \\* vrna\\_exp\\_params\\_comparative](#) (unsigned int n\_seq, [vrna\\_md\\_t](#) \*md)  
*Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors (alifold version)*

- `vrna_exp_param_t * vrna_exp_params_copy (vrna_exp_param_t *par)`  
*Get a copy of the provided free energy parameters (provided as Boltzmann factors)*
- `void vrna_params_subst (vrna_fold_compound_t *vc, vrna_param_t *par)`  
*Update/Reset energy parameters data structure within a `vrna_fold_compound_t`.*
- `void vrna_exp_params_subst (vrna_fold_compound_t *vc, vrna_exp_param_t *params)`  
*Update the energy parameters for subsequent partition function computations.*
- `void vrna_exp_params_rescale (vrna_fold_compound_t *vc, double *mfe)`  
*Rescale Boltzmann factors for partition function computations.*
- `void vrna_params_reset (vrna_fold_compound_t *vc, vrna_md_t *md_p)`  
*Reset free energy parameters within a `vrna_fold_compound_t` according to provided, or default model details.*
- `void vrna_exp_params_reset (vrna_fold_compound_t *vc, vrna_md_t *md_p)`  
*Reset Boltzmann factors for partition function computations within a `vrna_fold_compound_t` according to provided, or default model details.*
- `vrna_exp_param_t * get_scaled_pf_parameters (void)`
- `vrna_exp_param_t * get_boltzmann_factors (double temperature, double betaScale, vrna_md_t md, double pf_scale)`  
*Get precomputed Boltzmann factors of the loop type dependent energy contributions with independent thermodynamic temperature.*
- `vrna_exp_param_t * get_boltzmann_factor_copy (vrna_exp_param_t *parameters)`  
*Get a copy of already precomputed Boltzmann factors.*
- `vrna_exp_param_t * get_scaled_alipf_parameters (unsigned int n_seq)`  
*Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant)*
- `vrna_exp_param_t * get_boltzmann_factors_ali (unsigned int n_seq, double temperature, double betaScale, vrna_md_t md, double pf_scale)`  
*Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant) with independent thermodynamic temperature.*
- `vrna_param_t * scale_parameters (void)`  
*Get precomputed energy contributions for all the known loop types.*
- `vrna_param_t * get_scaled_parameters (double temperature, vrna_md_t md)`  
*Get precomputed energy contributions for all the known loop types.*

## 16.7.2 Data Structure Documentation

### 16.7.2.1 struct vrna\_param\_s

The datastructure that contains temperature scaled energy parameters.

Collaboration diagram for `vrna_param_s`:

#### Data Fields

- double **temperature**  
*Temperature used for loop contribution scaling.*
- `vrna_md_t` **model\_details**  
*Model details to be used in the recursions.*
- char **param\_file** [256]  
*The filename the parameters were derived from, or empty string if they represent the default.*

### 16.7.2.2 struct vrna\_exp\_param\_s

The data structure that contains temperature scaled Boltzmann weights of the energy parameters.

Collaboration diagram for `vrna_exp_param_s`:

## Data Fields

- int `id`  
*An identifier for the data structure.*
- double `pf_scale`  
*Scaling factor to avoid over-/underflows.*
- double `temperature`  
*Temperature used for loop contribution scaling.*
- double `alpha`  
*Scaling factor for the thermodynamic temperature.*
- `vrna_md_t` `model_details`  
*Model details to be used in the recursions.*
- char `param_file` [256]  
*The filename the parameters were derived from, or empty string if they represent the default.*

### 16.7.2.2.1 Field Documentation

**16.7.2.2.1.1 `id`** `int vrna_exp_param_s::id`  
An identifier for the data structure.

**Deprecated** This attribute will be removed in version 3

**16.7.2.2.1.2 `alpha`** `double vrna_exp_param_s::alpha`  
Scaling factor for the thermodynamic temperature.  
This allows for temperature scaling in Boltzmann factors independently from the energy contributions. The resulting Boltzmann factors are then computed by  $e^{-E/(\alpha \cdot K \cdot T)}$

## 16.7.3 Typedef Documentation

### 16.7.3.1 `paramT`

```
typedef struct vrna_param_s paramT
#include <ViennaRNA/params/basic.h>
```

Old typename of `vrna_param_s`.

**Deprecated** Use `vrna_param_t` instead!

### 16.7.3.2 `pf_paramT`

```
typedef struct vrna_exp_param_s pf_paramT
#include <ViennaRNA/params/basic.h>
```

Old typename of `vrna_exp_param_s`.

**Deprecated** Use `vrna_exp_param_t` instead!

## 16.7.4 Function Documentation

#### 16.7.4.1 vrna\_params()

```
vrna_param_t * vrna_params (
    vrna_md_t * md )
#include <ViennaRNA/params/basic.h>
```

Get a data structure containing prescaled free energy parameters.

If a NULL pointer is passed for the model details parameter, the default model parameters are stored within the requested `vrna_param_t` structure.

See also

[vrna\\_md\\_t](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_exp\\_params\(\)](#)

##### Parameters

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| <i>md</i> | A pointer to the model details to store inside the structure (Maybe NULL) |
|-----------|---------------------------------------------------------------------------|

##### Returns

A pointer to the memory location where the requested parameters are stored

#### 16.7.4.2 vrna\_params\_copy()

```
vrna_param_t * vrna_params_copy (
    vrna_param_t * par )
#include <ViennaRNA/params/basic.h>
```

Get a copy of the provided free energy parameters.

If NULL is passed as parameter, a default set of energy parameters is created and returned.

See also

[vrna\\_params\(\)](#), [vrna\\_param\\_t](#)

##### Parameters

|            |                                                               |
|------------|---------------------------------------------------------------|
| <i>par</i> | The free energy parameters that are to be copied (Maybe NULL) |
|------------|---------------------------------------------------------------|

##### Returns

A copy or a default set of the (provided) parameters

#### 16.7.4.3 vrna\_exp\_params()

```
vrna_exp_param_t * vrna_exp_params (
    vrna_md_t * md )
#include <ViennaRNA/params/basic.h>
```

Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors.

This function returns a data structure that contains all necessary precomputed energy contributions for each type of loop.

In contrast to [vrna\\_params\(\)](#), the free energies within this data structure are stored as their Boltzmann factors, i.e.

$\exp(-E/kT)$

where  $E$  is the free energy.

If a NULL pointer is passed for the model details parameter, the default model parameters are stored within the requested `vrna_exp_param_t` structure.



See also

[vrna\\_md\\_t](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_params\(\)](#), [vrna\\_rescale\\_pf\\_params\(\)](#)

Parameters

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| <i>md</i> | A pointer to the model details to store inside the structure (Maybe NULL) |
|-----------|---------------------------------------------------------------------------|

Returns

A pointer to the memory location where the requested parameters are stored

#### 16.7.4.4 vrna\_exp\_params\_comparative()

```
vrna_exp_param_t * vrna_exp_params_comparative (
    unsigned int n_seq,
    vrna_md_t * md )
```

```
#include <ViennaRNA/params/basic.h>
```

Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors (alifold version)

If a NULL pointer is passed for the model details parameter, the default model parameters are stored within the requested [vrna\\_exp\\_param\\_t](#) structure.

See also

[vrna\\_md\\_t](#), [vrna\\_md\\_set\\_default\(\)](#), [vrna\\_exp\\_params\(\)](#), [vrna\\_params\(\)](#)

Parameters

|              |                                                                           |
|--------------|---------------------------------------------------------------------------|
| <i>n_seq</i> | The number of sequences in the alignment                                  |
| <i>md</i>    | A pointer to the model details to store inside the structure (Maybe NULL) |

Returns

A pointer to the memory location where the requested parameters are stored

#### 16.7.4.5 vrna\_exp\_params\_copy()

```
vrna_exp_param_t * vrna_exp_params_copy (
    vrna_exp_param_t * par )
```

```
#include <ViennaRNA/params/basic.h>
```

Get a copy of the provided free energy parameters (provided as Boltzmann factors)

If NULL is passed as parameter, a default set of energy parameters is created and returned.

See also

[vrna\\_exp\\_params\(\)](#), [vrna\\_exp\\_param\\_t](#)

Parameters

|            |                                                               |
|------------|---------------------------------------------------------------|
| <i>par</i> | The free energy parameters that are to be copied (Maybe NULL) |
|------------|---------------------------------------------------------------|

## Returns

A copy or a default set of the (provided) parameters

16.7.4.6 `vrna_params_subst()`

```
void vrna_params_subst (
    vrna_fold_compound_t * vc,
    vrna_param_t * par )
#include <ViennaRNA/params/basic.h>
```

Update/Reset energy parameters data structure within a `vrna_fold_compound_t`.

Passing `NULL` as second argument leads to a reset of the energy parameters within `vc` to their default values. Otherwise, the energy parameters provided will be copied over into `vc`.

## See also

[vrna\\_params\\_reset\(\)](#), [vrna\\_param\\_t](#), [vrna\\_md\\_t](#), [vrna\\_params\(\)](#)

## Parameters

|                  |                                                                                                  |
|------------------|--------------------------------------------------------------------------------------------------|
| <code>vc</code>  | The <a href="#">vrna_fold_compound_t</a> that is about to receive updated energy parameters      |
| <code>par</code> | The energy parameters used to substitute those within <code>vc</code> (Maybe <code>NULL</code> ) |

**SWIG Wrapper Notes** This function is attached to `vrna_fc_s` objects as overloaded `params_subst()` method.

When no parameter is passed, the resulting action is the same as passing `NULL` as second parameter to [vrna\\_params\\_subst\(\)](#), i.e. resetting the parameters to the global defaults.

16.7.4.7 `vrna_exp_params_subst()`

```
void vrna_exp_params_subst (
    vrna_fold_compound_t * vc,
    vrna_exp_param_t * params )
#include <ViennaRNA/params/basic.h>
```

Update the energy parameters for subsequent partition function computations.

This function can be used to properly assign new energy parameters for partition function computations to a [vrna\\_fold\\_compound\\_t](#). For this purpose, the data of the provided pointer `params` will be copied into `vc` and a recomputation of the partition function scaling factor is issued, if the `pf_scale` attribute of `params` is less than 1.0.

Passing `NULL` as second argument leads to a reset of the energy parameters within `vc` to their default values

## See also

[vrna\\_exp\\_params\\_reset\(\)](#), [vrna\\_exp\\_params\\_rescale\(\)](#), [vrna\\_exp\\_param\\_t](#), [vrna\\_md\\_t](#), [vrna\\_exp\\_params\(\)](#)

## Parameters

|                     |                                        |
|---------------------|----------------------------------------|
| <code>vc</code>     | The fold compound data structure       |
| <code>params</code> | A pointer to the new energy parameters |

**SWIG Wrapper Notes** This function is attached to `vrna_fc_s` objects as overloaded `exp_params_subst()` method.

When no parameter is passed, the resulting action is the same as passing `NULL` as second parameter to [vrna\\_exp\\_params\\_subst\(\)](#), i.e. resetting the parameters to the global defaults.

#### 16.7.4.8 vrna\_exp\_params\_rescale()

```
void vrna_exp_params_rescale (
    vrna_fold_compound_t * vc,
    double * mfe )
#include <ViennaRNA/params/basic.h>
```

Rescale Boltzmann factors for partition function computations.

This function may be used to (automatically) rescale the Boltzmann factors used in partition function computations. Since partition functions over subsequences can easily become extremely large, the RNAlib internally rescales them to avoid numerical over- and/or underflow. Therefore, a proper scaling factor  $s$  needs to be chosen that in turn is then used to normalize the corresponding partition functions  $\hat{q}[i, j] = q[i, j]/s^{(j-i+1)}$ .

This function provides two ways to automatically adjust the scaling factor.

1. Automatic guess
2. Automatic adjustment according to MFE

Passing `NULL` as second parameter activates the *automatic guess mode*. Here, the scaling factor is recomputed according to a mean free energy of `184.3*length` cal for random sequences.

##### Note

This recomputation only takes place if the `pf_scale` attribute of the `exp_params` data structure contained in `vc` has a value below `1.0`.

On the other hand, if the MFE for a sequence is known, it can be used to recompute a more robust scaling factor, since it represents the lowest free energy of the entire ensemble of structures, i.e. the highest Boltzmann factor. To activate this second mode of *automatic adjustment according to MFE*, a pointer to the MFE value needs to be passed as second argument. This value is then taken to compute the scaling factor as  $s = \exp((sfact * MFE)/kT/length)$ , where `sfact` is an additional scaling weight located in the `vrna_md_t` data structure of `exp_params` in `vc`.

The computed scaling factor  $s$  will be stored as `pf_scale` attribute of the `exp_params` data structure in `vc`.

##### See also

[vrna\\_exp\\_params\\_subst\(\)](#), [vrna\\_md\\_t](#), [vrna\\_exp\\_param\\_t](#), [vrna\\_fold\\_compound\\_t](#)

##### Parameters

|                  |                                                         |
|------------------|---------------------------------------------------------|
| <code>vc</code>  | The fold compound data structure                        |
| <code>mfe</code> | A pointer to the MFE (in kcal/mol) or <code>NULL</code> |

**SWIG Wrapper Notes** This function is attached to `vrna_fc_s` objects as overloaded `exp_params_rescale()` method.

When no parameter is passed to this method, the resulting action is the same as passing `NULL` as second parameter to `vrna_exp_params_rescale()`, i.e. default scaling of the partition function. Passing an energy in kcal/mol, e.g. as retrieved by a previous call to the `mfe()` method, instructs all subsequent calls to scale the partition function accordingly.

#### 16.7.4.9 vrna\_params\_reset()

```
void vrna_params_reset (
    vrna_fold_compound_t * vc,
    vrna_md_t * md_p )
#include <ViennaRNA/params/basic.h>
```

Reset free energy parameters within a `vrna_fold_compound_t` according to provided, or default model details.

This function allows one to rescale free energy parameters for subsequent structure prediction or evaluation according to a set of model details, e.g. temperature values. To do so, the caller provides either a pointer to a set of model details to be used for rescaling, or `NULL` if global default setting should be used.

See also

[vrna\\_exp\\_params\\_reset\(\)](#), [vrna\\_params\\_subs\(\)](#)

#### Parameters

|             |                                                                    |
|-------------|--------------------------------------------------------------------|
| <i>vc</i>   | The fold compound data structure                                   |
| <i>md_p</i> | A pointer to the new model details (or NULL for reset to defaults) |

**SWIG Wrapper Notes** This function is attached to [vrna\\_fc\\_s](#) objects as overloaded **params\_reset()** method.

When no parameter is passed to this method, the resulting action is the same as passing *NULL* as second parameter to [vrna\\_params\\_reset\(\)](#), i.e. global default model settings are used. Passing an object of type [vrna\\_md\\_s](#) resets the fold compound according to the specifications stored within the [vrna\\_md\\_s](#) object.

#### 16.7.4.10 vrna\_exp\_params\_reset()

```
vrna_exp_params_reset (
    vrna_fold_compound_t * vc,
    vrna_md_t * md_p )
#include <ViennaRNA/params/basic.h>
```

Reset Boltzmann factors for partition function computations within a [vrna\\_fold\\_compound\\_t](#) according to provided, or default model details.

This function allows one to rescale Boltzmann factors for subsequent partition function computations according to a set of model details, e.g. temperature values. To do so, the caller provides either a pointer to a set of model details to be used for rescaling, or NULL if global default setting should be used.

See also

[vrna\\_params\\_reset\(\)](#), [vrna\\_exp\\_params\\_subst\(\)](#), [vrna\\_exp\\_params\\_rescale\(\)](#)

#### Parameters

|             |                                                                    |
|-------------|--------------------------------------------------------------------|
| <i>vc</i>   | The fold compound data structure                                   |
| <i>md_p</i> | A pointer to the new model details (or NULL for reset to defaults) |

**SWIG Wrapper Notes** This function is attached to [vrna\\_fc\\_s](#) objects as overloaded **exp\_params\_reset()** method.

When no parameter is passed to this method, the resulting action is the same as passing *NULL* as second parameter to [vrna\\_exp\\_params\\_reset\(\)](#), i.e. global default model settings are used. Passing an object of type [vrna\\_md\\_s](#) resets the fold compound according to the specifications stored within the [vrna\\_md\\_s](#) object.

#### 16.7.4.11 get\_scaled\_pf\_parameters()

```
vrna_exp_param_t * get_scaled_pf_parameters (
    void )
#include <ViennaRNA/params/basic.h>
```

get a data structure of type [vrna\\_exp\\_param\\_t](#) which contains the Boltzmann weights of several energy parameters scaled according to the current temperature

**Deprecated** Use [vrna\\_exp\\_params\(\)](#) instead!

#### Returns

The data structure containing Boltzmann weights for use in partition function calculations

#### 16.7.4.12 `get_boltzmann_factors()`

```
vrna_exp_param_t * get_boltzmann_factors (
    double temperature,
    double betaScale,
    vrna_md_t md,
    double pf_scale )
```

```
#include <ViennaRNA/params/basic.h>
```

Get precomputed Boltzmann factors of the loop type dependent energy contributions with independent thermodynamic temperature.

This function returns a data structure that contains all necessary precalculated Boltzmann factors for each loop type contribution.

In contrast to [get\\_scaled\\_pf\\_parameters\(\)](#), this function enables setting of independent temperatures for both, the individual energy contributions as well as the thermodynamic temperature used in  $\exp(-\Delta G/kT)$

**Deprecated** Use [vrna\\_exp\\_params\(\)](#) instead!

#### See also

[get\\_scaled\\_pf\\_parameters\(\)](#), [get\\_boltzmann\\_factor\\_copy\(\)](#)

#### Parameters

|                    |                                                                                                    |
|--------------------|----------------------------------------------------------------------------------------------------|
| <i>temperature</i> | The temperature in degrees Celcius used for (re-)scaling the energy contributions                  |
| <i>betaScale</i>   | A scaling value that is used as a multiplication factor for the absolute temperature of the system |
| <i>md</i>          | The model details to be used                                                                       |
| <i>pf_scale</i>    | The scaling factor for the Boltzmann factors                                                       |

#### Returns

A set of precomputed Boltzmann factors

#### 16.7.4.13 `get_boltzmann_factor_copy()`

```
vrna_exp_param_t * get_boltzmann_factor_copy (
    vrna_exp_param_t * parameters )
```

```
#include <ViennaRNA/params/basic.h>
```

Get a copy of already precomputed Boltzmann factors.

**Deprecated** Use [vrna\\_exp\\_params\\_copy\(\)](#) instead!

#### See also

[get\\_boltzmann\\_factors\(\)](#), [get\\_scaled\\_pf\\_parameters\(\)](#)

#### Parameters

|                   |                                               |
|-------------------|-----------------------------------------------|
| <i>parameters</i> | The input data structure that shall be copied |
|-------------------|-----------------------------------------------|

**Returns**

A copy of the provided Boltzmann factor data set

**16.7.4.14 get\_scaled\_alipf\_parameters()**

```
vrna_exp_param_t * get_scaled_alipf_parameters (
    unsigned int n_seq )
#include <ViennaRNA/params/basic.h>
```

Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant)

**Deprecated** Use `vrna_exp_params_comparative()` instead!

**16.7.4.15 get\_boltzmann\_factors\_ali()**

```
vrna_exp_param_t * get_boltzmann_factors_ali (
    unsigned int n_seq,
    double temperature,
    double betaScale,
    vrna_md_t md,
    double pf_scale )
#include <ViennaRNA/params/basic.h>
```

Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant) with independent thermodynamic temperature.

**Deprecated** Use `vrna_exp_params_comparative()` instead!

**16.7.4.16 scale\_parameters()**

```
vrna_param_t * scale_parameters (
    void )
#include <ViennaRNA/params/basic.h>
```

Get precomputed energy contributions for all the known loop types.

**Note**

OpenMP: This function relies on several global model settings variables and thus is not to be considered threadsafe. See [get\\_scaled\\_parameters\(\)](#) for a completely threadsafe implementation.

**Deprecated** Use `vrna_params()` instead!

**Returns**

A set of precomputed energy contributions

**16.7.4.17 get\_scaled\_parameters()**

```
vrna_param_t * get_scaled_parameters (
    double temperature,
    vrna_md_t md )
#include <ViennaRNA/params/basic.h>
```

Get precomputed energy contributions for all the known loop types.

Call this function to retrieve precomputed energy contributions, i.e. scaled according to the temperature passed. Furthermore, this function assumes a data structure that contains the model details as well, such that subsequent folding recursions are able to retrieve the correct model settings

**Deprecated** Use `vrna_params()` instead!

See also

[vrna\\_md\\_t, set\\_model\\_details\(\)](#)

Parameters

|                    |                                    |
|--------------------|------------------------------------|
| <i>temperature</i> | The temperature in degrees Celcius |
| <i>md</i>          | The model details                  |

Returns

precomputed energy contributions and model settings

## 16.8 Extending the Folding Grammar with Additional Domains

This module covers simple and straight-forward extensions to the RNA folding grammar.

### 16.8.1 Detailed Description

This module covers simple and straight-forward extensions to the RNA folding grammar.

Collaboration diagram for Extending the Folding Grammar with Additional Domains:

#### Modules

- [Unstructured Domains](#)  
*Add and modify unstructured domains to the RNA folding grammar.*
- [Structured Domains](#)  
*Add and modify structured domains to the RNA folding grammar.*

## 16.9 Unstructured Domains

Add and modify unstructured domains to the RNA folding grammar.

### 16.9.1 Detailed Description

Add and modify unstructured domains to the RNA folding grammar.

This module provides the tools to add and modify unstructured domains to the production rules of the RNA folding grammar. Usually this functionality is utilized for incorporating ligand binding to unpaired stretches of an RNA.

**Bug** Although the additional production rule(s) for unstructured domains as described in [Unstructured Domains](#) are always treated as 'segments possibly bound to one or more ligands', the current implementation requires that at least one ligand is bound. The default implementation already takes care of the required changes, however, upon using callback functions other than the default ones, one has to take care of this fact. Please also note, that this behavior might change in one of the next releases, such that the decomposition schemes as shown above comply with the actual implementation.

A default implementation allows one to readily use this feature by simply adding sequence motifs and corresponding binding free energies with the function [vrna\\_ud\\_add\\_motif\(\)](#) (see also [Ligands Binding to Unstructured Domains](#)). The grammar extension is realized using a callback function that

- evaluates the binding free energy of a ligand to its target sequence segment (white boxes in the figures above), or
- returns the free energy of an unpaired stretch possibly bound by a ligand, stored in the additional *UDP* matrix.

The callback is passed the segment positions, the loop context, and which of the two above mentioned evaluations are required. A second callback implements the pre-processing step that prepares the *UDP* matrix by evaluating all possible cases of the additional production rule. Both callbacks have a default implementation in *RNAlib*, but may be over-written by a user-implementation, making it fully user-customizable.

For equilibrium probability computations, two additional callbacks exist. One to store/add and one to retrieve the probability of unstructured domains at particular positions. Our implementation already takes care of computing the probabilities, but users of the unstructured domain feature are required to provide a mechanism to efficiently store/add the corresponding values into some external data structure. Collaboration diagram for Unstructured Domains:

## Files

- file [unstructured\\_domains.h](#)

*Functions to modify unstructured domains, e.g. to incorporate ligands binding to unpaired stretches.*

## Data Structures

- struct [vrna\\_unstructured\\_domain\\_s](#)

*Data structure to store all functionality for ligand binding. [More...](#)*

## Macros

- `#define VRNA_UNSTRUCTURED_DOMAIN_EXT_LOOP 1U`  
*Flag to indicate ligand bound to unpaired stretch in the exterior loop.*
- `#define VRNA_UNSTRUCTURED_DOMAIN_HP_LOOP 2U`  
*Flag to indicate ligand bound to unpaired stretch in a hairpin loop.*
- `#define VRNA_UNSTRUCTURED_DOMAIN_INT_LOOP 4U`  
*Flag to indicate ligand bound to unpaired stretch in an interior loop.*
- `#define VRNA_UNSTRUCTURED_DOMAIN_MB_LOOP 8U`  
*Flag to indicate ligand bound to unpaired stretch in a multibranch loop.*
- `#define VRNA_UNSTRUCTURED_DOMAIN_MOTIF 16U`  
*Flag to indicate ligand binding without additional unbound nucleotides (motif-only)*
- `#define VRNA_UNSTRUCTURED_DOMAIN_ALL_LOOPS`  
*Flag to indicate ligand bound to unpaired stretch in any loop (convenience macro)*

## Typedefs

- `typedef struct vrna\_unstructured\_domain\_s vrna_ud_t`  
*Typename for the ligand binding extension data structure [vrna\\_unstructured\\_domain\\_s](#).*
- `typedef int(vrna\_callback\_ud\_energy(vrna_fold_compound_t *vc, int i, int j, unsigned int loop_type, void *data))`  
*Callback to retrieve binding free energy of a ligand bound to an unpaired sequence segment.*
- `typedef FLT_OR_DBL(vrna\_callback\_ud\_exp\_energy(vrna_fold_compound_t *vc, int i, int j, unsigned int loop_type, void *data))`  
*Callback to retrieve Boltzmann factor of the binding free energy of a ligand bound to an unpaired sequence segment.*
- `typedef void(vrna\_callback\_ud\_production(vrna_fold_compound_t *vc, void *data))`  
*Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature.*
- `typedef void(vrna\_callback\_ud\_exp\_production(vrna_fold_compound_t *vc, void *data))`  
*Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature (partition function variant)*
- `typedef void(vrna\_callback\_ud\_probs\_add(vrna_fold_compound_t *vc, int i, int j, unsigned int loop_type, FLT_OR_DBL exp_energy, void *data))`  
*Callback to store/add equilibrium probability for a ligand bound to an unpaired sequence segment.*
- `typedef FLT_OR_DBL(vrna\_callback\_ud\_probs\_get(vrna_fold_compound_t *vc, int i, int j, unsigned int loop_type, int motif, void *data))`  
*Callback to retrieve equilibrium probability for a ligand bound to an unpaired sequence segment.*



## Functions

- `vrna_ud_motif_t * vrna_ud_motifs_centroid (vrna_fold_compound_t *fc, const char *structure)`  
*Detect unstructured domains in centroid structure.*
- `vrna_ud_motif_t * vrna_ud_motifs_MEA (vrna_fold_compound_t *fc, const char *structure, vrna_ep_t *probability_list)`  
*Detect unstructured domains in MEA structure.*
- `vrna_ud_motif_t * vrna_ud_motifs_MFE (vrna_fold_compound_t *fc, const char *structure)`  
*Detect unstructured domains in MFE structure.*
- `void vrna_ud_add_motif (vrna_fold_compound_t *vc, const char *motif, double motif_en, const char *motif_name, unsigned int loop_type)`  
*Add an unstructured domain motif, e.g. for ligand binding.*
- `void vrna_ud_remove (vrna_fold_compound_t *vc)`  
*Remove ligand binding to unpaired stretches.*
- `void vrna_ud_set_data (vrna_fold_compound_t *vc, void *data, vrna_callback_free_auxdata *free_cb)`  
*Attach an auxiliary data structure.*
- `void vrna_ud_set_prod_rule_cb (vrna_fold_compound_t *vc, vrna_callback_ud_production *pre_cb, vrna_callback_ud_energy *e_cb)`  
*Attach production rule callbacks for free energies computations.*
- `void vrna_ud_set_exp_prod_rule_cb (vrna_fold_compound_t *vc, vrna_callback_ud_exp_production *pre_cb, vrna_callback_ud_exp_energy *exp_e_cb)`  
*Attach production rule for partition function.*

## 16.9.2 Data Structure Documentation

### 16.9.2.1 struct vrna\_unstructured\_domain\_s

Data structure to store all functionality for ligand binding.

#### Data Fields

- `int uniq_motif_count`  
*The unique number of motifs of different lengths.*
- `unsigned int * uniq_motif_size`  
*An array storing a unique list of motif lengths.*
- `int motif_count`  
*Total number of distinguished motifs.*
- `char ** motif`  
*Motif sequences.*
- `char ** motif_name`  
*Motif identifier/name.*
- `unsigned int * motif_size`  
*Motif lengths.*
- `double * motif_en`  
*Ligand binding free energy contribution.*
- `unsigned int * motif_type`  
*Type of motif, i.e. loop type the ligand binds to.*
- `vrna_callback_ud_production * prod_cb`  
*Callback to ligand binding production rule, i.e. create/fill DP free energy matrices.*
- `vrna_callback_ud_exp_production * exp_prod_cb`  
*Callback to ligand binding production rule, i.e. create/fill DP partition function matrices.*
- `vrna_callback_ud_energy * energy_cb`  
*Callback to evaluate free energy of ligand binding to a particular unpaired stretch.*

- `vrna_callback_ud_exp_energy` \* `exp_energy_cb`  
Callback to evaluate Boltzmann factor of ligand binding to a particular unpaired stretch.
- `void` \* `data`  
Auxiliary data structure passed to energy evaluation callbacks.
- `vrna_callback_free_auxdata` \* `free_data`  
Callback to free auxiliary data structure.
- `vrna_callback_ud_probs_add` \* `probs_add`  
Callback to store/add outside partition function.
- `vrna_callback_ud_probs_get` \* `probs_get`  
Callback to retrieve outside partition function.

### 16.9.2.1.1 Field Documentation

**16.9.2.1.1.1 prod\_cb** `vrna_callback_ud_production`\* `vrna_unstructured_domain_s::prod_cb`

Callback to ligand binding production rule, i.e. create/fill DP free energy matrices.

This callback will be executed right before the actual secondary structure decompositions, and, therefore, any implementation must not interleave with the regular DP matrices.

## 16.9.3 Typedef Documentation

### 16.9.3.1 vrna\_callback\_ud\_energy

```
typedef int() vrna_callback_ud_energy(vrna_fold_compound_t *vc, int i, int j, unsigned int
loop_type, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback to retrieve binding free energy of a ligand bound to an unpaired sequence segment.

**Notes on Callback Functions** This function will be called to determine the additional energy contribution of a specific unstructured domain, e.g. the binding free energy of some ligand.

#### Parameters

|                        |                                               |
|------------------------|-----------------------------------------------|
| <code>vc</code>        | The current <code>vrna_fold_compound_t</code> |
| <code>i</code>         | The start of the unstructured domain (5' end) |
| <code>j</code>         | The end of the unstructured domain (3' end)   |
| <code>loop_type</code> | The loop context of the unstructured domain   |
| <code>data</code>      | Auxiliary data                                |

#### Returns

The auxiliary energy contribution in deka-cal/mol

### 16.9.3.2 vrna\_callback\_ud\_exp\_energy

```
typedef FLT_OR_DBL() vrna_callback_ud_exp_energy(vrna_fold_compound_t *vc, int i, int j, unsigned
int loop_type, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback to retrieve Boltzmann factor of the binding free energy of a ligand bound to an unpaired sequence segment.

**Notes on Callback Functions** This function will be called to determine the additional energy contribution of a specific unstructured domain, e.g. the binding free energy of some ligand (Partition function variant, i.e. the Boltzmann factors instead of actual free energies).

## Parameters

|                  |                                                  |
|------------------|--------------------------------------------------|
| <i>vc</i>        | The current <a href="#">vrna_fold_compound_t</a> |
| <i>i</i>         | The start of the unstructured domain (5' end)    |
| <i>j</i>         | The end of the unstructured domain (3' end)      |
| <i>loop_type</i> | The loop context of the unstructured domain      |
| <i>data</i>      | Auxiliary data                                   |

## Returns

The auxiliary energy contribution as Boltzmann factor

**16.9.3.3 vrna\_callback\_ud\_production**

```
typedef void() vrna_callback_ud_production(vrna_fold_compound_t *vc, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature.

**Notes on Callback Functions** The production rule for the unstructured domain grammar extension

**16.9.3.4 vrna\_callback\_ud\_exp\_production**

```
typedef void() vrna_callback_ud_exp_production(vrna_fold_compound_t *vc, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature (partition function variant)

**Notes on Callback Functions** The production rule for the unstructured domain grammar extension (Partition function variant)

**16.9.3.5 vrna\_callback\_ud\_probs\_add**

```
typedef void() vrna_callback_ud_probs_add(vrna_fold_compound_t *vc, int i, int j, unsigned int
loop_type, FLT_OR_DBL exp_energy, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback to store/add equilibrium probability for a ligand bound to an unpaired sequence segment.

**Notes on Callback Functions** A callback function to store equilibrium probabilities for the unstructured domain feature

**16.9.3.6 vrna\_callback\_ud\_probs\_get**

```
typedef FLT_OR_DBL() vrna_callback_ud_probs_get(vrna_fold_compound_t *vc, int i, int j, unsigned
int loop_type, int motif, void *data)
#include <ViennaRNA/unstructured_domains.h>
```

Callback to retrieve equilibrium probability for a ligand bound to an unpaired sequence segment.

**Notes on Callback Functions** A callback function to retrieve equilibrium probabilities for the unstructured domain feature

**16.9.4 Function Documentation**

#### 16.9.4.1 vrna\_ud\_motifs\_centroid()

```
vrna_ud_motif_t * vrna_ud_motifs_centroid (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/unstructured_domains.h>
```

Detect unstructured domains in centroid structure.

Given a centroid structure and a set of unstructured domains compute the list of unstructured domain motifs present in the centroid. Since we do not explicitly annotate unstructured domain motifs in dot-bracket strings, this function can be used to check for the presence and location of unstructured domain motifs under the assumption that the dot-bracket string is the centroid structure of the equilibrium ensemble.

See also

[vrna\\_centroid\(\)](#)

##### Parameters

|                  |                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------|
| <i>fc</i>        | The fold_compound data structure with pre-computed equilibrium probabilities and model settings |
| <i>structure</i> | The centroid structure in dot-bracket notation                                                  |

##### Returns

A list of unstructured domain motifs (possibly NULL). The last element terminates the list with `start=0`, `number=-1`

#### 16.9.4.2 vrna\_ud\_motifs\_MEA()

```
vrna_ud_motif_t * vrna_ud_motifs_MEA (
    vrna_fold_compound_t * fc,
    const char * structure,
    vrna_ep_t * probability_list )
#include <ViennaRNA/unstructured_domains.h>
```

Detect unstructured domains in MEA structure.

Given an MEA structure and a set of unstructured domains compute the list of unstructured domain motifs present in the MEA structure. Since we do not explicitly annotate unstructured domain motifs in dot-bracket strings, this function can be used to check for the presence and location of unstructured domain motifs under the assumption that the dot-bracket string is the MEA structure of the equilibrium ensemble.

See also

[MEA\(\)](#)

##### Parameters

|                         |                                                                                                 |
|-------------------------|-------------------------------------------------------------------------------------------------|
| <i>fc</i>               | The fold_compound data structure with pre-computed equilibrium probabilities and model settings |
| <i>structure</i>        | The MEA structure in dot-bracket notation                                                       |
| <i>probability_list</i> | The list of probabilities to extract the MEA structure from                                     |

##### Returns

A list of unstructured domain motifs (possibly NULL). The last element terminates the list with `start=0`, `number=-1`

### 16.9.4.3 vrna\_ud\_motifs\_MFE()

```
vrna_ud_motif_t * vrna_ud_motifs_MFE (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/unstructured_domains.h>
```

Detect unstructured domains in MFE structure.

Given an MFE structure and a set of unstructured domains compute the list of unstructured domain motifs present in the MFE structure. Since we do not explicitly annotate unstructured domain motifs in dot-bracket strings, this function can be used to check for the presence and location of unstructured domain motifs under the assumption that the dot-bracket string is the MFE structure of the equilibrium ensemble.

See also

[vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                      |
|------------------|------------------------------------------------------|
| <i>fc</i>        | The fold_compound data structure with model settings |
| <i>structure</i> | The MFE structure in dot-bracket notation            |

#### Returns

A list of unstructured domain motifs (possibly NULL). The last element terminates the list with `start=0`, `number=-1`

### 16.9.4.4 vrna\_ud\_add\_motif()

```
void vrna_ud_add_motif (
    vrna_fold_compound_t * vc,
    const char * motif,
    double motif_en,
    const char * motif_name,
    unsigned int loop_type )
#include <ViennaRNA/unstructured_domains.h>
```

Add an unstructured domain motif, e.g. for ligand binding.

This function adds a ligand binding motif and the associated binding free energy to the `vrna_ud_t` attribute of a `vrna_fold_compound_t`. The motif data will then be used in subsequent secondary structure predictions. Multiple calls to this function with different motifs append all additional data to a list of ligands, which all will be evaluated. Ligand motif data can be removed from the `vrna_fold_compound_t` again using the `vrna_ud_remove()` function. The loop type parameter allows one to limit the ligand binding to particular loop type, such as the exterior loop, hairpin loops, interior loops, or multibranch loops.

See also

[VRNA\\_UNSTRUCTURED\\_DOMAIN\\_EXT\\_LOOP](#), [VRNA\\_UNSTRUCTURED\\_DOMAIN\\_HP\\_LOOP](#), [VRNA\\_UNSTRUCTURED\\_DOMAIN\\_MB\\_LOOP](#), [VRNA\\_UNSTRUCTURED\\_DOMAIN\\_ALL\\_LOOPS](#), [vrna\\_ud\\_remove\(\)](#)

#### Parameters

|                   |                                                                                          |
|-------------------|------------------------------------------------------------------------------------------|
| <i>vc</i>         | The <code>vrna_fold_compound_t</code> data structure the ligand motif should be bound to |
| <i>motif</i>      | The sequence motif the ligand binds to                                                   |
| <i>motif_en</i>   | The binding free energy of the ligand in kcal/mol                                        |
| <i>motif_name</i> | The name/id of the motif (may be NULL)                                                   |
| <i>loop_type</i>  | The loop type the ligand binds to                                                        |

#### 16.9.4.5 vrna\_ud\_remove()

```
void vrna_ud_remove (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/unstructured_domains.h>
```

Remove ligand binding to unpaired stretches.

This function removes all ligand motifs that were bound to a `vrna_fold_compound_t` using the `vrna_ud_add_motif()` function.

##### Parameters

|    |                                                                                                   |
|----|---------------------------------------------------------------------------------------------------|
| vc | The <code>vrna_fold_compound_t</code> data structure the ligand motif data should be removed from |
|----|---------------------------------------------------------------------------------------------------|

**SWIG Wrapper Notes** This function is attached as method `ud_remove()` to objects of type `fold_compound`

#### 16.9.4.6 vrna\_ud\_set\_data()

```
void vrna_ud_set_data (
    vrna_fold_compound_t * vc,
    void * data,
    vrna_callback_free_auxdata * free_cb )
#include <ViennaRNA/unstructured_domains.h>
```

Attach an auxiliary data structure.

This function binds an arbitrary, auxiliary data structure for user-implemented ligand binding. The optional callback `free_cb` will be passed the bound data structure whenever the `vrna_fold_compound_t` is removed from memory to avoid memory leaks.

##### See also

`vrna_ud_set_prod_rule_cb()`, `vrna_ud_set_exp_prod_rule_cb()`, `vrna_ud_remove()`

##### Parameters

|         |                                                                                                      |
|---------|------------------------------------------------------------------------------------------------------|
| vc      | The <code>vrna_fold_compound_t</code> data structure the auxiliary data structure should be bound to |
| data    | A pointer to the auxiliary data structure                                                            |
| free_cb | A pointer to a callback function that free's memory occupied by <code>data</code>                    |

**SWIG Wrapper Notes** This function is attached as method `ud_set_data()` to objects of type `fold_compound`

#### 16.9.4.7 vrna\_ud\_set\_prod\_rule\_cb()

```
void vrna_ud_set_prod_rule_cb (
    vrna_fold_compound_t * vc,
    vrna_callback_ud_production * pre_cb,
    vrna_callback_ud_energy * e_cb )
#include <ViennaRNA/unstructured_domains.h>
```

Attach production rule callbacks for free energies computations.

Use this function to bind a user-implemented grammar extension for unstructured domains.

The callback `e_cb` needs to evaluate the free energy contribution  $f(i, j)$  of the unpaired segment  $[i, j]$ . It will be executed in each of the regular secondary structure production rules. Whenever the callback is passed the `VRNA_UNSTRUCTURED_DOMAIN_MOTIF` flag via its `loop_type` parameter the contribution of

any ligand that consecutively binds from position  $i$  to  $j$  (the white box) is requested. Otherwise, the callback usually performs a lookup in the precomputed  $B$  matrices. Which  $B$  matrix is addressed will be indicated by the flags `VRNA_UNSTRUCTURED_DOMAIN_EXT_LOOP`, `VRNA_UNSTRUCTURED_DOMAIN_HP_LOOP`, `VRNA_UNSTRUCTURED_DOMAIN_INT_LOOP`, and `VRNA_UNSTRUCTURED_DOMAIN_MB_LOOP`. As their names already imply, they specify exterior loops (F production rule), hairpin loops and interior loops (C production rule), and multibranch loops (M and M1 production rule).

$$f(i,j) = \boxed{\phantom{ij}} \mid \overbrace{\phantom{ij}}^B$$

$i \qquad j \qquad i \qquad j$

The `pre_cb` callback will be executed as a pre-processing step right before the regular secondary structure rules. Usually one would use this callback to fill the dynamic programming matrices  $U$  and preparations of the auxiliary data structure `vrna_unstructured_domain_s.data`

$$\overbrace{\phantom{ij}}^B = \overbrace{\phantom{ij-1j}}^B \bullet \mid \overbrace{\phantom{ij}}^B \boxed{\phantom{u+1j}}$$

$i \qquad j \qquad i \qquad j-1 \quad j \qquad i \qquad u \quad u+1 \quad j$

#### Parameters

|                     |                                                                                    |
|---------------------|------------------------------------------------------------------------------------|
| <code>vc</code>     | The <code>vrna_fold_compound_t</code> data structure the callback will be bound to |
| <code>pre_cb</code> | A pointer to a callback function for the $B$ production rule                       |
| <code>e_cb</code>   | A pointer to a callback function for free energy evaluation                        |

**SWIG Wrapper Notes** This function is attached as method `ud_set_prod_rule_cb()` to objects of type `fold_compound`

#### 16.9.4.8 `vrna_ud_set_exp_prod_rule_cb()`

```
void vrna_ud_set_exp_prod_rule_cb (
    vrna_fold_compound_t * vc,
    vrna_callback_ud_exp_production * pre_cb,
    vrna_callback_ud_exp_energy * exp_e_cb )
#include <ViennaRNA/unstructured_domains.h>
```

Attach production rule for partition function.

This function is the partition function companion of `vrna_ud_set_prod_rule_cb()`.

Use it to bind callbacks to (i) fill the  $U$  production rule dynamic programming matrices and/or prepare the `vrna_unstructured_domain_s.data`, and (ii) provide a callback to retrieve partition functions for subsegments  $[i, j]$ .

$$\overbrace{\phantom{ij}}^B = \overbrace{\phantom{ij-1j}}^B \bullet \mid \overbrace{\phantom{ij}}^B \boxed{\phantom{u+1j}}$$

$i \qquad j \qquad i \qquad j-1 \quad j \qquad i \qquad u \quad u+1 \quad j$

$$f(i,j) = \boxed{\phantom{B}} \mid \overbrace{\phantom{B}}^B$$

*i*                      *j*                      *i*                      *j*

See also

[vrna\\_ud\\_set\\_prod\\_rule\\_cb\(\)](#)

#### Parameters

|                       |                                                                                                                                         |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| <code>vc</code>       | The <a href="#">vrna_fold_compound_t</a> data structure the callback will be bound to                                                   |
| <code>pre_cb</code>   | A pointer to a callback function for the B production rule                                                                              |
| <code>exp_e_cb</code> | A pointer to a callback function that retrieves the partition function for a segment $[i, j]$ that may be bound by one or more ligands. |

**SWIG Wrapper Notes** This function is attached as method `ud_set_exp_prod_rule_cb()` to objects of type `fold_compound`

## 16.10 Structured Domains

Add and modify structured domains to the RNA folding grammar.

### 16.10.1 Detailed Description

Add and modify structured domains to the RNA folding grammar.

This module provides the tools to add and modify structured domains to the production rules of the RNA folding grammar. Usually this functionality is utilized for incorporating self-enclosed structural modules that exhibit a more or less complex base pairing pattern. Collaboration diagram for Structured Domains:

#### Files

- file [structured\\_domains.h](#)

*This module provides interfaces that deal with additional structured domains in the folding grammar.*

## 16.11 Constraining the RNA Folding Grammar

This module provides general functions that allow for an easy control of constrained secondary structure prediction and evaluation.

### 16.11.1 Detailed Description

This module provides general functions that allow for an easy control of constrained secondary structure prediction and evaluation.

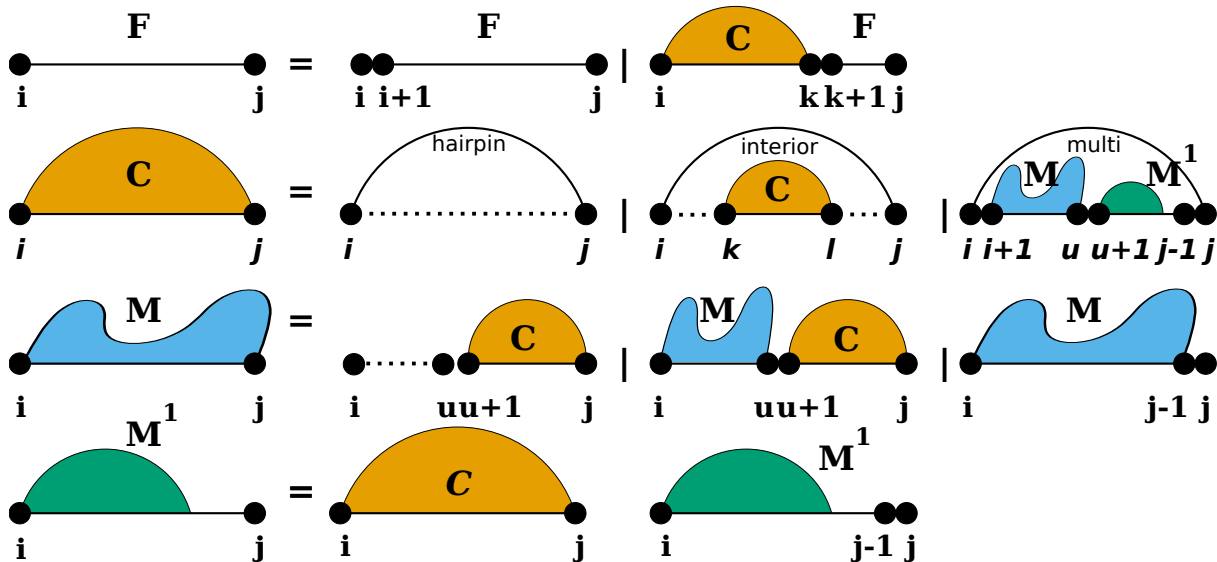
Secondary Structure constraints can be subdivided into two groups:

- [Hard Constraints](#), and
- [Soft Constraints](#).



While Hard-Constraints directly influence the production rules used in the folding recursions by allowing, disallowing, or enforcing certain decomposition steps, Soft-constraints on the other hand are used to change position specific contributions in the recursions by adding bonuses/penalties in form of pseudo free energies to certain loop configurations.

Secondary structure constraints are always applied at decomposition level, i.e. in each step of the recursive structure decomposition, for instance during MFE prediction. Below is a visualization of the decomposition scheme



For **Hard Constraints** the following option flags may be used to constrain the pairing behavior of single, or pairs of nucleotides:

- **VRNA\_CONSTRAINT\_CONTEXT\_EXT\_LOOP** - Hard constraints flag, base pair in the exterior loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_HP\_LOOP** - Hard constraints flag, base pair encloses hairpin loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_INT\_LOOP** - Hard constraints flag, base pair encloses an interior loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_INT\_LOOP\_ENC** - Hard constraints flag, base pair encloses a multi branch loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_MB\_LOOP** - Hard constraints flag, base pair is enclosed in an interior loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_MB\_LOOP\_ENC** - Hard constraints flag, base pair is enclosed in a multi branch loop.
- **VRNA\_CONSTRAINT\_CONTEXT\_ENFORCE** - Hard constraint flag to indicate enforcement of constraints.
- **VRNA\_CONSTRAINT\_CONTEXT\_NO\_REMOVE** - Hard constraint flag to indicate not to remove base pairs that conflict with a given constraint.
- **VRNA\_CONSTRAINT\_CONTEXT\_ALL\_LOOPS** - Constraint context flag indicating any loop context.

However, for **Soft Constraints** we do not allow for simple loop type dependent constraining. But soft constraints are equipped with generic constraint support. This enables the user to pass arbitrary callback functions that return auxiliary energy contributions for evaluation the evaluation of any decomposition.

The callback will then always be notified about the type of decomposition that is happening, and the corresponding delimiting sequence positions. The following decomposition steps are distinguished, and should be captured by the user's implementation of the callback:

- **VRNA\_DECOMP\_PAIR\_HP** - Flag passed to generic softt constraints callback to indicate hairpin loop decomposition step.
- **VRNA\_DECOMP\_PAIR\_IL** - Indicator for interior loop decomposition step.

- [VRNA\\_DECOMP\\_PAIR\\_ML](#) - Indicator for multibranch loop decomposition step.
- [VRNA\\_DECOMP\\_ML\\_ML\\_ML](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_ML\\_STEM](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_ML\\_ML](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_ML\\_UP](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_ML\\_ML\\_STEM](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_ML\\_COAXIAL](#) - Indicator for decomposition of multibranch loop part.
- [VRNA\\_DECOMP\\_EXT\\_EXT](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_UP](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_STEM](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_EXT\\_EXT](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_STEM\\_EXT](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_STEM\\_OUTSIDE](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM](#) - Indicator for decomposition of exterior loop part.
- [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM1](#) - Indicator for decomposition of exterior loop part.

Simplified interfaces to the soft constraints framework can be obtained by the implementations in the submodules

- [SHAPE Reactivity Data](#) and
- [Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints](#).

An implementation that generates soft constraints for unpaired nucleotides by minimizing the discrepancy between their predicted and expected pairing probability is available in submodule [Generate Soft Constraints from Data](#). Collaboration diagram for Constraining the RNA Folding Grammar:

## Modules

- [Hard Constraints](#)  
*This module covers all functionality for hard constraints in secondary structure prediction.*
- [Soft Constraints](#)  
*Functions and data structures for secondary structure soft constraints.*

## Files

- file [basic.h](#)  
*Functions and data structures for constraining secondary structure predictions and evaluation.*

## Macros

- `#define VRNA_CONSTRAINT_FILE 0`  
*Flag for [vrna\\_constraints\\_add\(\)](#) to indicate that constraints are present in a text file.*
- `#define VRNA_CONSTRAINT_SOFT_MFE 0`  
*Indicate generation of constraints for MFE folding.*
- `#define VRNA_CONSTRAINT_SOFT_PF VRNA_OPTION_PF`  
*Indicate generation of constraints for partition function computation.*
- `#define VRNA_DECOMP_PAIR_HP (unsigned char)1`  
*Flag passed to generic softt constraints callback to indicate hairpin loop decomposition step.*

- #define `VRNA_DECOMP_PAIR_IL` (unsigned char)2  
*Indicator for interior loop decomposition step.*
- #define `VRNA_DECOMP_PAIR_ML` (unsigned char)3  
*Indicator for multibranch loop decomposition step.*
- #define `VRNA_DECOMP_ML_ML_ML` (unsigned char)5  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_STEM` (unsigned char)6  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_ML` (unsigned char)7  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_UP` (unsigned char)8  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_ML_STEM` (unsigned char)9  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_COAXIAL` (unsigned char)10  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_ML_COAXIAL_ENC` (unsigned char)11  
*Indicator for decomposition of multibranch loop part.*
- #define `VRNA_DECOMP_EXT_EXT` (unsigned char)12  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_UP` (unsigned char)13  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_STEM` (unsigned char)14  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_EXT_EXT` (unsigned char)15  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_STEM_EXT` (unsigned char)16  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_STEM_OUTSIDE` (unsigned char)17  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_EXT_STEM` (unsigned char)18  
*Indicator for decomposition of exterior loop part.*
- #define `VRNA_DECOMP_EXT_EXT_STEM1` (unsigned char)19  
*Indicator for decomposition of exterior loop part.*

## Functions

- void `vrna_constraints_add` (`vrna_fold_compound_t` \*vc, const char \*constraint, unsigned int options)  
*Add constraints to a `vrna_fold_compound_t` data structure.*
- void `vrna_message_constraint_options` (unsigned int option)  
*Print a help message for pseudo dot-bracket structure constraint characters to stdout. (constraint support is specified by option parameter)*
- void `vrna_message_constraint_options_all` (void)  
*Print structure constraint characters to stdout (full constraint support)*

### 16.11.2 Macro Definition Documentation

### 16.11.2.1 VRNA\_CONSTRAINT\_FILE

```
#define VRNA_CONSTRAINT_FILE 0
```

```
#include <ViennaRNA/constraints/basic.h>
```

Flag for `vrna_constraints_add()` to indicate that constraints are present in a text file.

See also

`vrna_constraints_add()`

**Deprecated** Use 0 instead!

### 16.11.2.2 VRNA\_CONSTRAINT\_SOFT\_MFE

```
#define VRNA_CONSTRAINT_SOFT_MFE 0
```

```
#include <ViennaRNA/constraints/basic.h>
```

Indicate generation of constraints for MFE folding.

**Deprecated** This flag has no meaning anymore, since constraints are now always stored!

### 16.11.2.3 VRNA\_CONSTRAINT\_SOFT\_PF

```
#define VRNA_CONSTRAINT_SOFT_PF VRNA_OPTION_PF
```

```
#include <ViennaRNA/constraints/basic.h>
```

Indicate generation of constraints for partition function computation.

**Deprecated** Use `VRNA_OPTION_PF` instead!

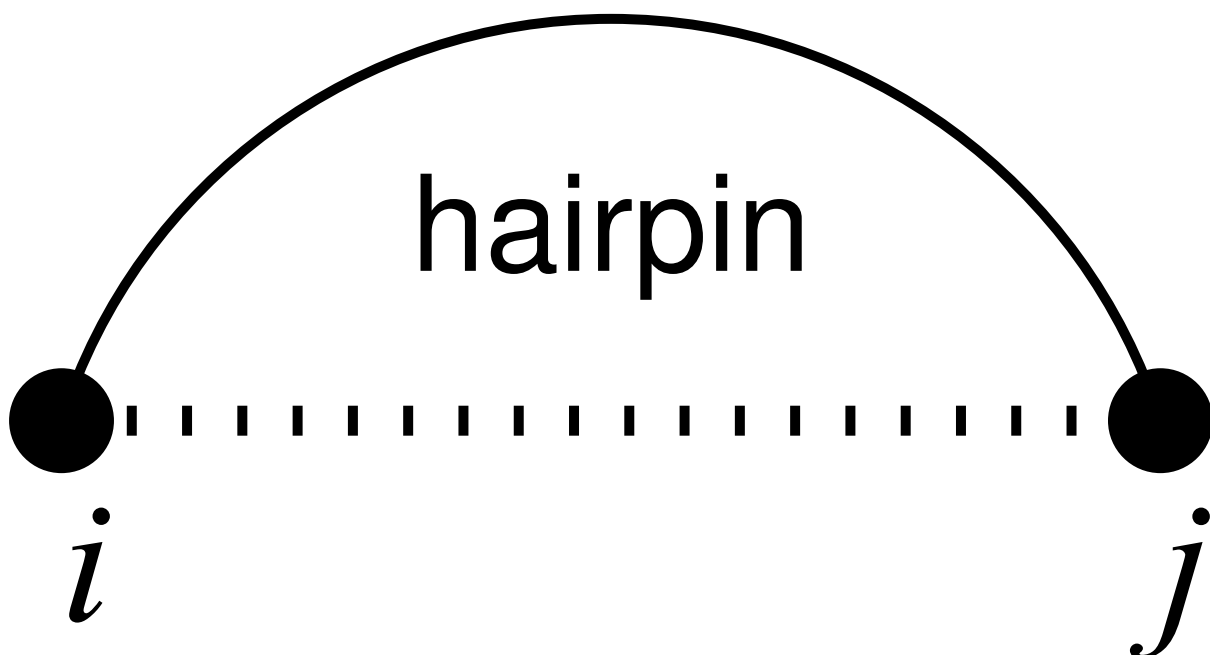
### 16.11.2.4 VRNA\_DECOMP\_PAIR\_HP

```
#define VRNA_DECOMP_PAIR_HP (unsigned char)1
```

```
#include <ViennaRNA/constraints/basic.h>
```

Flag passed to generic softt constraints callback to indicate hairpin loop decomposition step.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a hairpin loop enclosed by the base pair  $(i, j)$ .

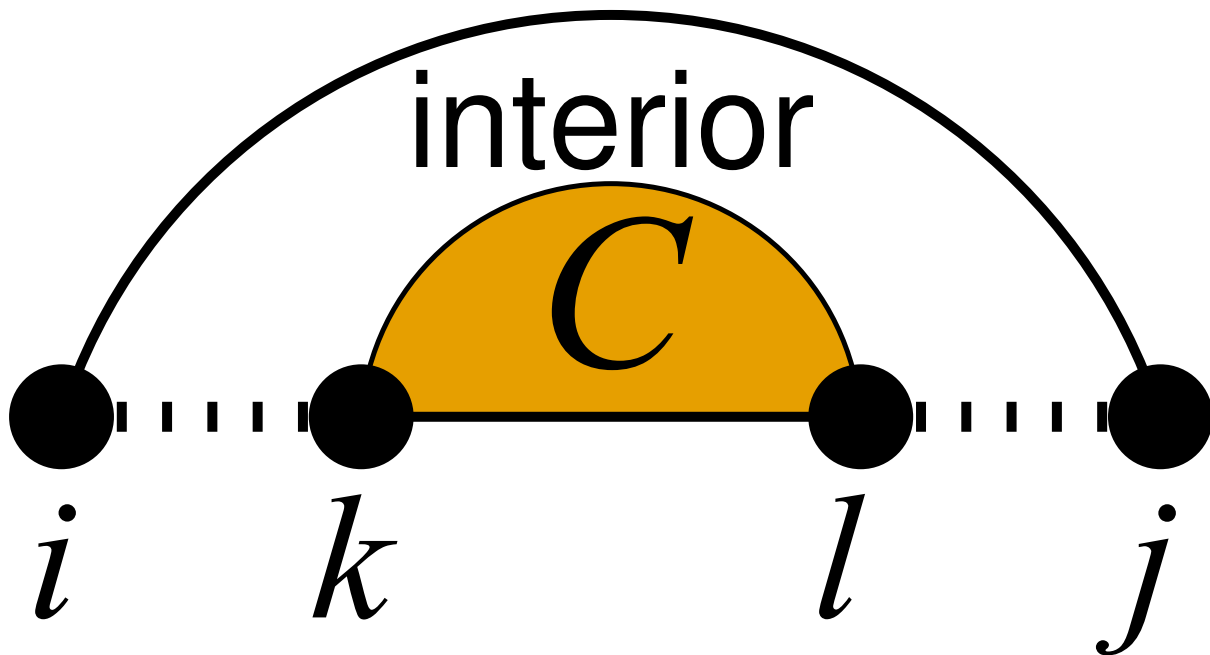


## 16.11.2.5 VRNA\_DECOMP\_PAIR\_IL

```
#define VRNA_DECOMP_PAIR_IL (unsigned char)2
#include <ViennaRNA/constraints/basic.h>
```

Indicator for interior loop decomposition step.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an interior loop enclosed by the base pair  $(i, j)$ , and enclosing the base pair  $(k, l)$ .

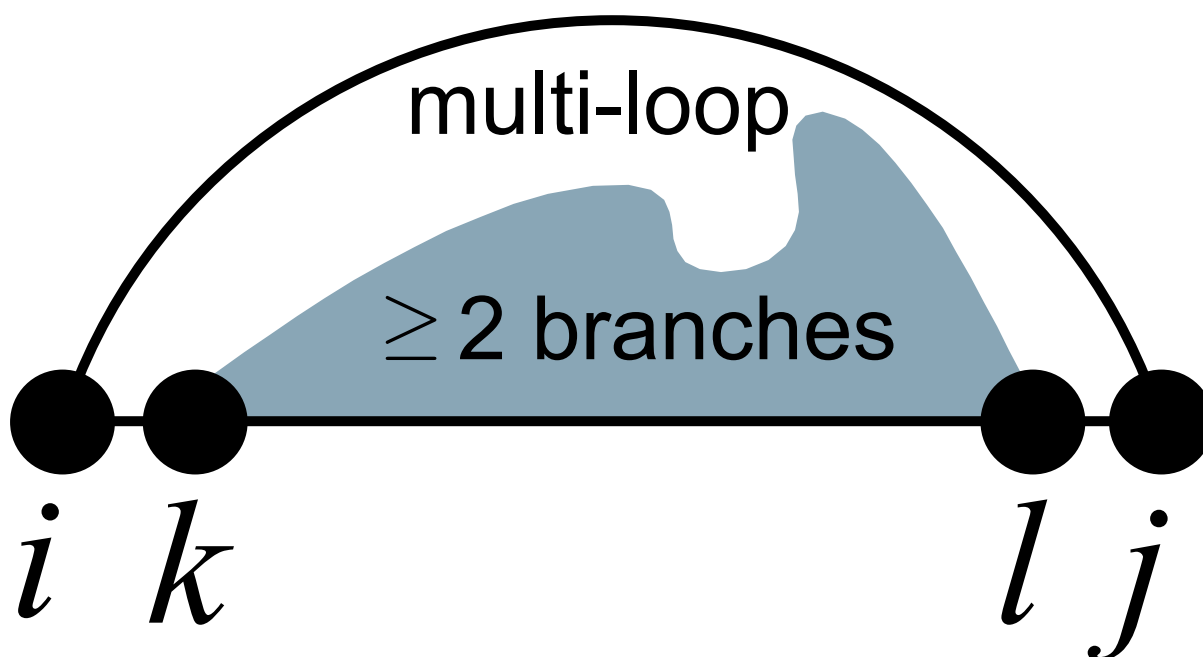


## 16.11.2.6 VRNA\_DECOMP\_PAIR\_ML

```
#define VRNA_DECOMP_PAIR_ML (unsigned char)3
#include <ViennaRNA/constraints/basic.h>
```

Indicator for multibranch loop decomposition step.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multi-branch loop enclosed by the base pair  $(i, j)$ , and consisting of some enclosed multi loop content from  $k$  to  $l$ .

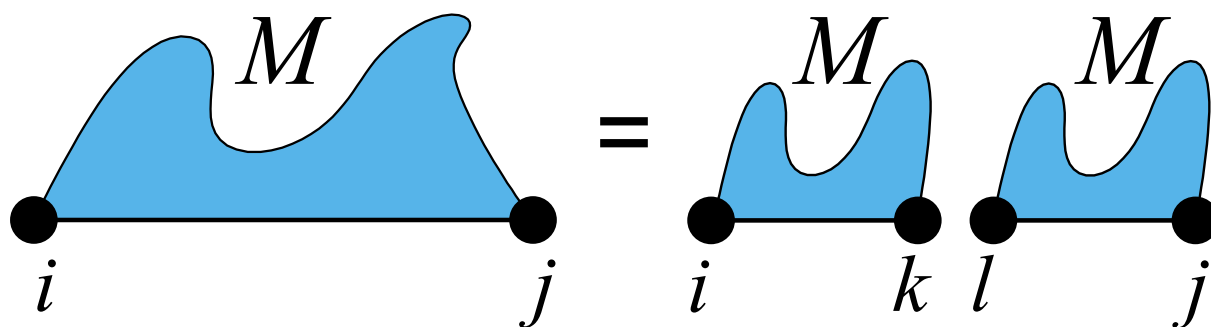


#### 16.11.2.7 VRNA\_DECOMP\_ML\_ML\_ML

```
#define VRNA_DECOMP_ML_ML_ML (unsigned char)5
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multi-branch loop part in the interval  $[i : j]$ , which will be decomposed into two multibranch loop parts  $[i : k]$ , and  $[l : j]$ .

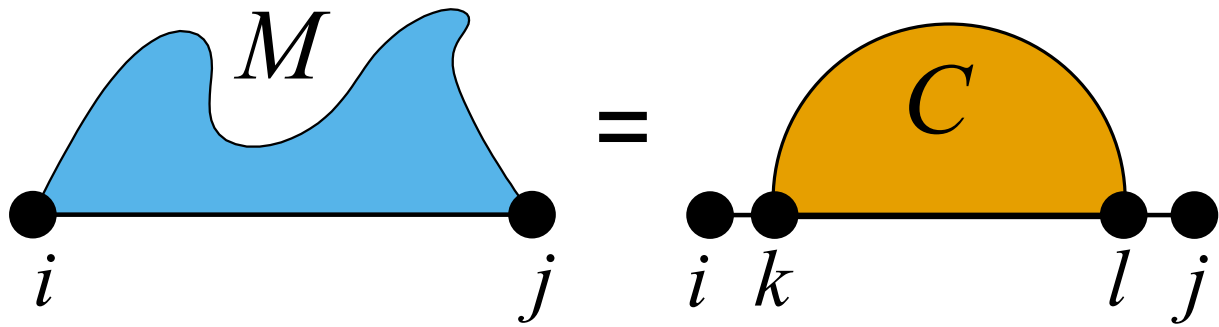


#### 16.11.2.8 VRNA\_DECOMP\_ML\_STEM

```
#define VRNA_DECOMP_ML_STEM (unsigned char)6
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multi-branch loop part in the interval  $[i : j]$ , which will be considered a single stem branching off with base pair  $(k, l)$ .



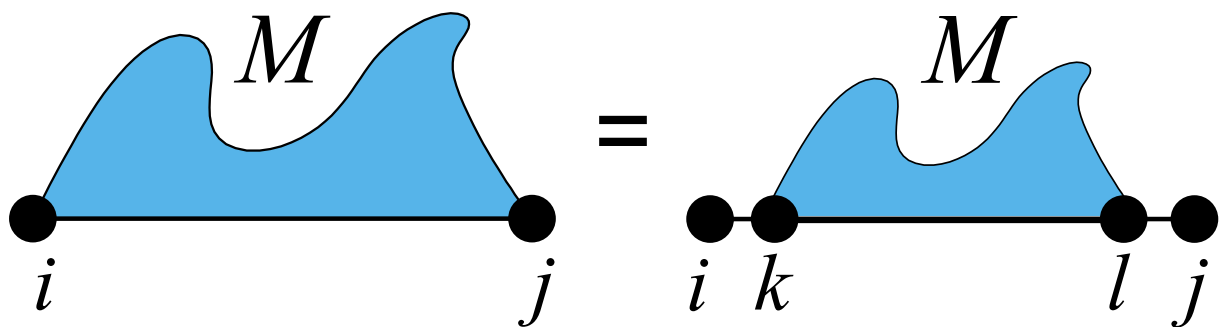
### 16.11.2.9 VRNA\_DECOMP\_ML\_ML

```
#define VRNA_DECOMP_ML_ML (unsigned char)7
```

```
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multibranch loop part in the interval  $[i : j]$ , which will be decomposed into a (usually) smaller multibranch loop part  $[k : l]$ .



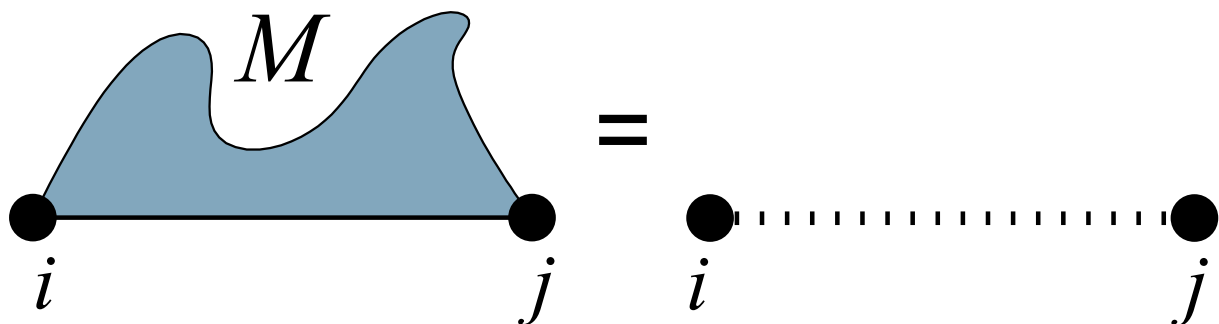
### 16.11.2.10 VRNA\_DECOMP\_ML\_UP

```
#define VRNA_DECOMP_ML_UP (unsigned char)8
```

```
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multibranch loop part in the interval  $[i : j]$ , which will be considered a multibranch loop part that only consists of unpaired nucleotides.

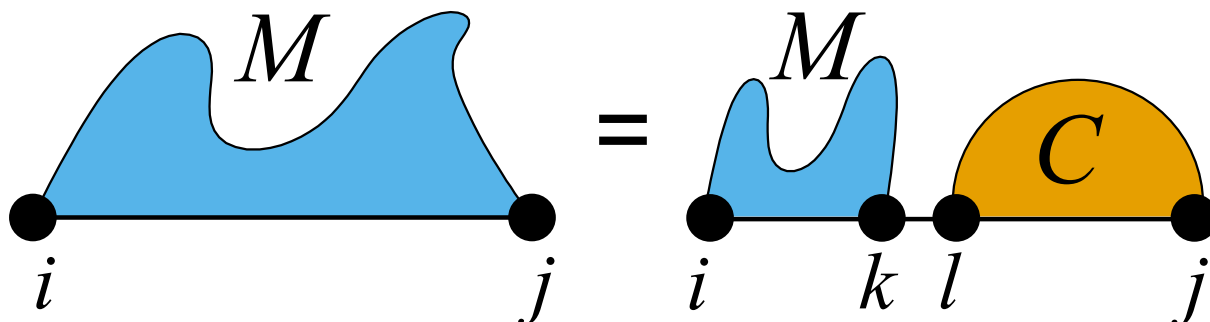


### 16.11.2.11 VRNA\_DECOMP\_ML\_ML\_STEM

```
#define VRNA_DECOMP_ML_ML_STEM (unsigned char)9
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multibranch loop part in the interval  $[i : j]$ , which will be decomposed into a multibranch loop part  $[i : k]$ , and a stem with enclosing base pair  $(l, j)$ .

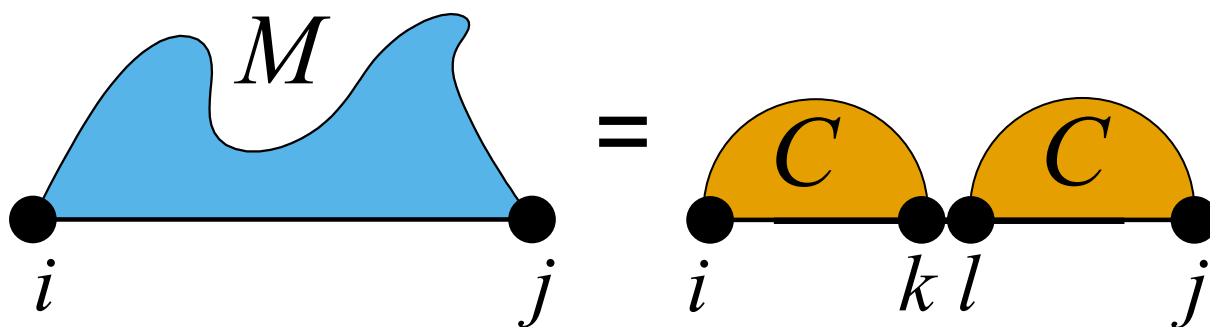


### 16.11.2.12 VRNA\_DECOMP\_ML\_COAXIAL

```
#define VRNA_DECOMP_ML_COAXIAL (unsigned char)10
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multibranch loop part in the interval  $[i : j]$ , where two stems with enclosing pairs  $(i, k)$  and  $(l, j)$  are coaxially stacking onto each other.



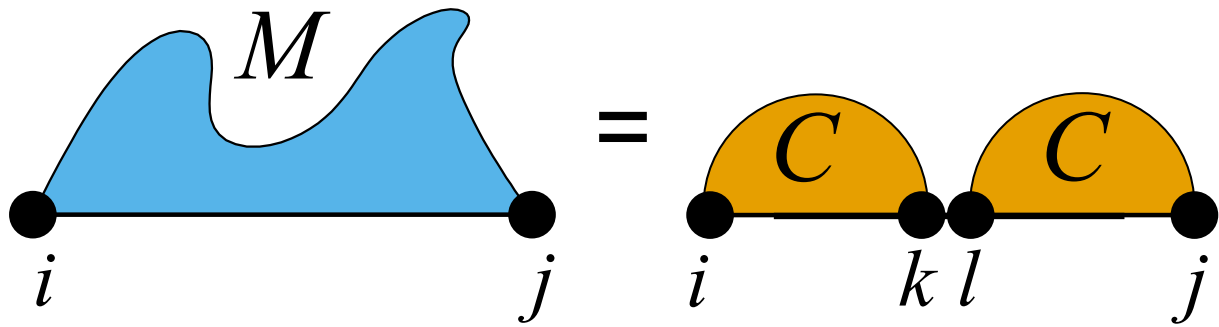
### 16.11.2.13 VRNA\_DECOMP\_ML\_COAXIAL\_ENC

```
#define VRNA_DECOMP_ML_COAXIAL_ENC (unsigned char)11
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of multibranch loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates a multibranch loop part in the interval  $[i : j]$ , where two stems with enclosing pairs  $(i, k)$  and  $(l, j)$  are coaxially stacking onto each other.



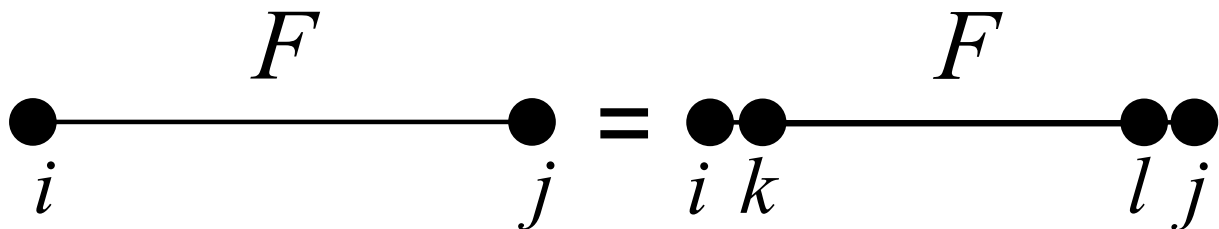


#### 16.11.2.14 VRNA\_DECOMP\_EXT\_EXT

```
#define VRNA_DECOMP_EXT_EXT (unsigned char)12
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be decomposed into a (usually) smaller exterior loop part  $[k : l]$ .

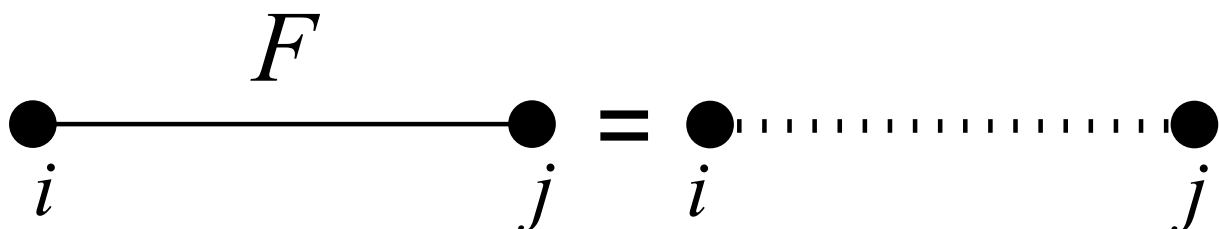


#### 16.11.2.15 VRNA\_DECOMP\_EXT\_UP

```
#define VRNA_DECOMP_EXT_UP (unsigned char)13
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be considered as an exterior loop component consisting of only unpaired nucleotides.

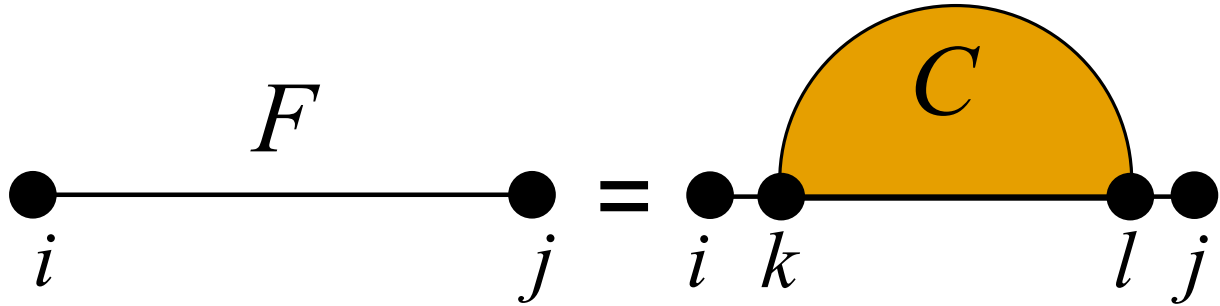


#### 16.11.2.16 VRNA\_DECOMP\_EXT\_STEM

```
#define VRNA_DECOMP_EXT_STEM (unsigned char)14
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be considered a stem with enclosing pair  $(k, l)$ .

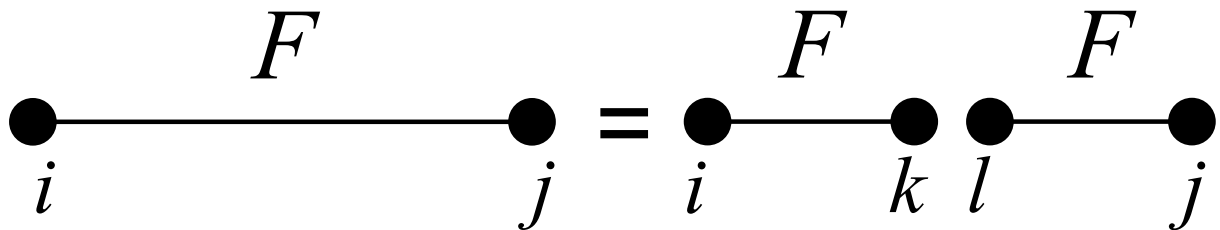


#### 16.11.2.17 VRNA\_DECOMP\_EXT\_EXT\_EXT

```
#define VRNA_DECOMP_EXT_EXT_EXT (unsigned char)15
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be decomposed into two exterior loop parts  $[i : k]$  and  $[l : j]$ .

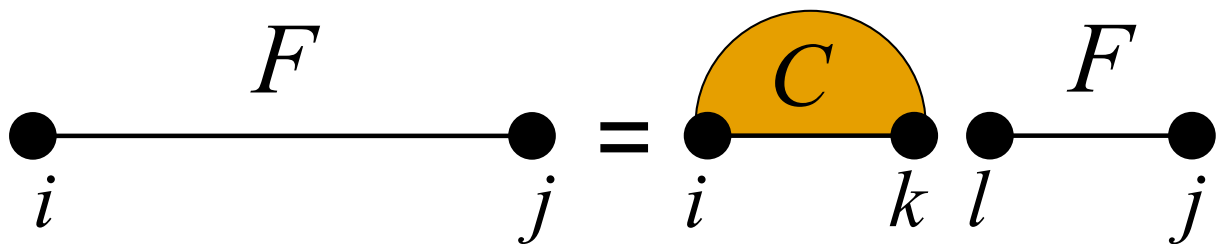


#### 16.11.2.18 VRNA\_DECOMP\_EXT\_STEM\_EXT

```
#define VRNA_DECOMP_EXT_STEM_EXT (unsigned char)16
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be decomposed into a stem branching off with base pair  $(i, k)$ , and an exterior loop part  $[l : j]$ .

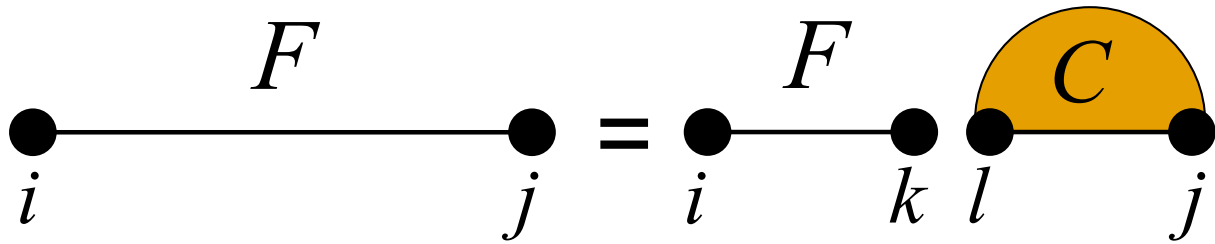


#### 16.11.2.19 VRNA\_DECOMP\_EXT\_EXT\_STEM

```
#define VRNA_DECOMP_EXT_EXT_STEM (unsigned char)18
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be decomposed into an exterior loop part  $[i : k]$ , and a stem branching off with base pair  $(l, j)$ .

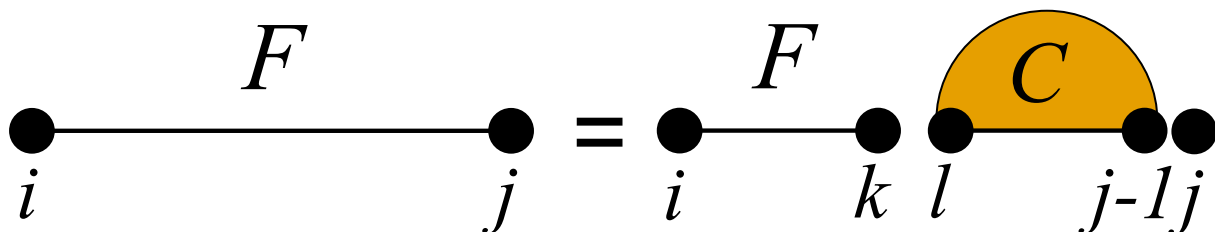


#### 16.11.2.20 VRNA\_DECOMP\_EXT\_EXT\_STEM1

```
#define VRNA_DECOMP_EXT_EXT_STEM1 (unsigned char)19
#include <ViennaRNA/constraints/basic.h>
```

Indicator for decomposition of exterior loop part.

This flag notifies the soft or hard constraint callback function that the current decomposition step evaluates an exterior loop part in the interval  $[i : j]$ , which will be decomposed into an exterior loop part  $[i : k]$ , and a stem branching off with base pair  $(l, j - 1)$ .



### 16.11.3 Function Documentation

#### 16.11.3.1 vrna\_constraints\_add()

```
void vrna_constraints_add (
    vrna_fold_compound_t * vc,
    const char * constraint,
    unsigned int options )
#include <ViennaRNA/constraints/basic.h>
```

Add constraints to a `vrna_fold_compound_t` data structure.

Use this function to add/update the hard/soft constraints. The function allows for passing a string 'constraint' that can either be a filename that points to a constraints definition file or it may be a pseudo dot-bracket notation indicating hard constraints. For the latter, the user has to pass the `VRNA_CONSTRAINT_DB` option. Also, the user has to specify, which characters are allowed to be interpreted as constraints by passing the corresponding options via the third parameter.

See also

`vrna_hc_init()`, `vrna_hc_add_up()`, `vrna_hc_add_up_batch()`, `vrna_hc_add_bp()`, `vrna_sc_init()`, `vrna_sc_set_up()`, `vrna_sc_set_bp()`, `vrna_sc_add_SHAPE_deigan()`, `vrna_sc_add_SHAPE_zarringham()`, `vrna_hc_free()`, `vrna_sc_free()`, `VRNA_CONSTRAINT_DB`, `VRNA_CONSTRAINT_DB_DEFAULT`, `VRNA_CONSTRAINT_DB_PIPE`, `VRNA_CONSTRAINT_DB_DOT`, `VRNA_CONSTRAINT_DB_X`, `VRNA_CONSTRAINT_DB_ANG_BRACK`, `VRNA_CONSTRAINT_DB_RND_BRACK`, `VRNA_CONSTRAINT_DB_INTRAMOL`, `VRNA_CONSTRAINT_DB_INTERMOL`, `VRNA_CONSTRAINT_DB_GQUAD`

The following is an example for adding hard constraints given in pseudo dot-bracket notation. Here, `vc` is the `vrna_fold_compound_t` object, `structure` is a char array with the hard constraint in dot-bracket notation, and `enforceConstraints` is a flag indicating whether or not constraints for base pairs should be enforced instead of just doing a removal of base pair that conflict with the constraint.

```

unsigned int constraint_options = VRNA_CONSTRAINT_DB_DEFAULT;
if (enforceConstraints)
    constraint_options |= VRNA_CONSTRAINT_DB_ENFORCE_BP;
if (canonicalBPonly)
    constraint_options |= VRNA_CONSTRAINT_DB_CANONICAL_BP;
vrna_constraints_add(fc, (const char *)cstruc, constraint_options);

```

In constrat to the above, constraints may also be read from file:

```
vrna_constraints_add(fc, constraints_file, VRNA_OPTION_DEFAULT);
```

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_hc\\_add\\_up\(\)](#), [vrna\\_hc\\_add\\_up\\_batch\(\)](#) [vrna\\_hc\\_add\\_bp\\_unspecific\(\)](#),  
[vrna\\_hc\\_add\\_bp\(\)](#)

#### Parameters

|                   |                                                                                                                                       |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| <i>vc</i>         | The fold compound                                                                                                                     |
| <i>constraint</i> | A string with either the filename of the constraint definitions or a pseudo dot-bracket notation of the hard constraint. May be NULL. |
| <i>options</i>    | The option flags                                                                                                                      |

### 16.11.3.2 vrna\_message\_constraint\_options()

```

void vrna_message_constraint_options (
    unsigned int option )
#include <ViennaRNA/constraints/hard.h>

```

Print a help message for pseudo dot-bracket structure constraint characters to stdout. (constraint support is specified by option parameter)

Currently available options are:

[VRNA\\_CONSTRAINT\\_DB\\_PIPE](#) (paired with another base)  
[VRNA\\_CONSTRAINT\\_DB\\_DOT](#) (no constraint at all)  
[VRNA\\_CONSTRAINT\\_DB\\_X](#) (base must not pair)  
[VRNA\\_CONSTRAINT\\_DB\\_ANG\\_BRACK](#) (paired downstream/upstream)  
[VRNA\\_CONSTRAINT\\_DB\\_RND\\_BRACK](#) (base i pairs base j)  
pass a collection of options as one value like this:

```
vrna_message_constraints(option_1 | option_2 | option_n)
```

See also

[vrna\\_message\\_constraint\\_options\\_all\(\)](#), [vrna\\_constraints\\_add\(\)](#), [VRNA\\_CONSTRAINT\\_DB](#), [VRNA\\_CONSTRAINT\\_DB\\_PIPE](#),  
[VRNA\\_CONSTRAINT\\_DB\\_DOT](#), [VRNA\\_CONSTRAINT\\_DB\\_X](#), [VRNA\\_CONSTRAINT\\_DB\\_ANG\\_BRACK](#),  
[VRNA\\_CONSTRAINT\\_DB\\_RND\\_BRACK](#), [VRNA\\_CONSTRAINT\\_DB\\_INTERMOL](#), [VRNA\\_CONSTRAINT\\_DB\\_INTRAMOL](#)

#### Parameters

|               |                                                                |
|---------------|----------------------------------------------------------------|
| <i>option</i> | Option switch that tells which constraint help will be printed |
|---------------|----------------------------------------------------------------|

### 16.11.3.3 vrna\_message\_constraint\_options\_all()

```

void vrna_message_constraint_options_all (
    void )
#include <ViennaRNA/constraints/hard.h>

```

Print structure constraint characters to stdout (full constraint support)

See also

[vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_constraints\\_add\(\)](#), [VRNA\\_CONSTRAINT\\_DB](#), [VRNA\\_CONSTRAINT\\_DB\\_PIPE](#), [VRNA\\_CONSTRAINT\\_DB\\_DOT](#), [VRNA\\_CONSTRAINT\\_DB\\_X](#), [VRNA\\_CONSTRAINT\\_DB\\_ANG\\_BRACK](#), [VRNA\\_CONSTRAINT\\_DB\\_RND\\_BRACK](#), [VRNA\\_CONSTRAINT\\_DB\\_INTERMOL](#), [VRNA\\_CONSTRAINT\\_DB\\_INTRAMOL](#)

## 16.12 Hard Constraints

This module covers all functionality for hard constraints in secondary structure prediction.

### 16.12.1 Detailed Description

This module covers all functionality for hard constraints in secondary structure prediction.  
Collaboration diagram for Hard Constraints:

#### Files

- file [hard.h](#)  
*Functions and data structures for handling of secondary structure hard constraints.*

#### Data Structures

- struct [vrna\\_hc\\_s](#)  
*The hard constraints data structure. [More...](#)*
- struct [vrna\\_hc\\_up\\_s](#)  
*A single hard constraint for a single nucleotide. [More...](#)*

#### Macros

- `#define VRNA_CONSTRAINT_DB 16384U`  
*Flag for [vrna\\_constraints\\_add\(\)](#) to indicate that constraint is passed in pseudo dot-bracket notation.*
- `#define VRNA_CONSTRAINT_DB_ENFORCE_BP 32768U`  
*Switch for dot-bracket structure constraint to enforce base pairs.*
- `#define VRNA_CONSTRAINT_DB_PIPE 65536U`  
*Flag that is used to indicate the pipe '|' sign in pseudo dot-bracket notation of hard constraints.*
- `#define VRNA_CONSTRAINT_DB_DOT 131072U`  
*dot '.' switch for structure constraints (no constraint at all)*
- `#define VRNA_CONSTRAINT_DB_X 262144U`  
*'x' switch for structure constraint (base must not pair)*
- `#define VRNA_CONSTRAINT_DB_RND_BRACK 1048576U`  
*round brackets '(',')' switch for structure constraint (base i pairs base j)*
- `#define VRNA_CONSTRAINT_DB_INTRAMOL 2097152U`  
*Flag that is used to indicate the character 'I' in pseudo dot-bracket notation of hard constraints.*
- `#define VRNA_CONSTRAINT_DB_INTERMOL 4194304U`  
*Flag that is used to indicate the character 'e' in pseudo dot-bracket notation of hard constraints.*
- `#define VRNA_CONSTRAINT_DB_GQUAD 8388608U`  
*'+' switch for structure constraint (base is involved in a gquad)*
- `#define VRNA_CONSTRAINT_DB_WUSS 33554432U`  
*Flag to indicate Washington University Secondary Structure (WUSS) notation of the hard constraint string.*
- `#define VRNA_CONSTRAINT_DB_DEFAULT`  
*Switch for dot-bracket structure constraint with default symbols.*
- `#define VRNA_CONSTRAINT_CONTEXT_EXT_LOOP (unsigned char)0x01`  
*Hard constraints flag, base pair in the exterior loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_HP_LOOP (unsigned char)0x02`

- *Hard constraints flag, base pair encloses hairpin loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_INT_LOOP` (unsigned char)0x04
- *Hard constraints flag, base pair encloses an interior loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_INT_LOOP_ENC` (unsigned char)0x08
- *Hard constraints flag, base pair encloses a multi branch loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_MB_LOOP` (unsigned char)0x10
- *Hard constraints flag, base pair is enclosed in an interior loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_MB_LOOP_ENC` (unsigned char)0x20
- *Hard constraints flag, base pair is enclosed in a multi branch loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_ALL_LOOPS`
- *Constraint context flag indicating any loop context.*

## Typedefs

- typedef struct [vrna\\_hc\\_s](#) [vrna\\_hc\\_t](#)  
*Typename for the hard constraints data structure [vrna\\_hc\\_s](#).*
- typedef struct [vrna\\_hc\\_up\\_s](#) [vrna\\_hc\\_up\\_t](#)  
*Typename for the single nucleotide hard constraint data structure [vrna\\_hc\\_up\\_s](#).*
- typedef unsigned char() [vrna\\_callback\\_hc\\_evaluate](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to evaluate whether or not a particular decomposition step is contributing to the solution space.*

## Functions

- void [vrna\\_hc\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Initialize/Reset hard constraints to default values.*
- void [vrna\\_hc\\_add\\_up](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, unsigned char option)  
*Make a certain nucleotide unpaired.*
- int [vrna\\_hc\\_add\\_up\\_batch](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_hc\\_up\\_t](#) \*constraints)  
*Apply a list of hard constraints for single nucleotides.*
- int [vrna\\_hc\\_add\\_bp](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, unsigned char option)  
*Favorize/Enforce a certain base pair (i,j)*
- void [vrna\\_hc\\_add\\_bp\\_nonspecific](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int d, unsigned char option)  
*Enforce a nucleotide to be paired (upstream/downstream)*
- void [vrna\\_hc\\_free](#) ([vrna\\_hc\\_t](#) \*hc)  
*Free the memory allocated by a [vrna\\_hc\\_t](#) data structure.*
- int [vrna\\_hc\\_add\\_from\\_db](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*constraint, unsigned int options)  
*Add hard constraints from pseudo dot-bracket notation.*

## 16.12.2 Data Structure Documentation

### 16.12.2.1 struct [vrna\\_hc\\_s](#)

The hard constraints data structure.

The content of this data structure determines the decomposition pattern used in the folding recursions. Attribute 'matrix' is used as source for the branching pattern of the decompositions during all folding recursions. Any entry in matrix[i,j] consists of the 6 LSB that allows one to distinguish the following types of base pairs:

- in the exterior loop ([VRNA\\_CONSTRAINT\\_CONTEXT\\_EXT\\_LOOP](#))
- enclosing a hairpin ([VRNA\\_CONSTRAINT\\_CONTEXT\\_HP\\_LOOP](#))
- enclosing an interior loop ([VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP](#))
- enclosed by an exterior loop ([VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP\\_ENC](#))
- enclosing a multi branch loop ([VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP](#))

- enclosed by a multi branch loop ([VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP\\_ENC](#))

The four linear arrays 'up\_xxx' provide the number of available unpaired nucleotides (including position i) 3' of each position in the sequence.

See also

[vrna\\_hc\\_init\(\)](#), [vrna\\_hc\\_free\(\)](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_EXT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_HP\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP\\_ENC](#)

### Data Fields

- int \* **up\_ext**  
*A linear array that holds the number of allowed unpaired nucleotides in an exterior loop.*
- int \* **up\_hp**  
*A linear array that holds the number of allowed unpaired nucleotides in a hairpin loop.*
- int \* **up\_int**  
*A linear array that holds the number of allowed unpaired nucleotides in an interior loop.*
- int \* **up\_ml**  
*A linear array that holds the number of allowed unpaired nucleotides in a multi branched loop.*
- [vrna\\_callback\\_hc\\_evaluate](#) \* **f**  
*A function pointer that returns whether or not a certain decomposition may be evaluated.*
- void \* **data**  
*A pointer to some structure where the user may store necessary data to evaluate its generic hard constraint function.*
- [vrna\\_callback\\_free\\_auxdata](#) \* **free\_data**  
*A pointer to a function to free memory occupied by auxiliary data.*

#### 16.12.2.1.1 Field Documentation

##### 16.12.2.1.1.1 **free\_data** [vrna\\_callback\\_free\\_auxdata](#)\* `vrna_hc_s::free_data`

A pointer to a function to free memory occupied by auxiliary data.

The function this pointer is pointing to will be called upon destruction of the [vrna\\_hc\\_s](#), and provided with the [vrna\\_hc\\_s.data](#) pointer that may hold auxiliary data. Hence, to avoid leaking memory, the user may use this pointer to free memory occupied by auxiliary data.

#### 16.12.2.2 struct `vrna_hc_up_s`

A single hard constraint for a single nucleotide.

### Data Fields

- int **position**  
*The sequence position (1-based)*
- unsigned char **options**  
*The hard constraint option*

### 16.12.3 Macro Definition Documentation

### 16.12.3.1 VRNA\_CONSTRAINT\_DB

```
#define VRNA_CONSTRAINT_DB 16384U
#include <ViennaRNA/constraints/hard.h>
```

Flag for `vrna_constraints_add()` to indicate that constraint is passed in pseudo dot-bracket notation.

See also

[vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.2 VRNA\_CONSTRAINT\_DB\_ENFORCE\_BP

```
#define VRNA_CONSTRAINT_DB_ENFORCE_BP 32768U
#include <ViennaRNA/constraints/hard.h>
```

Switch for dot-bracket structure constraint to enforce base pairs.

This flag should be used to really enforce base pairs given in dot-bracket constraint rather than just weakly-enforcing them.

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.3 VRNA\_CONSTRAINT\_DB\_PIPE

```
#define VRNA_CONSTRAINT_DB_PIPE 65536U
#include <ViennaRNA/constraints/hard.h>
```

Flag that is used to indicate the pipe '|' sign in pseudo dot-bracket notation of hard constraints.

Use this definition to indicate the pipe sign '|' (paired with another base)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.4 VRNA\_CONSTRAINT\_DB\_DOT

```
#define VRNA_CONSTRAINT_DB_DOT 131072U
#include <ViennaRNA/constraints/hard.h>
```

dot '.' switch for structure constraints (no constraint at all)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.5 VRNA\_CONSTRAINT\_DB\_X

```
#define VRNA_CONSTRAINT_DB_X 262144U
#include <ViennaRNA/constraints/hard.h>
```

'x' switch for structure constraint (base must not pair)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)



### 16.12.3.6 VRNA\_CONSTRAINT\_DB\_RND\_BRACK

```
#define VRNA_CONSTRAINT_DB_RND_BRACK 1048576U
#include <ViennaRNA/constraints/hard.h>
round brackets '(',')' switch for structure constraint (base i pairs base j)
```

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.7 VRNA\_CONSTRAINT\_DB\_INTRAMOL

```
#define VRNA_CONSTRAINT_DB_INTRAMOL 2097152U
#include <ViennaRNA/constraints/hard.h>
```

Flag that is used to indicate the character 'I' in pseudo dot-bracket notation of hard constraints.  
Use this definition to indicate the usage of 'I' character (intramolecular pairs only)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.8 VRNA\_CONSTRAINT\_DB\_INTERMOL

```
#define VRNA_CONSTRAINT_DB_INTERMOL 4194304U
#include <ViennaRNA/constraints/hard.h>
```

Flag that is used to indicate the character 'e' in pseudo dot-bracket notation of hard constraints.  
Use this definition to indicate the usage of 'e' character (intermolecular pairs only)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 16.12.3.9 VRNA\_CONSTRAINT\_DB\_GQUAD

```
#define VRNA_CONSTRAINT_DB_GQUAD 8388608U
#include <ViennaRNA/constraints/hard.h>
'+' switch for structure constraint (base is involved in a quad)
```

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### Warning

This flag is for future purposes only! No implementation recognizes it yet.

### 16.12.3.10 VRNA\_CONSTRAINT\_DB\_WUSS

```
#define VRNA_CONSTRAINT_DB_WUSS 33554432U
#include <ViennaRNA/constraints/hard.h>
```

Flag to indicate Washington University Secondary Structure (WUSS) notation of the hard constraint string.  
This secondary structure notation for RNAs is usually used as consensus secondary structure (SS\_cons) entry in Stockholm formatted files

### 16.12.3.11 VRNA\_CONSTRAINT\_DB\_DEFAULT

```
#define VRNA_CONSTRAINT_DB_DEFAULT
#include <ViennaRNA/constraints/hard.h>
```

**Value:**

```
(VRNA_CONSTRAINT_DB \
 | VRNA_CONSTRAINT_DB_PIPE \
 | VRNA_CONSTRAINT_DB_DOT \
 | VRNA_CONSTRAINT_DB_X \
 | VRNA_CONSTRAINT_DB_ANG_BRACK \
 | VRNA_CONSTRAINT_DB_RND_BRACK \
 | VRNA_CONSTRAINT_DB_INTRAMOL \
 | VRNA_CONSTRAINT_DB_INTERMOL \
 | VRNA_CONSTRAINT_DB_GQUAD \
)
```

Switch for dot-bracket structure constraint with default symbols.

This flag conveniently combines all possible symbols in dot-bracket notation for hard constraints and [VRNA\\_CONSTRAINT\\_DB](#)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

## 16.12.4 Typedef Documentation

### 16.12.4.1 vrna\_callback\_hc\_evaluate

```
typedef unsigned char() vrna_callback_hc_evaluate(int i, int j, int k, int l, unsigned char d,
void *data)
```

```
#include <ViennaRNA/constraints/hard.h>
```

Callback to evaluate whether or not a particular decomposition step is contributing to the solution space.

This is the prototype for callback functions used by the folding recursions to evaluate generic hard constraints. The first four parameters passed indicate the delimiting nucleotide positions of the decomposition, and the parameter `data` denotes the decomposition step. The last parameter `data` is the auxiliary data structure associated to the hard constraints via [vrna\\_hc\\_add\\_data\(\)](#), or NULL if no auxiliary data was added.

**Notes on Callback Functions** This callback enables one to over-rule default hard constraints in secondary structure decompositions.

See also

[VRNA\\_DECOMP\\_PAIR\\_HP](#), [VRNA\\_DECOMP\\_PAIR\\_IL](#), [VRNA\\_DECOMP\\_PAIR\\_ML](#), [VRNA\\_DECOMP\\_ML\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_UP](#), [VRNA\\_DECOMP\\_ML\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_COAXIAL](#), [VRNA\\_DECOMP\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_UP](#), [VRNA\\_DECOMP\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_STEM\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM1](#), [vrna\\_hc\\_add\\_f\(\)](#), [vrna\\_hc\\_add\\_data\(\)](#)

Parameters

|             |                                               |
|-------------|-----------------------------------------------|
| <i>i</i>    | Left (5') delimiter position of substructure  |
| <i>j</i>    | Right (3') delimiter position of substructure |
| <i>k</i>    | Left delimiter of decomposition               |
| <i>l</i>    | Right delimiter of decomposition              |
| <i>d</i>    | Decomposition step indicator                  |
| <i>data</i> | Auxiliary data                                |

## Returns

A non-zero value if the decomposition is valid, 0 otherwise

## 16.12.5 Function Documentation

16.12.5.1 `vrna_hc_init()`

```
void vrna_hc_init (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/constraints/hard.h>
```

Initialize/Reset hard constraints to default values.

This function resets the hard constraints to their default values, i.e. all positions may be unpaired in all contexts, and base pairs are allowed in all contexts, if they resemble canonical pairs. Previously set hard constraints will be removed before initialization.

## See also

[vrna\\_hc\\_add\\_bp\(\)](#), [vrna\\_hc\\_add\\_bp\\_nonspecific\(\)](#), [vrna\\_hc\\_add\\_up\(\)](#)

## Parameters

|                 |                   |
|-----------------|-------------------|
| <code>vc</code> | The fold compound |
|-----------------|-------------------|

**SWIG Wrapper Notes** This function is attached as method `hc_init()` to objects of type `fold_compound`

16.12.5.2 `vrna_hc_add_up()`

```
void vrna_hc_add_up (
    vrna_fold_compound_t * vc,
    int i,
    unsigned char option )
#include <ViennaRNA/constraints/hard.h>
```

Make a certain nucleotide unpaired.

## See also

[vrna\\_hc\\_add\\_bp\(\)](#), [vrna\\_hc\\_add\\_bp\\_nonspecific\(\)](#), [vrna\\_hc\\_init\(\)](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_EXT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_HP\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_ALL\\_LOOPS](#)

## Parameters

|                     |                                                                                   |
|---------------------|-----------------------------------------------------------------------------------|
| <code>vc</code>     | The <a href="#">vrna_fold_compound_t</a> the hard constraints are associated with |
| <code>i</code>      | The position that needs to stay unpaired (1-based)                                |
| <code>option</code> | The options flag indicating how/where to store the hard constraints               |

16.12.5.3 `vrna_hc_add_up_batch()`

```
int vrna_hc_add_up_batch (
    vrna_fold_compound_t * vc,
    vrna_hc_up_t * constraints )
```

```
#include <ViennaRNA/constraints/hard.h>
```

Apply a list of hard constraints for single nucleotides.

#### Parameters

|                    |                                                                                     |
|--------------------|-------------------------------------------------------------------------------------|
| <i>vc</i>          | The <a href="#">vrna_fold_compound_t</a> the hard constraints are associated with   |
| <i>constraints</i> | The list off constraints to apply, last entry must have position attribute set to 0 |

#### 16.12.5.4 vrna\_hc\_add\_bp()

```
int vrna_hc_add_bp (
    vrna_fold_compound_t * vc,
    int i,
    int j,
    unsigned char option )
#include <ViennaRNA/constraints/hard.h>
```

Favorize/Enforce a certain base pair (i,j)

#### See also

[vrna\\_hc\\_add\\_bp\\_nonspecific\(\)](#), [vrna\\_hc\\_add\\_up\(\)](#), [vrna\\_hc\\_init\(\)](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_EXT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_HP\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP\\_ENC](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_ENFORCE](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_ALL\\_LOOPS](#)

#### Parameters

|               |                                                                                   |
|---------------|-----------------------------------------------------------------------------------|
| <i>vc</i>     | The <a href="#">vrna_fold_compound_t</a> the hard constraints are associated with |
| <i>i</i>      | The 5' located nucleotide position of the base pair (1-based)                     |
| <i>j</i>      | The 3' located nucleotide position of the base pair (1-based)                     |
| <i>option</i> | The options flag indicating how/where to store the hard constraints               |

#### 16.12.5.5 vrna\_hc\_add\_bp\_nonspecific()

```
void vrna_hc_add_bp_nonspecific (
    vrna_fold_compound_t * vc,
    int i,
    int d,
    unsigned char option )
#include <ViennaRNA/constraints/hard.h>
```

Enforce a nucleotide to be paired (upstream/downstream)

#### See also

[vrna\\_hc\\_add\\_bp\(\)](#), [vrna\\_hc\\_add\\_up\(\)](#), [vrna\\_hc\\_init\(\)](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_EXT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_HP\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_INT\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_MB\\_LOOP\\_ENC](#), [VRNA\\_CONSTRAINT\\_CONTEXT\\_ALL\\_LOOPS](#)

#### Parameters

|           |                                                                                   |
|-----------|-----------------------------------------------------------------------------------|
| <i>vc</i> | The <a href="#">vrna_fold_compound_t</a> the hard constraints are associated with |
| <i>i</i>  | The position that needs to stay unpaired (1-based)                                |

## Parameters

|               |                                                                                                                |
|---------------|----------------------------------------------------------------------------------------------------------------|
| <i>d</i>      | The direction of base pairing ( $d < 0$ : pairs upstream, $d > 0$ : pairs downstream, $d == 0$ : no direction) |
| <i>option</i> | The options flag indicating in which loop type context the pairs may appear                                    |

**16.12.5.6 vrna\_hc\_free()**

```
void vrna_hc_free (
    vrna_hc_t * hc )
#include <ViennaRNA/constraints/hard.h>
Free the memory allocated by a vrna\_hc\_t data structure.
Use this function to free all memory that was allocated for a data structure of type vrna\_hc\_t.
```

## See also

[get\\_hard\\_constraints\(\)](#), [vrna\\_hc\\_t](#)

**16.12.5.7 vrna\_hc\_add\_from\_db()**

```
int vrna_hc_add_from_db (
    vrna_fold_compound_t * vc,
    const char * constraint,
    unsigned int options )
#include <ViennaRNA/constraints/hard.h>
Add hard constraints from pseudo dot-bracket notation.
This function allows one to apply hard constraints from a pseudo dot-bracket notation. The options parameter controls, which characters are recognized by the parser. Use the VRNA\_CONSTRAINT\_DB\_DEFAULT convenience macro, if you want to allow all known characters
```

## See also

[VRNA\\_CONSTRAINT\\_DB\\_PIPE](#), [VRNA\\_CONSTRAINT\\_DB\\_DOT](#), [VRNA\\_CONSTRAINT\\_DB\\_X](#), [VRNA\\_CONSTRAINT\\_DB\\_](#)  
[VRNA\\_CONSTRAINT\\_DB\\_RND\\_BRACK](#), [VRNA\\_CONSTRAINT\\_DB\\_INTRAMOL](#), [VRNA\\_CONSTRAINT\\_DB\\_INTERMOL](#),  
[VRNA\\_CONSTRAINT\\_DB\\_GQUAD](#)

## Parameters

|                   |                                                       |
|-------------------|-------------------------------------------------------|
| <i>vc</i>         | The fold compound                                     |
| <i>constraint</i> | A pseudo dot-bracket notation of the hard constraint. |
| <i>options</i>    | The option flags                                      |

**SWIG Wrapper Notes** This function is attached as method [hc\\_add\\_from\\_db\(\)](#) to objects of type *fold\_compound*

## 16.13 Soft Constraints

Functions and data structures for secondary structure soft constraints.

### 16.13.1 Detailed Description

Functions and data structures for secondary structure soft constraints.  
Soft-constraints are used to change position specific contributions in the recursions by adding bonuses/penalties in form of pseudo free energies to certain loop configurations. Collaboration diagram for Soft Constraints:

## Files

- file [soft.h](#)

*Functions and data structures for secondary structure soft constraints.*

## Data Structures

- struct [vrna\\_sc\\_s](#)

*The soft constraints data structure. [More...](#)*

## Typedefs

- typedef struct [vrna\\_sc\\_s](#) [vrna\\_sc\\_t](#)  
*Typename for the soft constraints data structure [vrna\\_sc\\_s](#).*
- typedef int() [vrna\\_callback\\_sc\\_energy](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve pseudo energy contribution for soft constraint feature.*
- typedef [FLT\\_OR\\_DBL](#)() [vrna\\_callback\\_sc\\_exp\\_energy](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve pseudo energy contribution as Boltzmann Factors for soft constraint feature.*
- typedef [vrna\\_basepair\\_t](#) \*() [vrna\\_callback\\_sc\\_backtrack](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve auxiliary base pairs for soft constraint feature.*

## Functions

- void [vrna\\_sc\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Initialize an empty soft constraints data structure within a [vrna\\_fold\\_compound\\_t](#).*
- int [vrna\\_sc\\_set\\_bp](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const [FLT\\_OR\\_DBL](#) \*\*constraints, unsigned int options)  
*Set soft constraints for paired nucleotides.*
- int [vrna\\_sc\\_add\\_bp](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, [FLT\\_OR\\_DBL](#) energy, unsigned int options)  
*Add soft constraints for paired nucleotides.*
- int [vrna\\_sc\\_set\\_up](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const [FLT\\_OR\\_DBL](#) \*constraints, unsigned int options)  
*Set soft constraints for unpaired nucleotides.*
- int [vrna\\_sc\\_add\\_up](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, [FLT\\_OR\\_DBL](#) energy, unsigned int options)  
*Add soft constraints for unpaired nucleotides.*
- void [vrna\\_sc\\_remove](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Remove soft constraints from [vrna\\_fold\\_compound\\_t](#).*
- void [vrna\\_sc\\_free](#) ([vrna\\_sc\\_t](#) \*sc)  
*Free memory occupied by a [vrna\\_sc\\_t](#) data structure.*
- int [vrna\\_sc\\_add\\_data](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, void \*data, [vrna\\_callback\\_free\\_auxdata](#) \*free\_data)  
*Add an auxiliary data structure for the generic soft constraints callback function.*
- int [vrna\\_sc\\_add\\_f](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_energy](#) \*f)  
*Bind a function pointer for generic soft constraint feature (MFE version)*
- int [vrna\\_sc\\_add\\_bt](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_backtrack](#) \*f)  
*Bind a backtracking function pointer for generic soft constraint feature.*
- int [vrna\\_sc\\_add\\_exp\\_f](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_exp\\_energy](#) \*exp\_f)  
*Bind a function pointer for generic soft constraint feature (PF version)*

## 16.13.2 Data Structure Documentation

### 16.13.2.1 struct [vrna\\_sc\\_s](#)

The soft constraints data structure.

Collaboration diagram for [vrna\\_sc\\_s](#):

## Data Fields

- `int ** energy_up`  
*Energy contribution for stretches of unpaired nucleotides.*
- `FLT_OR_DBL ** exp_energy_up`  
*Boltzmann Factors of the energy contributions for unpaired sequence stretches.*
- `int * up_storage`  
*Storage container for energy contributions per unpaired nucleotide.*
- `vrna_sc_bp_storage_t ** bp_storage`  
*Storage container for energy contributions per base pair.*
- `int * energy_stack`  
*Pseudo Energy contribution per base pair involved in a stack.*
- `FLT_OR_DBL * exp_energy_stack`  
*Boltzmann weighted pseudo energy contribution per nucleotide involved in a stack.*
- `vrna_callback_sc_energy * f`  
*A function pointer used for pseudo energy contribution in MFE calculations.*
- `vrna_callback_sc_backtrack * bt`  
*A function pointer used to obtain backtraced base pairs in loop regions that were altered by soft constrained pseudo energy contributions.*
- `vrna_callback_sc_exp_energy * exp_f`  
*A function pointer used for pseudo energy contribution boltzmann factors in PF calculations.*
- `void * data`  
*A pointer to the data object provided for for pseudo energy contribution functions of the generic soft constraints feature.*
- `int * energy_bp`  
*Energy contribution for base pairs.*
- `FLT_OR_DBL * exp_energy_bp`  
*Boltzmann Factors of the energy contribution for base pairs.*
- `int ** energy_bp_local`  
*Energy contribution for base pairs (sliding window approach)*
- `FLT_OR_DBL ** exp_energy_bp_local`  
*Boltzmann Factors of the energy contribution for base pairs (sliding window approach)*

### 16.13.2.1.1 Field Documentation

#### 16.13.2.1.1.1 `f vrna_callback_sc_energy* vrna_sc_s::f`

A function pointer used for pseudo energy contribution in MFE calculations.

See also

`vrna_sc_add_f()`

#### 16.13.2.1.1.2 `bt vrna_callback_sc_backtrack* vrna_sc_s::bt`

A function pointer used to obtain backtraced base pairs in loop regions that were altered by soft constrained pseudo energy contributions.

See also

`vrna_sc_add_bt()`

#### 16.13.2.1.1.3 `exp_f vrna_callback_sc_exp_energy* vrna_sc_s::exp_f`

A function pointer used for pseudo energy contribution boltzmann factors in PF calculations.

See also

[vrna\\_sc\\_add\\_exp\\_f\(\)](#)

### 16.13.3 Typedef Documentation

#### 16.13.3.1 `vrna_callback_sc_energy`

```
typedef int() vrna_callback_sc_energy(int i, int j, int k, int l, unsigned char d, void *data)
#include <ViennaRNA/constraints/soft.h>
```

Callback to retrieve pseudo energy contribution for soft constraint feature.

This is the prototype for callback functions used by the folding recursions to evaluate generic soft constraints. The first four parameters passed indicate the delimiting nucleotide positions of the decomposition, and the parameter `denotes` the decomposition step. The last parameter `data` is the auxiliary data structure associated to the hard constraints via [vrna\\_sc\\_add\\_data\(\)](#), or NULL if no auxiliary data was added.

**Notes on Callback Functions** This callback enables one to add (pseudo-)energy contributions to individual decompositions of the secondary structure.

See also

[VRNA\\_DECOMP\\_PAIR\\_HP](#), [VRNA\\_DECOMP\\_PAIR\\_IL](#), [VRNA\\_DECOMP\\_PAIR\\_ML](#), [VRNA\\_DECOMP\\_ML\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_UP](#), [VRNA\\_DECOMP\\_ML\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_COAXIAL](#), [VRNA\\_DECOMP\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_UP](#), [VRNA\\_DECOMP\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_STEM\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM1](#), [vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#), [vrna\\_sc\\_add\\_bt\(\)](#), [vrna\\_sc\\_add\\_data\(\)](#)

#### Parameters

|             |                                               |
|-------------|-----------------------------------------------|
| <i>i</i>    | Left (5') delimiter position of substructure  |
| <i>j</i>    | Right (3') delimiter position of substructure |
| <i>k</i>    | Left delimiter of decomposition               |
| <i>l</i>    | Right delimiter of decomposition              |
| <i>d</i>    | Decomposition step indicator                  |
| <i>data</i> | Auxiliary data                                |

#### Returns

Pseudo energy contribution in deka-kalories per mol

#### 16.13.3.2 `vrna_callback_sc_exp_energy`

```
typedef FLT_OR_DBL() vrna_callback_sc_exp_energy(int i, int j, int k, int l, unsigned char d, void *data)
#include <ViennaRNA/constraints/soft.h>
```

Callback to retrieve pseudo energy contribution as Boltzmann Factors for soft constraint feature.

This is the prototype for callback functions used by the partition function recursions to evaluate generic soft constraints. The first four parameters passed indicate the delimiting nucleotide positions of the decomposition, and the parameter `denotes` the decomposition step. The last parameter `data` is the auxiliary data structure associated to the hard constraints via [vrna\\_sc\\_add\\_data\(\)](#), or NULL if no auxiliary data was added.



**Notes on Callback Functions** This callback enables one to add (pseudo-)energy contributions to individual decompositions of the secondary structure (Partition function variant, i.e. contributions must be returned as Boltzmann factors).

See also

[VRNA\\_DECOMP\\_PAIR\\_HP](#), [VRNA\\_DECOMP\\_PAIR\\_IL](#), [VRNA\\_DECOMP\\_PAIR\\_ML](#), [VRNA\\_DECOMP\\_ML\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_UP](#), [VRNA\\_DECOMP\\_ML\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_COAXIAL](#), [VRNA\\_DECOMP\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_UP](#), [VRNA\\_DECOMP\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_STEM\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM1](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#), [vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_bt\(\)](#), [vrna\\_sc\\_add\\_data\(\)](#)

Parameters

|             |                                               |
|-------------|-----------------------------------------------|
| <i>i</i>    | Left (5') delimiter position of substructure  |
| <i>j</i>    | Right (3') delimiter position of substructure |
| <i>k</i>    | Left delimiter of decomposition               |
| <i>l</i>    | Right delimiter of decomposition              |
| <i>d</i>    | Decomposition step indicator                  |
| <i>data</i> | Auxiliary data                                |

Returns

Pseudo energy contribution in deka-kalories per mol

### 16.13.3.3 vrna\_callback\_sc\_backtrack

```
typedef vrna\_basepair\_t *() vrna_callback_sc_backtrack(int i, int j, int k, int l, unsigned char d, void *data)
```

```
#include <ViennaRNA/constraints/soft.h>
```

Callback to retrieve auxiliary base pairs for soft constraint feature.

**Notes on Callback Functions** This callback enables one to add auxiliary base pairs in the backtracking steps of hairpin- and interior loops.

See also

[VRNA\\_DECOMP\\_PAIR\\_HP](#), [VRNA\\_DECOMP\\_PAIR\\_IL](#), [VRNA\\_DECOMP\\_PAIR\\_ML](#), [VRNA\\_DECOMP\\_ML\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_ML](#), [VRNA\\_DECOMP\\_ML\\_UP](#), [VRNA\\_DECOMP\\_ML\\_ML\\_STEM](#), [VRNA\\_DECOMP\\_ML\\_COAXIAL](#), [VRNA\\_DECOMP\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_UP](#), [VRNA\\_DECOMP\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_STEM\\_EXT](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM](#), [VRNA\\_DECOMP\\_EXT\\_EXT\\_STEM1](#), [vrna\\_sc\\_add\\_bt\(\)](#), [vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#), [vrna\\_sc\\_add\\_data\(\)](#)

Parameters

|             |                                               |
|-------------|-----------------------------------------------|
| <i>i</i>    | Left (5') delimiter position of substructure  |
| <i>j</i>    | Right (3') delimiter position of substructure |
| <i>k</i>    | Left delimiter of decomposition               |
| <i>l</i>    | Right delimiter of decomposition              |
| <i>d</i>    | Decomposition step indicator                  |
| <i>data</i> | Auxiliary data                                |

## Returns

List of additional base pairs

## 16.13.4 Function Documentation

### 16.13.4.1 `vrna_sc_init()`

```
void vrna_sc_init (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/constraints/soft.h>
```

Initialize an empty soft constraints data structure within a `vrna_fold_compound_t`.

This function adds a proper soft constraints data structure to the `vrna_fold_compound_t` data structure. If soft constraints already exist within the fold compound, they are removed.

## Note

Accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE` and `VRNA_FC_TYPE_COMPARATIVE`

## See also

`vrna_sc_set_bp()`, `vrna_sc_set_up()`, `vrna_sc_add_SHAPE_deigan()`, `vrna_sc_add_SHAPE_zarringhalam()`, `vrna_sc_remove()`, `vrna_sc_add_f()`, `vrna_sc_add_exp_f()`, `vrna_sc_add_pre()`, `vrna_sc_add_post()`

## Parameters

|                 |                                                                                                |
|-----------------|------------------------------------------------------------------------------------------------|
| <code>vc</code> | The <code>vrna_fold_compound_t</code> where an empty soft constraint feature is to be added to |
|-----------------|------------------------------------------------------------------------------------------------|

**SWIG Wrapper Notes** This function is attached as method `sc_init()` to objects of type `fold_compound`

### 16.13.4.2 `vrna_sc_set_bp()`

```
int vrna_sc_set_bp (
    vrna_fold_compound_t * vc,
    const FLT_OR_DBL ** constraints,
    unsigned int options )
#include <ViennaRNA/constraints/soft.h>
```

Set soft constraints for paired nucleotides.

## Note

This function replaces any pre-existing soft constraints with the ones supplied in `constraints`.

## See also

`vrna_sc_add_bp()`, `vrna_sc_set_up()`, `vrna_sc_add_up()`

## Parameters

|                          |                                                                                |
|--------------------------|--------------------------------------------------------------------------------|
| <code>vc</code>          | The <code>vrna_fold_compound_t</code> the soft constraints are associated with |
| <code>constraints</code> | A two-dimensional array of pseudo free energies in <i>kcal/mol</i>             |
| <code>options</code>     | The options flag indicating how/where to store the soft constraints            |

**Returns**

Non-zero on successful application of the constraint, 0 otherwise.

**SWIG Wrapper Notes** This function is attached as method **sc\_set\_bp()** to objects of type *fold\_compound*

**16.13.4.3 vrna\_sc\_add\_bp()**

```
int vrna_sc_add_bp (
    vrna_fold_compound_t * vc,
    int i,
    int j,
    FLT_OR_DBL energy,
    unsigned int options )
```

```
#include <ViennaRNA/constraints/soft.h>
```

Add soft constraints for paired nucleotides.

**See also**

[vrna\\_sc\\_set\\_bp\(\)](#), [vrna\\_sc\\_set\\_up\(\)](#), [vrna\\_sc\\_add\\_up\(\)](#)

**Parameters**

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| <i>vc</i>      | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>i</i>       | The 5' position of the base pair the soft constraint is added for                 |
| <i>j</i>       | The 3' position of the base pair the soft constraint is added for                 |
| <i>energy</i>  | The free energy (soft-constraint) in <i>kcal/mol</i>                              |
| <i>options</i> | The options flag indicating how/where to store the soft constraints               |

**Returns**

Non-zero on successful application of the constraint, 0 otherwise.

**SWIG Wrapper Notes** This function is attached as an overloaded method **sc\_add\_bp()** to objects of type *fold\_compound*. The method either takes arguments for a single base pair (i,j) with the corresponding energy value:

```
fold_compound.sc_add_bp(i, j, energy, options)
```

or an entire 2-dimensional matrix with dimensions  $n \times n$  that stores free energy contributions for any base pair (i,j) with  $1 \leq i < j \leq n$ :

```
fold_compound.sc_add_bp(matrix, options)
```

In both variants, the *options* argument is optional and may be omitted.

**16.13.4.4 vrna\_sc\_set\_up()**

```
int vrna_sc_set_up (
    vrna_fold_compound_t * vc,
    const FLT_OR_DBL * constraints,
    unsigned int options )
```

```
#include <ViennaRNA/constraints/soft.h>
```

Set soft constraints for unpaired nucleotides.

**Note**

This function replaces any pre-existing soft constraints with the ones supplied in *constraints*.

**See also**

[vrna\\_sc\\_add\\_up\(\)](#), [vrna\\_sc\\_set\\_bp\(\)](#), [vrna\\_sc\\_add\\_bp\(\)](#)

## Parameters

|                    |                                                                                   |
|--------------------|-----------------------------------------------------------------------------------|
| <i>vc</i>          | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>constraints</i> | A vector of pseudo free energies in <i>kcal/mol</i>                               |
| <i>options</i>     | The options flag indicating how/where to store the soft constraints               |

## Returns

Non-zero on successful application of the constraint, 0 otherwise.

**SWIG Wrapper Notes** This function is attached as method `sc_set_up()` to objects of type *fold\_compound*

**16.13.4.5 vrna\_sc\_add\_up()**

```
int vrna_sc_add_up (
    vrna_fold_compound_t * vc,
    int i,
    FLT_OR_DBL energy,
    unsigned int options )
#include <ViennaRNA/constraints/soft.h>
Add soft constraints for unpaired nucleotides.
```

## See also

[vrna\\_sc\\_set\\_up\(\)](#), [vrna\\_sc\\_add\\_bp\(\)](#), [vrna\\_sc\\_set\\_bp\(\)](#)

## Parameters

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| <i>vc</i>      | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>i</i>       | The nucleotide position the soft constraint is added for                          |
| <i>energy</i>  | The free energy (soft-constraint) in <i>kcal/mol</i>                              |
| <i>options</i> | The options flag indicating how/where to store the soft constraints               |

## Returns

Non-zero on successful application of the constraint, 0 otherwise.

**SWIG Wrapper Notes** This function is attached as an overloaded method `sc_add_up()` to objects of type *fold\_compound*. The method either takes arguments for a single nucleotide *i* with the corresponding energy value:

```
fold_compound.sc_add_up(i, energy, options)
or an entire vector that stores free energy contributions for each nucleotide i with 1 ≤ i ≤ n:
fold_compound.sc_add_bp(vector, options)
In both variants, the options argument is optional can may be omitted.
```

**16.13.4.6 vrna\_sc\_remove()**

```
void vrna_sc_remove (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/constraints/soft.h>
Remove soft constraints from vrna\_fold\_compound\_t.
```

## Note

Accepts [vrna\\_fold\\_compound\\_t](#) of type [VRNA\\_FC\\_TYPE\\_SINGLE](#) and [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#)

## Parameters

|    |                                                                               |
|----|-------------------------------------------------------------------------------|
| vc | The <a href="#">vrna_fold_compound_t</a> possibly containing soft constraints |
|----|-------------------------------------------------------------------------------|

**SWIG Wrapper Notes** This function is attached as method **sc\_remove()** to objects of type *fold\_compound*

**16.13.4.7 vrna\_sc\_free()**

```
void vrna_sc_free (
    vrna_sc_t * sc )
#include <ViennaRNA/constraints/soft.h>
Free memory occupied by a vrna\_sc\_t data structure.
```

## Parameters

|    |                                        |
|----|----------------------------------------|
| sc | The data structure to free from memory |
|----|----------------------------------------|

**16.13.4.8 vrna\_sc\_add\_data()**

```
int vrna_sc_add_data (
    vrna_fold_compound_t * vc,
    void * data,
    vrna_callback_free_auxdata * free_data )
#include <ViennaRNA/constraints/soft.h>
Add an auxiliary data structure for the generic soft constraints callback function.
```

## See also

[vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#), [vrna\\_sc\\_add\\_bt\(\)](#)

## Parameters

|           |                                                                                     |
|-----------|-------------------------------------------------------------------------------------|
| vc        | The fold compound the generic soft constraint function should be bound to           |
| data      | A pointer to the data structure that holds required data for function 'f'           |
| free_data | A pointer to a function that free's the memory occupied by <i>data</i> (Maybe NULL) |

## Returns

Non-zero on successful binding the data (and free-function), 0 otherwise

**SWIG Wrapper Notes** This function is attached as method **sc\_add\_data()** to objects of type *fold\_compound*

**16.13.4.9 vrna\_sc\_add\_f()**

```
int vrna_sc_add_f (
    vrna_fold_compound_t * vc,
    vrna_callback_sc_energy * f )
#include <ViennaRNA/constraints/soft.h>
```

Bind a function pointer for generic soft constraint feature (MFE version)

This function allows one to easily bind a function pointer and corresponding data structure to the soft constraint part [vrna\\_sc\\_t](#) of the [vrna\\_fold\\_compound\\_t](#). The function for evaluating the generic soft constraint feature has to return a pseudo free energy  $\hat{E}$  in *dacal/mol*, where  $1\text{dacal/mol} = 10\text{cal/mol}$ .

See also

[vrna\\_sc\\_add\\_data\(\)](#), [vrna\\_sc\\_add\\_bt\(\)](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#)

#### Parameters

|           |                                                                              |
|-----------|------------------------------------------------------------------------------|
| <i>vc</i> | The fold compound the generic soft constraint function should be bound to    |
| <i>f</i>  | A pointer to the function that evaluates the generic soft constraint feature |

#### Returns

Non-zero on successful binding the callback function, 0 otherwise

**SWIG Wrapper Notes** This function is attached as method **sc\_add\_f()** to objects of type *fold\_compound*

#### 16.13.4.10 vrna\_sc\_add\_bt()

```
int vrna_sc_add_bt (
    vrna_fold_compound_t * vc,
    vrna_callback_sc_backtrack * f )
#include <ViennaRNA/constraints/soft.h>
```

Bind a backtracking function pointer for generic soft constraint feature.

This function allows one to easily bind a function pointer to the soft constraint part [vrna\\_sc\\_t](#) of the [vrna\\_fold\\_compound\\_t](#). The provided function should be used for backtracking purposes in loop regions that were altered via the generic soft constraint feature. It has to return an array of [vrna\\_basepair\\_t](#) data structures, where the last element in the list is indicated by a value of -1 in its *i* position.

See also

[vrna\\_sc\\_add\\_data\(\)](#), [vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_exp\\_f\(\)](#)

#### Parameters

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| <i>vc</i> | The fold compound the generic soft constraint function should be bound to |
| <i>f</i>  | A pointer to the function that returns additional base pairs              |

#### Returns

Non-zero on successful binding the callback function, 0 otherwise

**SWIG Wrapper Notes** This function is attached as method **sc\_add\_bt()** to objects of type *fold\_compound*

#### 16.13.4.11 vrna\_sc\_add\_exp\_f()

```
int vrna_sc_add_exp_f (
    vrna_fold_compound_t * vc,
    vrna_callback_sc_exp_energy * exp_f )
#include <ViennaRNA/constraints/soft.h>
```

Bind a function pointer for generic soft constraint feature (PF version)

This function allows one to easily bind a function pointer and corresponding data structure to the soft constraint part [vrna\\_sc\\_t](#) of the [vrna\\_fold\\_compound\\_t](#). The function for evaluating the generic soft constraint feature has to return a pseudo free energy  $\hat{E}$  as Boltzmann factor, i.e.  $\exp(-\hat{E}/kT)$ . The required unit for  $E$  is *cal/mol*.

See also

[vrna\\_sc\\_add\\_bt\(\)](#), [vrna\\_sc\\_add\\_f\(\)](#), [vrna\\_sc\\_add\\_data\(\)](#)

Parameters

|                          |                                                                              |
|--------------------------|------------------------------------------------------------------------------|
| <code>vc</code>          | The fold compound the generic soft constraint function should be bound to    |
| <code>exp↔<br/>_f</code> | A pointer to the function that evaluates the generic soft constraint feature |

Returns

Non-zero on successful binding the callback function, 0 otherwise

**SWIG Wrapper Notes** This function is attached as method `sc_add_exp_f()` to objects of type *fold\_compound*

## 16.14 The RNA Secondary Structure Landscape

### 16.14.1 Detailed Description

Collaboration diagram for The RNA Secondary Structure Landscape:

#### Modules

- [Neighborhood Relation and Move Sets for Secondary Structures](#)  
*Different functions to generate structural neighbors of a secondary structure according to a particular Move Set.*
- [\(Re-\)folding Paths, Saddle Points, Energy Barriers, and Local Minima](#)  
*API for various RNA folding path algorithms.*

## 16.15 Minimum Free Energy (MFE) Algorithms

Predicting the Minimum Free Energy (MFE) and a corresponding (consensus) secondary structure.

### 16.15.1 Detailed Description

Predicting the Minimum Free Energy (MFE) and a corresponding (consensus) secondary structure.

In a nutshell we provide two different flavors for MFE prediction:

- [Global MFE Prediction](#) - to compute the MFE for the entire sequence
- [Local \(sliding window\) MFE Prediction](#) - to compute MFEs for each window using a sliding window approach

Each of these flavors, again, provides two implementations to either compute the MFE based on

- single RNA (DNA) sequence(s), or
- a comparative approach using multiple sequence alignments (MSA).

For the latter, a consensus secondary structure is predicted and our implementations compute an average of free energies for each sequence in the MSA plus an additional covariance pseudo-energy term.

The implementations for [Backtracking MFE structures](#) are generally agnostic with respect to whether local or global structure prediction is in place. Collaboration diagram for Minimum Free Energy (MFE) Algorithms:

#### Modules

- [Global MFE Prediction](#)  
*Variations of the global Minimum Free Energy (MFE) prediction algorithm.*
- [Local \(sliding window\) MFE Prediction](#)  
*Variations of the local (sliding window) Minimum Free Energy (MFE) prediction algorithm.*
- [Backtracking MFE structures](#)  
*Backtracking related interfaces.*

## Files

- file [mfe.h](#)  
*Compute Minimum Free energy (MFE) and backtrace corresponding secondary structures from RNA sequence data.*
- file [mfe\\_window.h](#)  
*Compute local Minimum Free Energy (MFE) using a sliding window approach and backtrace corresponding secondary structures.*

## 16.16 Partition Function and Equilibrium Properties

Compute the partition function to assess various equilibrium properties.

### 16.16.1 Detailed Description

Compute the partition function to assess various equilibrium properties.

Similar to our [Minimum Free Energy \(MFE\) Algorithms](#), we provide two different flavors for partition function computations:

- [Global Partition Function and Equilibrium Probabilities](#) - to compute the partition function for a full length sequence
- [Local \(sliding window\) Partition Function and Equilibrium Probabilities](#) - to compute the partition function of each window using a sliding window approach

While the global partition function approach supports predictions using single sequences as well as consensus partition functions for multiple sequence alignments (MSA), we currently do not support MSA input for the local variant.

Comparative prediction computes an average of the free energy contributions plus an additional covariance pseudo-energy term, exactly as we do for the [Minimum Free Energy \(MFE\) Algorithms](#) implementation.

Boltzmann weights for the free energy contributions of individual loops can be found in [Energy Evaluation for Individual Loops](#). Our implementations also provide a stochastic backtracking procedure to draw [Random Structure Samples from the Ensemble](#) according to their equilibrium probability. Collaboration diagram for Partition Function and Equilibrium Properties:

## Modules

- [Global Partition Function and Equilibrium Probabilities](#)  
*Variations of the global partition function algorithm.*
- [Local \(sliding window\) Partition Function and Equilibrium Probabilities](#)  
*Scanning version using a sliding window approach to compute equilibrium probabilities.*

## Files

- file [concentrations.h](#)  
*Concentration computations for RNA-RNA interactions.*
- file [part\\_func.h](#)  
*Partition function implementations.*
- file [part\\_func\\_window.h](#)  
*Partition function and equilibrium probability implementation for the sliding window algorithm.*

## Functions

- int [vrna\\_pf\\_float\\_precision](#) (void)  
*Find out whether partition function computations are using single precision floating points.*

### 16.16.2 Function Documentation



**16.16.2.1 vrna\_pf\_float\_precision()**

```
int vrna_pf_float_precision (
    void )
#include <ViennaRNA/part_func.h>
```

Find out whether partition function computations are using single precision floating points.

See also

[FLT\\_OR\\_DBL](#)

Returns

1 if single precision is used, 0 otherwise

**16.17 Global MFE Prediction**

Variations of the global Minimum Free Energy (MFE) prediction algorithm.

**16.17.1 Detailed Description**

Variations of the global Minimum Free Energy (MFE) prediction algorithm.

We provide implementations of the global MFE prediction algorithm for

- Single sequences,
- Multiple sequence alignments (MSA), and
- RNA-RNA hybrids

Collaboration diagram for Global MFE Prediction:

**Modules**

- [Computing MFE representatives of a Distance Based Partitioning](#)  
*Compute the minimum free energy (MFE) and secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures basepair distance to two fixed reference structures.*
- [Deprecated Interface for Global MFE Prediction](#)

**Files**

- file [mfe.h](#)  
*Compute Minimum Free energy (MFE) and backtrace corresponding secondary structures from RNA sequence data.*

**Basic global MFE prediction interface**

- float [vrna\\_mfe](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Compute minimum free energy and an appropriate secondary structure of an RNA sequence, or RNA sequence alignment.*
- float [vrna\\_mfe\\_dimer](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Compute the minimum free energy of two interacting RNA molecules.*

**Simplified global MFE prediction using sequence(s) or multiple sequence alignment(s)**

- float [vrna\\_fold](#) (const char \*sequence, char \*structure)  
*Compute Minimum Free Energy (MFE), and a corresponding secondary structure for an RNA sequence.*
- float [vrna\\_circfold](#) (const char \*sequence, char \*structure)  
*Compute Minimum Free Energy (MFE), and a corresponding secondary structure for a circular RNA sequence.*

- float [vrna\\_alifold](#) (const char \*\*sequences, char \*structure)  
*Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for an RNA sequence alignment using a comparative method.*
- float [vrna\\_circalifold](#) (const char \*\*sequences, char \*structure)  
*Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for a sequence alignment of circular RNAs using a comparative method.*
- float [vrna\\_cofold](#) (const char \*sequence, char \*structure)  
*Compute Minimum Free Energy (MFE), and a corresponding secondary structure for two dimerized RNA sequences.*

## 16.17.2 Function Documentation

### 16.17.2.1 vrna\_mfe()

```
float vrna_mfe (
    vrna_fold_compound_t * vc,
    char * structure )
```

```
#include <ViennaRNA/mfe.h>
```

Compute minimum free energy and an appropriate secondary structure of an RNA sequence, or RNA sequence alignment.

Depending on the type of the provided [vrna\\_fold\\_compound\\_t](#), this function predicts the MFE for a single sequence (or connected component of multiple sequences), or an averaged MFE for a sequence alignment. If backtracking is activated, it also constructs the corresponding secondary structure, or consensus structure. Therefore, the second parameter, *structure*, has to point to an allocated block of memory with a size of at least `strlen(sequence) + 1` to store the backtracked MFE structure. (For consensus structures, this is the length of the alignment + 1. If `NULL` is passed, no backtracking will be performed.

#### Note

This function is polymorphic. It accepts [vrna\\_fold\\_compound\\_t](#) of type [VRNA\\_FC\\_TYPE\\_SINGLE](#), and [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#).

#### See also

[vrna\\_fold\\_compound\\_t](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\(\)](#), [vrna\\_circfold\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_alifold\(\)](#), [vrna\\_circalifold\(\)](#)

#### Parameters

|                  |                                                                                                                                      |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------|
| <i>vc</i>        | fold compound                                                                                                                        |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to (Maybe <code>NULL</code> ) |

#### Returns

the minimum free energy (MFE) in kcal/mol

**SWIG Wrapper Notes** This function is attached as method **mfe()** to objects of type *fold\_compound*

### 16.17.2.2 vrna\_mfe\_dimer()

```
float vrna_mfe_dimer (
    vrna_fold_compound_t * vc,
    char * structure )
#include <ViennaRNA/mfe.h>
```

Compute the minimum free energy of two interacting RNA molecules.  
The code is analog to the [vrna\\_mfe\(\)](#) function.

**Deprecated** This function is obsolete since [vrna\\_mfe\(\)](#) can handle complexes multiple sequences since v2.5.0. Use [vrna\\_mfe\(\)](#) for connected component MFE instead and compute MFEs of unconnected states separately.

See also

[vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                           |
|------------------|-----------------------------------------------------------|
| <i>vc</i>        | fold compound                                             |
| <i>structure</i> | Will hold the barcket dot structure of the dimer molecule |

#### Returns

minimum free energy of the structure

**SWIG Wrapper Notes** This function is attached as method **mfe\_dimer()** to objects of type *fold\_compound*

#### 16.17.2.3 vrna\_fold()

```
float vrna_fold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/mfe.h>
```

Compute Minimum Free Energy (MFE), and a corresponding secondary structure for an RNA sequence. This simplified interface to [vrna\\_mfe\(\)](#) computes the MFE and, if required, a secondary structure for an RNA sequence using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing, e.g. suboptimal backtracking, etc.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

See also

[vrna\\_circfold\(\)](#), [vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | RNA sequence                                                                                              |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

**Returns**

the minimum free energy (MFE) in kcal/mol

**16.17.2.4 vrna\_circfold()**

```
float vrna_circfold (
    const char * sequence,
    char * structure )
```

```
#include <ViennaRNA/mfe.h>
```

Compute Minimum Free Energy (MFE), and a corresponding secondary structure for a circular RNA sequence.

This simplified interface to [vrna\\_mfe\(\)](#) computes the MFE and, if required, a secondary structure for a circular RNA sequence using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing, e.g. suboptimal backtracking, etc.

Folding of circular RNA sequences is handled as a post-processing step of the forward recursions. See [13] for further details.

**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

**See also**

[vrna\\_fold\(\)](#), [vrna\\_mfe\(\)](#)

**Parameters**

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | RNA sequence                                                                                              |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

**Returns**

the minimum free energy (MFE) in kcal/mol

**16.17.2.5 vrna\_alifold()**

```
float vrna_alifold (
    const char ** sequences,
    char * structure )
```

```
#include <ViennaRNA/mfe.h>
```

Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for an RNA sequence alignment using a comparative method.

This simplified interface to [vrna\\_mfe\(\)](#) computes the MFE and, if required, a consensus secondary structure for an RNA sequence alignment using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing, e.g. suboptimal backtracking, etc.

**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

See also

[vrna\\_circalifold\(\)](#), [vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequences</i> | RNA sequence alignment                                                                                    |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

#### Returns

the minimum free energy (MFE) in kcal/mol

#### 16.17.2.6 vrna\_circalifold()

```
float vrna_circalifold (
    const char ** sequences,
    char * structure )
```

```
#include <ViennaRNA/mfe.h>
```

Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for a sequence alignment of circular RNAs using a comparative method.

This simplified interface to [vrna\\_mfe\(\)](#) computes the MFE and, if required, a consensus secondary structure for an RNA sequence alignment using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing, e.g. suboptimal backtracking, etc.

Folding of circular RNA sequences is handled as a post-processing step of the forward recursions. See [13] for further details.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

See also

[vrna\\_alifold\(\)](#), [vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequences</i> | Sequence alignment of circular RNAs                                                                       |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

#### Returns

the minimum free energy (MFE) in kcal/mol

#### 16.17.2.7 vrna\_cofold()

```
float vrna_cofold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/mfe.h>
```

Compute Minimum Free Energy (MFE), and a corresponding secondary structure for two dimerized RNA sequences.

This simplified interface to [vrna\\_mfe\(\)](#) computes the MFE and, if required, a secondary structure for two RNA sequences upon dimerization using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing, e.g. suboptimal backtracking, etc.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

**Deprecated** This function is obsolete since [vrna\\_mfe\(\)](#)/[vrna\\_fold\(\)](#) can handle complexes multiple sequences since v2.5.0. Use [vrna\\_mfe\(\)](#)/[vrna\\_fold\(\)](#) for connected component MFE instead and compute MFEs of unconnected states separately.

#### See also

[vrna\\_fold\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#), [vrna\\_cut\\_point\\_insert\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | two RNA sequences separated by the '&' character                                                          |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

#### Returns

the minimum free energy (MFE) in kcal/mol

## 16.18 Local (sliding window) MFE Prediction

Variations of the local (sliding window) Minimum Free Energy (MFE) prediction algorithm.

### 16.18.1 Detailed Description

Variations of the local (sliding window) Minimum Free Energy (MFE) prediction algorithm.

We provide implementations for the local (sliding window) MFE prediction algorithm for

- Single sequences,
- Multiple sequence alignments (MSA), and

Note, that our implementation scans an RNA sequence (or MSA) from the 3' to the 5' end, and reports back locally optimal (consensus) structures, the corresponding free energy, and the position of the sliding window in global coordinates.

For any particular RNA sequence (or MSA) multiple locally optimal (consensus) secondary structures may be predicted. Thus, we tried to implement an interface that allows for an effortless conversion of the corresponding hits into any target data structure. As a consequence, we provide two distinct ways to retrieve the corresponding predictions, either

- through directly writing to an open `FILE` stream on-the-fly, or
- through a callback function mechanism.

The latter allows one to store the results in any possible target data structure. Our implementations then pass the results through the user-implemented callback as soon as the prediction for a particular window is finished. Collaboration diagram for Local (sliding window) MFE Prediction:

## Modules

- [Deprecated Interface for Local \(Sliding Window\) MFE Prediction](#)

## Files

- file [mfe\\_window.h](#)

*Compute local Minimum Free Energy (MFE) using a sliding window approach and backtrace corresponding secondary structures.*

## Typedefs

- typedef void() [vrna\\_mfe\\_window\\_callback](#)(int start, int end, const char \*structure, float en, void \*data)

*The default callback for sliding window MFE structure predictions.*

## Basic local (sliding window) MFE prediction interface

- float [vrna\\_mfe\\_window](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, FILE \*file)

*Local MFE prediction using a sliding window approach.*

- float [vrna\\_mfe\\_window\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)

- float [vrna\\_mfe\\_window\\_zscore](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double min\_z, FILE \*file)

*Local MFE prediction using a sliding window approach (with z-score cut-off)*

- float [vrna\\_mfe\\_window\\_zscore\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double min\_z, [vrna\\_mfe\\_window\\_zscore\\_callback](#) \*cb, void \*data)

## Simplified local MFE prediction using sequence(s) or multiple sequence alignment(s)

- float [vrna\\_Lfold](#) (const char \*string, int window\_size, FILE \*file)

*Local MFE prediction using a sliding window approach (simplified interface)*

- float [vrna\\_Lfold\\_cb](#) (const char \*string, int window\_size, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)

- float [vrna\\_Lfoldz](#) (const char \*string, int window\_size, double min\_z, FILE \*file)

*Local MFE prediction using a sliding window approach with z-score cut-off (simplified interface)*

- float [vrna\\_Lfoldz\\_cb](#) (const char \*string, int window\_size, double min\_z, [vrna\\_mfe\\_window\\_zscore\\_callback](#) \*cb, void \*data)

- float [vrna\\_aliLfold](#) (const char \*\*alignment, int maxdist, FILE \*fp)

- float [vrna\\_aliLfold\\_cb](#) (const char \*\*alignment, int maxdist, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)

## 16.18.2 Typedef Documentation

### 16.18.2.1 vrna\_mfe\_window\_callback

```
typedef void() vrna_mfe_window_callback(int start, int end, const char *structure, float en, void *data)
```

```
#include <ViennaRNA/mfe_window.h>
```

The default callback for sliding window MFE structure predictions.

**Notes on Callback Functions** This function will be called for each hit in a sliding window MFE prediction.

## Parameters

## See also

[vrna\\_mfe\\_window\(\)](#)

## Parameters

|                  |                                                                                            |
|------------------|--------------------------------------------------------------------------------------------|
| <i>start</i>     | provides the first position of the hit (1-based, relative to entire sequence/alignment)    |
| <i>end</i>       | provides the last position of the hit (1-based, relative to the entire sequence/alignment) |
| <i>structure</i> | provides the (sub)structure in dot-bracket notation                                        |
| <i>en</i>        | is the free energy of the structure hit in kcal/mol                                        |
| <i>data</i>      | is some arbitrary data pointer passed through by the function executing the callback       |

## 16.18.3 Function Documentation

### 16.18.3.1 vrna\_mfe\_window()

```
float vrna_mfe_window (
    vrna_fold_compound_t * vc,
    FILE * file )
#include <ViennaRNA/mfe_window.h>
```

Local MFE prediction using a sliding window approach.

Computes minimum free energy structures using a sliding window approach, where base pairs may not span outside the window. In contrast to [vrna\\_mfe\(\)](#), where a maximum base pair span may be set using the [vrna\\_md\\_t.max\\_bp\\_span](#) attribute and one globally optimal structure is predicted, this function uses a sliding window to retrieve all locally optimal structures within each window. The size of the sliding window is set in the [vrna\\_md\\_t.window\\_size](#) attribute, prior to the retrieval of the [vrna\\_fold\\_compound\\_t](#) using [vrna\\_fold\\_compound\(\)](#) with option [VRNA\\_OPTION\\_WINDOW](#)

The predicted structures are written on-the-fly, either to stdout, if a NULL pointer is passed as file parameter, or to the corresponding filehandle.

## See also

[vrna\\_fold\\_compound\(\)](#), [vrna\\_mfe\\_window\\_zscore\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_Lfold\(\)](#), [vrna\\_Lfoldz\(\)](#), [VRNA\\_OPTION\\_WINDOW](#), [vrna\\_md\\_t.max\\_bp\\_span](#), [vrna\\_md\\_t.window\\_size](#)

## Parameters

|             |                                                                                       |
|-------------|---------------------------------------------------------------------------------------|
| <i>vc</i>   | The <a href="#">vrna_fold_compound_t</a> with preallocated memory for the DP matrices |
| <i>file</i> | The output file handle where predictions are written to (maybe NULL)                  |

**SWIG Wrapper Notes** This function is attached as method **mfe\_window()** to objects of type *fold\_compound*

### 16.18.3.2 vrna\_mfe\_window\_zscore()

```
float vrna_mfe_window_zscore (
    vrna_fold_compound_t * vc,
    double min_z,
    FILE * file )
#include <ViennaRNA/mfe_window.h>
```



Local MFE prediction using a sliding window approach (with z-score cut-off)

Computes minimum free energy structures using a sliding window approach, where base pairs may not span outside the window. This function is the z-score version of [vrna\\_mfe\\_window\(\)](#), i.e. only predictions above a certain z-score cut-off value are printed. As for [vrna\\_mfe\\_window\(\)](#), the size of the sliding window is set in the [vrna\\_md\\_t.window\\_size](#) attribute, prior to the retrieval of the [vrna\\_fold\\_compound\\_t](#) using [vrna\\_fold\\_compound\(\)](#) with option [VRNA\\_OPTION\\_WINDOW](#).

The predicted structures are written on-the-fly, either to stdout, if a NULL pointer is passed as file parameter, or to the corresponding filehandle.

See also

[vrna\\_fold\\_compound\(\)](#), [vrna\\_mfe\\_window\\_zscore\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_Lfold\(\)](#), [vrna\\_Lfoldz\(\)](#), [VRNA\\_OPTION\\_WINDOW](#), [vrna\\_md\\_t.max\\_bp\\_span](#), [vrna\\_md\\_t.window\\_size](#)

#### Parameters

|              |                                                                                       |
|--------------|---------------------------------------------------------------------------------------|
| <i>vc</i>    | The <a href="#">vrna_fold_compound_t</a> with preallocated memory for the DP matrices |
| <i>min_z</i> | The minimal z-score for a predicted structure to appear in the output                 |
| <i>file</i>  | The output file handle where predictions are written to (maybe NULL)                  |

### 16.18.3.3 vrna\_Lfold()

```
float vrna_Lfold (
    const char * string,
    int window_size,
    FILE * file )
#include <ViennaRNA/mfe_window.h>
```

Local MFE prediction using a sliding window approach (simplified interface)

This simplified interface to [vrna\\_mfe\\_window\(\)](#) computes the MFE and locally optimal secondary structure using default options. Structures are predicted using a sliding window approach, where base pairs may not span outside the window. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\\_window\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

See also

[vrna\\_mfe\\_window\(\)](#), [vrna\\_Lfoldz\(\)](#), [vrna\\_mfe\\_window\\_zscore\(\)](#)

#### Parameters

|                    |                                                                                                |
|--------------------|------------------------------------------------------------------------------------------------|
| <i>string</i>      | The nucleic acid sequence                                                                      |
| <i>window_size</i> | The window size for locally optimal structures                                                 |
| <i>file</i>        | The output file handle where predictions are written to (if NULL, output is written to stdout) |

### 16.18.3.4 vrna\_Lfoldz()

```
float vrna_Lfoldz (
```

```
const char * string,
int window_size,
double min_z,
FILE * file )
```

```
#include <ViennaRNA/mfe_window.h>
```

Local MFE prediction using a sliding window approach with z-score cut-off (simplified interface)

This simplified interface to [vrna\\_mfe\\_window\\_zscore\(\)](#) computes the MFE and locally optimal secondary structure using default options. Structures are predicted using a sliding window approach, where base pairs may not span outside the window. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing. This function is the z-score version of [vrna\\_Lfold\(\)](#), i.e. only predictions above a certain z-score cut-off value are printed.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_mfe\\_window\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

#### See also

[vrna\\_mfe\\_window\\_zscore\(\)](#), [vrna\\_Lfold\(\)](#), [vrna\\_mfe\\_window\(\)](#)

#### Parameters

|                    |                                                                                                |
|--------------------|------------------------------------------------------------------------------------------------|
| <i>string</i>      | The nucleic acid sequence                                                                      |
| <i>window_size</i> | The window size for locally optimal structures                                                 |
| <i>min_z</i>       | The minimal z-score for a predicted structure to appear in the output                          |
| <i>file</i>        | The output file handle where predictions are written to (if NULL, output is written to stdout) |

## 16.19 Backtracking MFE structures

Backtracking related interfaces.

### 16.19.1 Detailed Description

Backtracking related interfaces.

Collaboration diagram for Backtracking MFE structures:

#### Functions

- float [vrna\\_backtrack5](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int length, char \*structure)  
*Backtrack an MFE (sub)structure.*
- int [vrna\\_BT\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int en, [vrna\\_bp\\_stack\\_t](#) \*bp\_stack, int \*stack\_count)  
*Backtrack a hairpin loop closed by (i, j).*
- int [vrna\\_BT\\_stack](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int \*i, int \*j, int \*en, [vrna\\_bp\\_stack\\_t](#) \*bp\_stack, int \*stack\_count)  
*Backtrack a stacked pair closed by (i, j).*
- int [vrna\\_BT\\_int\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int \*i, int \*j, int en, [vrna\\_bp\\_stack\\_t](#) \*bp\_stack, int \*stack\_count)  
*Backtrack an interior loop closed by (i, j).*
- int [vrna\\_BT\\_mb\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int \*i, int \*j, int \*k, int en, int \*component1, int \*component2)  
*Backtrack the decomposition of a multi branch loop closed by (i, j).*

## 16.19.2 Function Documentation

### 16.19.2.1 `vrna_backtrack5()`

```
float vrna_backtrack5 (
    vrna_fold_compound_t * fc,
    unsigned int length,
    char * structure )
#include <ViennaRNA/mfe.h>
```

Backtrack an MFE (sub)structure.

This function allows one to backtrack the MFE structure for a (sub)sequence

#### Note

On error, the function returns `INF / 100.` and stores the empty string in `structure`.

#### Precondition

Requires pre-filled MFE dynamic programming matrices, i.e. one has to call `vrna_mfe()` prior to calling this function

#### See also

`vrna_mfe()`, `vrna_pbacktrack5()`

#### Parameters

|                  |                                                                                                                                                                   |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>fc</i>        | fold compound                                                                                                                                                     |
| <i>length</i>    | The length of the subsequence, starting from the 5' end                                                                                                           |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to. (Must have size of at least $\$p \text{ length} + 1$ ) |

#### Returns

The minimum free energy (MFE) for the specified `length` in kcal/mol and a corresponding secondary structure in dot-bracket notation (stored in `structure`)

**SWIG Wrapper Notes** This function is attached as overloaded method `backtrack()` to objects of type `fold_compound` with default parameter `length` equal to the total length of the RNA.

### 16.19.2.2 `vrna_BT_hp_loop()`

```
int vrna_BT_hp_loop (
    vrna_fold_compound_t * fc,
    int i,
    int j,
    int en,
    vrna_bp_stack_t * bp_stack,
    int * stack_count )
#include <ViennaRNA/loops/hairpin.h>
```

Backtrack a hairpin loop closed by  $(i, j)$ .

#### Note

This function is polymorphic! The provided `vrna_fold_compound_t` may be of type `VRNA_FC_TYPE_SINGLE` or `VRNA_FC_TYPE_COMPARATIVE`

### 16.19.2.3 vrna\_BT\_mb\_loop()

```
int vrna_BT_mb_loop (
    vrna_fold_compound_t * fc,
    int * i,
    int * j,
    int * k,
    int en,
    int * component1,
    int * component2 )
#include <ViennaRNA/loops/multibranch.h>
Backtrack the decomposition of a multi branch loop closed by  $(i, j)$ .
```

#### Parameters

|                   |                                                                                                                                                |
|-------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>fc</i>         | The <code>vrna_fold_compound_t</code> filled with all relevant data for backtracking                                                           |
| <i>i</i>          | 5' position of base pair closing the loop (will be set to 5' position of leftmost decomposed block upon successful backtracking)               |
| <i>j</i>          | 3' position of base pair closing the loop (will be set to 3' position of rightmost decomposed block upon successful backtracking)              |
| <i>k</i>          | Split position that delimits leftmost from rightmost block, $[i, k]$ and $[k+1, j]$ , respectively. (Will be set upon successful backtracking) |
| <i>en</i>         | The energy contribution of the substructure enclosed by $(i, j)$                                                                               |
| <i>component1</i> | Type of leftmost block (1 = ML, 2 = C)                                                                                                         |
| <i>component2</i> | Type of rightmost block (1 = ML, 2 = C)                                                                                                        |

#### Returns

1, if backtracking succeeded, 0 otherwise.

## 16.20 Global Partition Function and Equilibrium Probabilities

Variations of the global partition function algorithm.

### 16.20.1 Detailed Description

Variations of the global partition function algorithm.

We provide implementations of the global partition function algorithm for

- Single sequences,
- Multiple sequence alignments (MSA), and
- RNA-RNA hybrids

Collaboration diagram for Global Partition Function and Equilibrium Probabilities:

#### Modules

- [Computing Partition Functions of a Distance Based Partitioning](#)  
*Compute the partition function and stochastically sample secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures.*
- [Predicting various thermodynamic properties](#)  
*Compute various thermodynamic properties using the partition function.*
- [Deprecated Interface for Global Partition Function Computation](#)

## Files

- file [part\\_func.h](#)  
*Partition function implementations.*

## Data Structures

- struct [vrna\\_dimer\\_pf\\_s](#)  
*Data structure returned by [vrna\\_pf\\_dimer\(\)](#) [More...](#)*
- struct [vrna\\_multimer\\_pf\\_s](#)

## Functions

- [vrna\\_ep\\_t](#) \* [vrna\\_plist\\_from\\_probs](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double cut\_off)  
*Create a [vrna\\_ep\\_t](#) from base pair probability matrix.*

## Basic global partition function interface

- [FLT\\_OR\\_DBL vrna\\_pf](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Compute the partition function  $Q$  for a given RNA sequence, or sequence alignment.*
- [vrna\\_dimer\\_pf\\_t vrna\\_pf\\_dimer](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.*
- [FLT\\_OR\\_DBL](#) \* [vrna\\_pf\\_substrands](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, size\_t complex\_size)
- [FLT\\_OR\\_DBL vrna\\_pf\\_add](#) ([FLT\\_OR\\_DBL](#) dG1, [FLT\\_OR\\_DBL](#) dG2, double kT)

## Simplified global partition function computation using sequence(s) or multiple sequence alignment(s)

- float [vrna\\_pf\\_fold](#) (const char \*sequence, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence using a comparative method.*
- float [vrna\\_pf\\_circfold](#) (const char \*sequence, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for a circular RNA sequences using a comparative method.*
- float [vrna\\_pf\\_alifold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence alignment using a comparative method.*
- float [vrna\\_pf\\_circalifold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an alignment of circular RNA sequences using a comparative method.*
- [vrna\\_dimer\\_pf\\_t vrna\\_pf\\_co\\_fold](#) (const char \*seq, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.*

## 16.20.2 Data Structure Documentation

### 16.20.2.1 struct vrna\_dimer\_pf\_s

Data structure returned by [vrna\\_pf\\_dimer\(\)](#)

#### Data Fields

- double **F0AB**  
*Null model without DuplexInit.*
- double **FAB**  
*all states with DuplexInit correction*
- double **FcAB**  
*true hybrid states only*

- double **FA**  
*monomer A*
- double **FB**  
*monomer B*

### 16.20.2.2 struct vrna\_multimer\_pf\_s

#### Data Fields

- double **F\_connected**  
*Fully connected ensemble (incl. DuplexInitiation and rotational symmetry correction).*
- double \* **F\_monomers**  
*monomers*
- size\_t **num\_monomers**  
*Number of monomers.*

## 16.20.3 Function Documentation

### 16.20.3.1 vrna\_pf()

```
float vrna_pf (
    vrna_fold_compound_t * vc,
    char * structure )
```

```
#include <ViennaRNA/part_func.h>
```

Compute the partition function  $Q$  for a given RNA sequence, or sequence alignment.

If *structure* is not a NULL pointer on input, it contains on return a string consisting of the letters ". , | { } ( ) " denoting bases that are essentially unpaired, weakly paired, strongly paired without preference, weakly upstream (downstream) paired, or strongly up- (down-)stream paired bases, respectively. If the model's compute\_bpp is set to 0 base pairing probabilities will not be computed (saving CPU time), otherwise after calculations took place *pr* will contain the probability that bases  $i$  and  $j$  pair.

#### Note

This function is polymorphic. It accepts *vrna\_fold\_compound\_t* of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

This function may return `INF` / 100. in case of contradicting constraints or numerical over-/underflow. In the latter case, a corresponding warning will be issued to `stdout`.

#### See also

[vrna\\_fold\\_compound\\_t](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_pf\\_fold\(\)](#), [vrna\\_pf\\_circfold\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_pf\\_alifold\(\)](#), [vrna\\_pf\\_circalifold\(\)](#), [vrna\\_db\\_from\\_probs\(\)](#), [vrna\\_exp\\_params\(\)](#), [vrna\\_aln\\_pinfol\(\)](#)

#### Parameters

|                |                  |                                                                                                      |
|----------------|------------------|------------------------------------------------------------------------------------------------------|
| <i>in, out</i> | <i>vc</i>        | The fold compound data structure                                                                     |
| <i>in, out</i> | <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |

#### Returns

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

**SWIG Wrapper Notes** This function is attached as method **pf()** to objects of type *fold\_compound*

**16.20.3.2 vrna\_pf\_dimer()**

```
vrna_dimer_pf_t vrna_pf_dimer (
    vrna_fold_compound_t * vc,
    char * structure )
#include <ViennaRNA/part_func.h>
```

Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers. This is the cofold partition function folding.

**Note**

This function may return [INF](#) / 100. for the FA, FB, FAB, F0AB members of the output data structure in case of contradicting constraints or numerical over-/underflow. In the latter case, a corresponding warning will be issued to `stdout`.

**See also**

[vrna\\_fold\\_compound\(\)](#) for how to retrieve the necessary data structure

**Parameters**

|                  |                                        |
|------------------|----------------------------------------|
| <i>vc</i>        | the fold compound data structure       |
| <i>structure</i> | Will hold the structure or constraints |

**Returns**

`vrna_dimer_pf_t` structure containing a set of energies needed for concentration computations.

**SWIG Wrapper Notes** This function is attached as method **pf\_dimer()** to objects of type *fold\_compound*

**16.20.3.3 vrna\_pf\_fold()**

```
float vrna_pf_fold (
    const char * sequence,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/part_func.h>
```

Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence using a comparative method. This simplified interface to [vrna\\_pf\(\)](#) computes the partition function and, if required, base pair probabilities for an RNA sequence using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_pf\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

**See also**

[vrna\\_pf\\_circfold\(\)](#), [vrna\\_pf\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#)

**Parameters**

|                  |                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | RNA sequence                                                                                         |
| <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <i>pl</i>        | A pointer to a list of <a href="#">vrna_ep_t</a> to store pairing probabilities (Maybe NULL)         |

**Returns**

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

**16.20.3.4 vrna\_pf\_circfold()**

```
float vrna_pf_circfold (
    const char * sequence,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/part_func.h>
```

Compute Partition function  $Q$  (and base pair probabilities) for a circular RNA sequences using a comparative method.

This simplified interface to [vrna\\_pf\(\)](#) computes the partition function and, if required, base pair probabilities for a circular RNA sequence using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_pf\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

Folding of circular RNA sequences is handled as a post-processing step of the forward recursions. See [13] for further details.

**See also**

[vrna\\_pf\\_fold\(\)](#), [vrna\\_pf\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#)

**Parameters**

|                  |                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | A circular RNA sequence                                                                              |
| <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <i>pl</i>        | A pointer to a list of <a href="#">vrna_ep_t</a> to store pairing probabilities (Maybe NULL)         |

**Returns**

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

**16.20.3.5 vrna\_pf\_alifold()**

```
float vrna_pf_alifold (
    const char ** sequences,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/part_func.h>
```

Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence alignment using a comparative method.

This simplified interface to [vrna\\_pf\(\)](#) computes the partition function and, if required, base pair probabilities for an RNA sequence alignment using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.



**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_pf\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

**See also**

[vrna\\_pf\\_circalifold\(\)](#), [vrna\\_pf\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_t](#)

**Parameters**

|                  |                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------|
| <i>sequences</i> | RNA sequence alignment                                                                               |
| <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <i>pl</i>        | A pointer to a list of <a href="#">vrna_ep_t</a> to store pairing probabilities (Maybe NULL)         |

**Returns**

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

**16.20.3.6 vrna\_pf\_circalifold()**

```
float vrna_pf_circalifold (
    const char ** sequences,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/part_func.h>
```

Compute Partition function  $Q$  (and base pair probabilities) for an alignment of circular RNA sequences using a comparative method.

This simplified interface to [vrna\\_pf\(\)](#) computes the partition function and, if required, base pair probabilities for an RNA sequence alignment using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

**Note**

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_pf\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

Folding of circular RNA sequences is handled as a post-processing step of the forward recursions. See [13] for further details.

**See also**

[vrna\\_pf\\_alifold\(\)](#), [vrna\\_pf\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_t](#)

**Parameters**

|                  |                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------|
| <i>sequences</i> | Sequence alignment of circular RNAs                                                                  |
| <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <i>pl</i>        | A pointer to a list of <a href="#">vrna_ep_t</a> to store pairing probabilities (Maybe NULL)         |

## Returns

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

16.20.3.7 `vrna_plist_from_probs()`

```
vrna_ep_t * vrna_plist_from_probs (
    vrna_fold_compound_t * vc,
    double cut_off )
#include <ViennaRNA/utils/structures.h>
```

Create a `vrna_ep_t` from base pair probability matrix.

The probability matrix provided via the `vrna_fold_compound_t` is parsed and all pair probabilities above the given threshold are used to create an entry in the plist

The end of the plist is marked by sequence positions *i* as well as *j* equal to 0. This condition should be used to stop looping over its entries

## Parameters

|    |                      |                   |
|----|----------------------|-------------------|
| in | <code>vc</code>      | The fold compound |
| in | <code>cut_off</code> | The cutoff value  |

## Returns

A pointer to the plist that is to be created

16.20.3.8 `vrna_pf_co_fold()`

```
vrna_dimer_pf_t vrna_pf_co_fold (
    const char * seq,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/part_func.h>
```

Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.

This simplified interface to `vrna_pf_dimer()` computes the partition function and, if required, base pair probabilities for an RNA-RNA interaction using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

## Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use `vrna_pf_dimer()`, and the data structure `vrna_fold_compound_t` instead.

## See also

[vrna\\_pf\\_dimer\(\)](#)

## Parameters

|                        |                                                                                                      |
|------------------------|------------------------------------------------------------------------------------------------------|
| <code>seq</code>       | Two concatenated RNA sequences with a delimiting '&' in between                                      |
| <code>structure</code> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <code>pl</code>        | A pointer to a list of <code>vrna_ep_t</code> to store pairing probabilities (Maybe NULL)            |

**Returns**

vrna\_dimer\_pf\_t structure containing a set of energies needed for concentration computations.

## 16.21 Local (sliding window) Partition Function and Equilibrium Probabilities

Scanning version using a sliding window approach to compute equilibrium probabilities.

### 16.21.1 Detailed Description

Scanning version using a sliding window approach to compute equilibrium probabilities.

Collaboration diagram for Local (sliding window) Partition Function and Equilibrium Probabilities:

**Modules**

- [Deprecated Interface for Local \(Sliding Window\) Partition Function Computation](#)

**Files**

- file [part\\_func\\_window.h](#)  
*Partition function and equilibrium probability implementation for the sliding window algorithm.*

**Macros**

- `#define VRNA_EXT_LOOP 1U`  
*Exterior loop.*
- `#define VRNA_HP_LOOP 2U`  
*Hairpin loop.*
- `#define VRNA_INT_LOOP 4U`  
*Internal loop.*
- `#define VRNA_MB_LOOP 8U`  
*Multibranch loop.*
- `#define VRNA_ANY_LOOP (VRNA_EXT_LOOP | VRNA_HP_LOOP | VRNA_INT_LOOP | VRNA_MB_LOOP)`  
*Any loop.*
- `#define VRNA_PROBS_WINDOW_BPP 4096U`  
*Trigger base pairing probabilities.*
- `#define VRNA_PROBS_WINDOW_UP 8192U`  
*Trigger unpaired probabilities.*
- `#define VRNA_PROBS_WINDOW_STACKP 16384U`  
*Trigger base pair stack probabilities.*
- `#define VRNA_PROBS_WINDOW_UP_SPLIT 32768U`  
*Trigger detailed unpaired probabilities split up into different loop type contexts.*
- `#define VRNA_PROBS_WINDOW_PF 65536U`  
*Trigger partition function.*

**Typedefs**

- typedef void() [vrna\\_probs\\_window\\_callback](#)(FLT\_OR\_DBL \*pr, int pr\_size, int i, int max, unsigned int type, void \*data)  
*Sliding window probability computation callback.*

## Basic local partition function interface

- `int vrna_probs_window (vrna_fold_compound_t *fc, int ulength, unsigned int options, vrna_probs_window_callback *cb, void *data)`

*Compute various equilibrium probabilities under a sliding window approach.*

## Simplified global partition function computation using sequence(s) or multiple sequence alignment(s)

- `vrna_ep_t * vrna_pfl_fold (const char *sequence, int window_size, int max_bp_span, float cutoff)`  
*Compute base pair probabilities using a sliding-window approach.*
- `int vrna_pfl_fold_cb (const char *sequence, int window_size, int max_bp_span, vrna_probs_window_callback *cb, void *data)`  
*Compute base pair probabilities using a sliding-window approach (callback version)*

- `double ** vrna_pfl_fold_up (const char *sequence, int ulength, int window_size, int max_bp_span)`  
*Compute probability of contiguous unpaired segments.*
- `int vrna_pfl_fold_up_cb (const char *sequence, int ulength, int window_size, int max_bp_span, vrna_probs_window_callback *cb, void *data)`  
*Compute probability of contiguous unpaired segments.*

## 16.21.2 Macro Definition Documentation

### 16.21.2.1 VRNA\_PROBS\_WINDOW\_BPP

```
#define VRNA_PROBS_WINDOW_BPP 4096U
#include <ViennaRNA/part_func_window.h>
```

Trigger base pairing probabilities.

Passing this flag to `vrna_probs_window()` activates callback execution for base pairing probabilities. In turn, the corresponding callback receives this flag through the `type` argument whenever base pairing probabilities are provided.

Detailed information for the algorithm to compute unpaired probabilities can be taken from [3].

See also

`vrna_probs_window()`

### 16.21.2.2 VRNA\_PROBS\_WINDOW\_UP

```
#define VRNA_PROBS_WINDOW_UP 8192U
#include <ViennaRNA/part_func_window.h>
```

Trigger unpaired probabilities.

Passing this flag to `vrna_probs_window()` activates callback execution for unpaired probabilities. In turn, the corresponding callback receives this flag through the `type` argument whenever unpaired probabilities are provided.

Detailed information for the algorithm to compute unpaired probabilities can be taken from [4].

See also

`vrna_probs_window()`

### 16.21.2.3 VRNA\_PROBS\_WINDOW\_STACKP

```
#define VRNA_PROBS_WINDOW_STACKP 16384U
#include <ViennaRNA/part_func_window.h>
```

Trigger base pair stack probabilities.

Passing this flag to [vrna\\_probs\\_window\(\)](#) activates callback execution for stacking probabilities. In turn, the corresponding callback receives this flag through the `type` argument whenever stack probabilities are provided.

**Bug** Currently, this flag is a placeholder doing nothing as the corresponding implementation for stack probability computation is missing.

See also

[vrna\\_probs\\_window\(\)](#)

### 16.21.2.4 VRNA\_PROBS\_WINDOW\_UP\_SPLIT

```
#define VRNA_PROBS_WINDOW_UP_SPLIT 32768U
#include <ViennaRNA/part_func_window.h>
```

Trigger detailed unpaired probabilities split up into different loop type contexts.

Passing this flag to [vrna\\_probs\\_window\(\)](#) activates callback execution for unpaired probabilities. In contrast to [VRNA\\_PROBS\\_WINDOW\\_UP](#) this flag requests unpaired probabilities to be split up into different loop type contexts. In turn, the corresponding callback receives the [VRNA\\_PROBS\\_WINDOW\\_UP](#) flag OR-ed together with the corresponding loop type, i.e.:

- [VRNA\\_EXT\\_LOOP](#) - Exterior loop.
- [VRNA\\_HP\\_LOOP](#) - Hairpin loop.
- [VRNA\\_INT\\_LOOP](#) - Internal loop.
- [VRNA\\_MB\\_LOOP](#) - Multibranch loop.
- [VRNA\\_ANY\\_LOOP](#) - Any loop.

See also

[vrna\\_probs\\_window\(\)](#), [VRNA\\_PROBS\\_WINDOW\\_UP](#)

### 16.21.2.5 VRNA\_PROBS\_WINDOW\_PF

```
#define VRNA_PROBS_WINDOW_PF 65536U
#include <ViennaRNA/part_func_window.h>
```

Trigger partition function.

Passing this flag to [vrna\\_probs\\_window\(\)](#) activates callback execution for partition function. In turn, the corresponding callback receives this flag through its `type` argument whenever partition function data is provided.

**Note**

Instead of actually providing the partition function  $Z$ , the callback is always provided with the corresponding ensemble free energy  $\Delta G = -RT \ln Z$ .

See also

[vrna\\_probs\\_window\(\)](#)

## 16.21.3 Typedef Documentation

### 16.21.3.1 vrna\_probs\_window\_callback

```
typedef void() vrna_probs_window_callback(FLT\_OR\_DBL *pr, int pr_size, int i, int max, unsigned
int type, void *data)
#include <ViennaRNA/part\_func\_window.h>
```

Sliding window probability computation callback.

**Notes on Callback Functions** This function will be called for each probability data set in the sliding window probability computation implementation of [vrna\\_probs\\_window\(\)](#). The argument *type* specifies the type of probability that is passed to this function.

#### Types:

- [VRNA\\_PROBS\\_WINDOW\\_BPP](#) - Trigger base pairing probabilities.
- [VRNA\\_PROBS\\_WINDOW\\_UP](#) - Trigger unpaired probabilities.
- [VRNA\\_PROBS\\_WINDOW\\_PF](#) - Trigger partition function.

The above types usually come exclusively. However, for unpaired probabilities, the [VRNA\\_PROBS\\_WINDOW\\_UP](#) flag is OR-ed together with one of the loop type contexts

- [VRNA\\_EXT\\_LOOP](#) - Exterior loop.
- [VRNA\\_HP\\_LOOP](#) - Hairpin loop.
- [VRNA\\_INT\\_LOOP](#) - Internal loop.
- [VRNA\\_MB\\_LOOP](#) - Multibranch loop.
- [VRNA\\_ANY\\_LOOP](#) - Any loop.

to indicate the particular type of data available through the *pr* pointer.

See also

[vrna\\_probs\\_window\(\)](#), [vrna\\_pfl\\_fold\\_up\\_cb\(\)](#)

#### Parameters

|                |                                                           |
|----------------|-----------------------------------------------------------|
| <i>pr</i>      | An array of probabilities                                 |
| <i>pr_size</i> | The length of the probability array                       |
| <i>i</i>       | The i-position (5') of the probabilities                  |
| <i>max</i>     | The (theoretical) maximum length of the probability array |
| <i>type</i>    | The type of data that is provided                         |
| <i>data</i>    | Auxiliary data                                            |

## 16.21.4 Function Documentation

### 16.21.4.1 vrna\_probs\_window()

```
int vrna_probs_window (
    vrna\_fold\_compound\_t * fc,
    int ulength,
    unsigned int options,
    vrna\_probs\_window\_callback * cb,
    void * data )
```

```
#include <ViennaRNA/part_func_window.h>
```

Compute various equilibrium probabilities under a sliding window approach.

This function applies a sliding window scan for the sequence provided with the argument `fc` and reports back equilibrium probabilities through the callback function `cb`. The data reported to the callback depends on the `options` flag.

#### Note

The parameter `ulength` only affects computation and resulting data if unpaired probability computations are requested through the `options` flag.

#### Options:

- `VRNA_PROBS_WINDOW_BPP` - Trigger base pairing probabilities.
- `VRNA_PROBS_WINDOW_UP` - Trigger unpaired probabilities.
- `VRNA_PROBS_WINDOW_UP_SPLIT` - Trigger detailed unpaired probabilities split up into different loop type contexts.

Options may be OR-ed together

#### See also

`vrna_pfl_fold_cb()`, `vrna_pfl_fold_up_cb()`

#### Parameters

|                      |                                                                                        |
|----------------------|----------------------------------------------------------------------------------------|
| <code>fc</code>      | The fold compound with sequence data, model settings and precomputed energy parameters |
| <code>ulength</code> | The maximal length of an unpaired segment (only for unpaired probability computations) |
| <code>cb</code>      | The callback function which collects the pair probability data for further processing  |
| <code>data</code>    | Some arbitrary data structure that is passed to the callback <code>cb</code>           |
| <code>options</code> | Option flags to control the behavior of this function                                  |

#### Returns

0 on failure, non-zero on success

#### 16.21.4.2 `vrna_pfl_fold()`

```
vrna_ep_t * vrna_pfl_fold (
    const char * sequence,
    int window_size,
    int max_bp_span,
    float cutoff )
```

```
#include <ViennaRNA/part_func_window.h>
```

Compute base pair probabilities using a sliding-window approach.

This is a simplified wrapper to `vrna_probs_window()` that given a nucleic acid sequence, a window size, a maximum base pair span, and a cutoff value computes the pair probabilities for any base pair in any window. The pair probabilities are returned as a list and the user has to take care to `free()` the memory occupied by the list.

#### Note

This function uses default model settings! For custom model settings, we refer to the function `vrna_probs_window()`.

In case of any computation errors, this function returns `NULL`

See also

[vrna\\_probs\\_window\(\)](#), [vrna\\_pfl\\_fold\\_cb\(\)](#), [vrna\\_pfl\\_fold\\_up\(\)](#)

#### Parameters

|                    |                                                                                        |
|--------------------|----------------------------------------------------------------------------------------|
| <i>sequence</i>    | The nucleic acid input sequence                                                        |
| <i>window_size</i> | The size of the sliding window                                                         |
| <i>max_bp_span</i> | The maximum distance along the backbone between two nucleotides that form a base pairs |
| <i>cutoff</i>      | A cutoff value that omits all pairs with lower probability                             |

#### Returns

A list of base pair probabilities, terminated by an entry with [vrna\\_ep\\_t.i](#) and [vrna\\_ep\\_t.j](#) set to 0

### 16.21.4.3 vrna\_pfl\_fold\_cb()

```
int vrna_pfl_fold_cb (
    const char * sequence,
    int window_size,
    int max_bp_span,
    vrna_probs_window_callback * cb,
    void * data )
#include <ViennaRNA/part_func_window.h>
```

Compute base pair probabilities using a sliding-window approach (callback version)

This is a simplified wrapper to [vrna\\_probs\\_window\(\)](#) that given a nucleic acid sequence, a window size, a maximum base pair span, and a cutoff value computes the pair probabilities for any base pair in any window. It is similar to [vrna\\_pfl\\_fold\(\)](#) but uses a callback mechanism to return the pair probabilities.

Read the details for [vrna\\_probs\\_window\(\)](#) for details on the callback implementation!

#### Note

This function uses default model settings! For custom model settings, we refer to the function [vrna\\_probs\\_window\(\)](#).

See also

[vrna\\_probs\\_window\(\)](#), [vrna\\_pfl\\_fold\(\)](#), [vrna\\_pfl\\_fold\\_up\\_cb\(\)](#)

#### Parameters

|                    |                                                                                        |
|--------------------|----------------------------------------------------------------------------------------|
| <i>sequence</i>    | The nucleic acid input sequence                                                        |
| <i>window_size</i> | The size of the sliding window                                                         |
| <i>max_bp_span</i> | The maximum distance along the backbone between two nucleotides that form a base pairs |
| <i>cb</i>          | The callback function which collects the pair probability data for further processing  |
| <i>data</i>        | Some arbitrary data structure that is passed to the callback <i>cb</i>                 |

#### Returns

0 on failure, non-zero on success

### 16.21.4.4 vrna\_pfl\_fold\_up()

```
double ** vrna_pfl_fold_up (
```



```

    const char * sequence,
    int ulength,
    int window_size,
    int max_bp_span )
#include <ViennaRNA/part_func_window.h>

```

Compute probability of contiguous unpaired segments.

This is a simplified wrapper to [vrna\\_probs\\_window\(\)](#) that given a nucleic acid sequence, a maximum length of unpaired segments (`ulength`), a window size, and a maximum base pair span computes the equilibrium probability of any segment not exceeding `ulength`. The probabilities to be unpaired are returned as a 1-based, 2-dimensional matrix with dimensions  $N \times M$ , where  $N$  is the length of the sequence and  $M$  is the maximum segment length. As an example, the probability of a segment of size 5 starting at position 100 is stored in the matrix entry  $X[100][5]$ . It is the users responsibility to free the memory occupied by this matrix.

#### Note

This function uses default model settings! For custom model settings, we refer to the function [vrna\\_probs\\_window\(\)](#).

#### Parameters

|                    |                                                                                        |
|--------------------|----------------------------------------------------------------------------------------|
| <i>sequence</i>    | The nucleic acid input sequence                                                        |
| <i>ulength</i>     | The maximal length of an unpaired segment                                              |
| <i>window_size</i> | The size of the sliding window                                                         |
| <i>max_bp_span</i> | The maximum distance along the backbone between two nucleotides that form a base pairs |

#### Returns

The probabilities to be unpaired for any segment not exceeding `ulength`

#### 16.21.4.5 vrna\_pfl\_fold\_up\_cb()

```

int vrna_pfl_fold_up_cb (
    const char * sequence,
    int ulength,
    int window_size,
    int max_bp_span,
    vrna_probs_window_callback * cb,
    void * data )
#include <ViennaRNA/part_func_window.h>

```

Compute probability of contiguous unpaired segments.

This is a simplified wrapper to [vrna\\_probs\\_window\(\)](#) that given a nucleic acid sequence, a maximum length of unpaired segments (`ulength`), a window size, and a maximum base pair span computes the equilibrium probability of any segment not exceeding `ulength`. It is similar to [vrna\\_pfl\\_fold\\_up\(\)](#) but uses a callback mechanism to return the unpaired probabilities.

Read the details for [vrna\\_probs\\_window\(\)](#) for details on the callback implementation!

#### Note

This function uses default model settings! For custom model settings, we refer to the function [vrna\\_probs\\_window\(\)](#).

#### Parameters

|                    |                                           |
|--------------------|-------------------------------------------|
| <i>sequence</i>    | The nucleic acid input sequence           |
| <i>ulength</i>     | The maximal length of an unpaired segment |
| <i>window_size</i> | The size of the sliding window            |

## Parameters

|                    |                                                                                        |
|--------------------|----------------------------------------------------------------------------------------|
| <i>max_bp_span</i> | The maximum distance along the backbone between two nucleotides that form a base pairs |
| <i>cb</i>          | The callback function which collects the pair probability data for further processing  |
| <i>data</i>        | Some arbitrary data structure that is passed to the callback <i>cb</i>                 |

## Returns

0 on failure, non-zero on success

## 16.22 Suboptimal and Representative Structures

Sample and enumerate suboptimal secondary structures from RNA sequence data.

### 16.22.1 Detailed Description

Sample and enumerate suboptimal secondary structures from RNA sequence data.  
Collaboration diagram for Suboptimal and Representative Structures:

#### Modules

- [Suboptimal Structures sensu Stiegler et al. 1984 / Zuker et al. 1989](#)
- [Suboptimal Structures within an Energy Band around the MFE](#)
- [Random Structure Samples from the Ensemble](#)  
*Functions to draw random structure samples from the ensemble according to their equilibrium probability.*
- [Compute the Structure with Maximum Expected Accuracy \(MEA\)](#)
- [Compute the Centroid Structure](#)

#### Files

- file [boltzmann\\_sampling.h](#)  
*Boltzmann Sampling of secondary structures from the ensemble.*
- file [centroid.h](#)  
*Centroid structure computation.*
- file [MEA.h](#)  
*Computes a MEA (maximum expected accuracy) structure.*
- file [mm.h](#)  
*Several Maximum Matching implementations.*
- file [subopt.h](#)  
*RNAsubopt and density of states declarations.*

## 16.23 Suboptimal Structures sensu Stiegler et al. 1984 / Zuker et al. 1989

### 16.23.1 Detailed Description

Collaboration diagram for Suboptimal Structures sensu Stiegler et al. 1984 / Zuker et al. 1989:

#### Functions

- [SOLUTION \\* zukersubopt](#) (const char \*string)  
*Compute Zuker type suboptimal structures.*
- [SOLUTION \\* zukersubopt\\_par](#) (const char \*string, [vrna\\_param\\_t](#) \*parameters)  
*Compute Zuker type suboptimal structures.*
- [vrna\\_subopt\\_solution\\_t \\* vrna\\_subopt\\_zuker](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)  
*Compute Zuker type suboptimal structures.*

## 16.23.2 Function Documentation

### 16.23.2.1 `zukersubopt()`

```
SOLUTION * zukersubopt (
    const char * string )
#include <ViennaRNA/subopt.h>
```

Compute Zuker type suboptimal structures.

Compute Suboptimal structures according to M. Zuker, i.e. for every possible base pair the minimum energy structure containing the resp. base pair. Returns a list of these structures and their energies.

**Deprecated** use `vrna_zukersubopt()` instead

#### Parameters

|                     |              |
|---------------------|--------------|
| <code>string</code> | RNA sequence |
|---------------------|--------------|

#### Returns

List of zuker suboptimal structures

### 16.23.2.2 `zukersubopt_par()`

```
SOLUTION * zukersubopt_par (
    const char * string,
    vrna_param_t * parameters )
#include <ViennaRNA/subopt.h>
```

Compute Zuker type suboptimal structures.

**Deprecated** use `vrna_zukersubopt()` instead

### 16.23.2.3 `vrna_subopt_zuker()`

```
vrna_subopt_solution_t * vrna_subopt_zuker (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/subopt_zuker.h>
```

Compute Zuker type suboptimal structures.

Compute Suboptimal structures according to M. Zuker [27], i.e. for every possible base pair the minimum energy structure containing the resp. base pair. Returns a list of these structures and their energies.

#### Note

This function internally uses the cofold implementation to compute the suboptimal structures. For that purpose, the function doubles the sequence and enlarges the DP matrices, which in fact will grow by a factor of 4 during the computation! At the end of the structure prediction, everything will be re-set to its original requirements, i.e. normal sequence, normal (empty) DP matrices.

**Bug** Due to resizing, any pre-existing constraints will be lost!

#### See also

[vrna\\_subopt\(\)](#), [zukersubopt\(\)](#), [zukersubopt\\_par\(\)](#)

## Parameters

|    |               |
|----|---------------|
| vc | fold compound |
|----|---------------|

## Returns

List of zucker suboptimal structures

**SWIG Wrapper Notes** This function is attached as method **subopt\_zucker()** to objects of type *fold\_compound*

## 16.24 Suboptimal Structures within an Energy Band around the MFE

### 16.24.1 Detailed Description

Collaboration diagram for Suboptimal Structures within an Energy Band around the MFE:

### Typedefs

- typedef void() [vrna\\_subopt\\_callback](#)(const char \*structure, float energy, void \*data)  
*Callback for [vrna\\_subopt\\_cb\(\)](#)*

### Functions

- [vrna\\_subopt\\_solution\\_t](#) \* [vrna\\_subopt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int delta, int sorted, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- void [vrna\\_subopt\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int delta, [vrna\\_subopt\\_callback](#) \*cb, void \*data)  
*Generate suboptimal structures within an energy band around the MFE.*
- [SOLUTION](#) \* [subopt](#) (char \*seq, char \*structure, int delta, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- [SOLUTION](#) \* [subopt\\_par](#) (char \*seq, char \*structure, [vrna\\_param\\_t](#) \*parameters, int delta, int is\_ $\leftrightarrow$  constrained, int is\_circular, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- [SOLUTION](#) \* [subopt\\_circ](#) (char \*seq, char \*sequence, int delta, FILE \*fp)  
*Returns list of circular subopt structures or writes to fp.*

### Variables

- double **print\_energy**  
*printing threshold for use with logML*
- int **subopt\_sorted**  
*Sort output by energy.*

### 16.24.2 Typedef Documentation

#### 16.24.2.1 vrna\_subopt\_callback

```
typedef void() vrna_subopt_callback(const char *structure, float energy, void *data)
#include <ViennaRNA/subopt.h>
Callback for vrna\_subopt\_cb\(\)
```

**Notes on Callback Functions** This function will be called for each suboptimal secondary structure that is successfully backtraced.

#### See also

[vrna\\_subopt\\_cb\(\)](#)

## Parameters

|                  |                                                                                      |
|------------------|--------------------------------------------------------------------------------------|
| <i>structure</i> | The suboptimal secondary structure in dot-bracket notation                           |
| <i>energy</i>    | The free energy of the secondary structure in kcal/mol                               |
| <i>data</i>      | Some arbitrary, auxiliary data address as passed to <a href="#">vrna_subopt_cb()</a> |

## 16.24.3 Function Documentation

16.24.3.1 [vrna\\_subopt\(\)](#)

```
vrna_subopt_solution_t * vrna_subopt (
    vrna_fold_compound_t * vc,
    int delta,
    int sorted,
    FILE * fp )
```

```
#include <ViennaRNA/subopt.h>
```

Returns list of subopt structures or writes to fp.

This function produces **all** suboptimal secondary structures within 'delta' \* 0.01 kcal/mol of the optimum, see [25]. The results are either directly written to a 'fp' (if 'fp' is not NULL), or (fp=NULL) returned in a [vrna\\_subopt\\_solution\\_t](#) \* list terminated by an entry where the 'structure' member is NULL.

## Note

This function requires all multibranch loop DP matrices for unique multibranch loop backtracing. Therefore, the supplied [vrna\\_fold\\_compound\\_t](#) vc (argument 1) must be initialized with [vrna\\_md\\_t.uniq\\_ML](#) = 1, for instance like this:

```
vrna_md_t md;
vrna_md_set_default(&md);
md.uniq_ML = 1;
vrna_fold_compound_t *vc=vrna_fold_compound("GGGGGAAAAACCCCC", &md, VRNA_OPTION_DEFAULT);
```

## See also

[vrna\\_subopt\\_cb\(\)](#), [vrna\\_subopt\\_zuker\(\)](#)

## Parameters

|               |                                           |
|---------------|-------------------------------------------|
| <i>fc</i>     |                                           |
| <i>delta</i>  |                                           |
| <i>sorted</i> | Sort results by energy in ascending order |
| <i>fp</i>     |                                           |

## Returns

**SWIG Wrapper Notes** This function is attached as method [subopt\(\)](#) to objects of type *fold\_compound*

16.24.3.2 [vrna\\_subopt\\_cb\(\)](#)

```
void vrna_subopt_cb (
    vrna_fold_compound_t * vc,
    int delta,
    vrna_subopt_callback * cb,
    void * data )
```

```
#include <ViennaRNA/subopt.h>
```

Generate suboptimal structures within an energy band around the MFE.

This is the most generic implementation of the suboptimal structure generator according to Wuchty et al. 1999 [25]. Identical to `vrna_subopt()`, it computes all secondary structures within an energy band `delta` around the MFE. However, this function does not print the resulting structures and their corresponding free energies to a file pointer, or returns them as a list. Instead, it calls a user-provided callback function which it passes the structure in dot-bracket format, the corresponding free energy in kcal/mol, and a user-provided data structure each time a structure was backtracked successfully. This function indicates the final output, i.e. the end of the backtracking procedure by passing `NULL` instead of an actual dot-bracket string to the callback.

#### Note

This function requires all multibranch loop DP matrices for unique multibranch loop backtracing. Therefore, the supplied `vrna_fold_compound_t` `vc` (argument 1) must be initialized with `vrna_md_t.uniq_ML = 1`, for instance like this:

```
vrna_md_t md;
vrna_md_set_default(&md);
md.uniq_ML = 1;
vrna_fold_compound_t *vc=vrna_fold_compound("GGGGGGAAAAACCCCC", &md, VRNA_OPTION_DEFAULT);
```

#### See also

[vrna\\_subopt\\_callback](#), [vrna\\_subopt\(\)](#), [vrna\\_subopt\\_zuker\(\)](#)

#### Parameters

|              |                                                                                                       |
|--------------|-------------------------------------------------------------------------------------------------------|
| <i>fc</i>    | fold compound with the sequence data                                                                  |
| <i>delta</i> | Energy band around the MFE in 10cal/mol, i.e. deka-calories                                           |
| <i>cb</i>    | Pointer to a callback function that handles the backtracked structure and its free energy in kcal/mol |
| <i>data</i>  | Pointer to some data structure that is passed along to the callback                                   |

**SWIG Wrapper Notes** This function is attached as method `subopt_cb()` to objects of type `fold_compound`

### 16.24.3.3 subopt()

```
SOLUTION * subopt (
    char * seq,
    char * structure,
    int delta,
    FILE * fp )
```

```
#include <ViennaRNA/subopt.h>
```

Returns list of subopt structures or writes to `fp`.

This function produces **all** suboptimal secondary structures within '`delta`' \* 0.01 kcal/mol of the optimum. The results are either directly written to a '`fp`' (if '`fp`' is not `NULL`), or (`fp`==`NULL`) returned in a `SOLUTION *` list terminated by an entry where the 'structure' pointer is `NULL`.

#### Parameters

|                  |  |
|------------------|--|
| <i>seq</i>       |  |
| <i>structure</i> |  |
| <i>delta</i>     |  |
| <i>fp</i>        |  |

## Returns

## 16.24.3.4 subopt\_circ()

```
SOLUTION * subopt_circ (
    char * seq,
    char * sequence,
    int delta,
    FILE * fp )
#include <ViennaRNA/subopt.h>
```

Returns list of circular subopt structures or writes to fp.

This function is similar to [subopt\(\)](#) but calculates secondary structures assuming the RNA sequence to be circular instead of linear

## Parameters

|                 |  |
|-----------------|--|
| <i>seq</i>      |  |
| <i>sequence</i> |  |
| <i>delta</i>    |  |
| <i>fp</i>       |  |

## Returns

## 16.25 Random Structure Samples from the Ensemble

Functions to draw random structure samples from the ensemble according to their equilibrium probability.

## 16.25.1 Detailed Description

Functions to draw random structure samples from the ensemble according to their equilibrium probability.  
Collaboration diagram for Random Structure Samples from the Ensemble:

## Modules

- [Stochastic Backtracking of Structures from Distance Based Partitioning](#)  
*Contains functions related to stochastic backtracking from a specified distance class.*
- [Deprecated Interface for Stochastic Backtracking](#)

## Macros

- `#define VRNA_PBACKTRACK_DEFAULT 0`  
*Boltzmann sampling flag indicating default backtracing mode.*
- `#define VRNA_PBACKTRACK_NON_REDUNDANT 1`  
*Boltzmann sampling flag indicating non-redundant backtracing mode.*

## Typedefs

- `typedef void() vrna_boltzmann_sampling_callback(const char *structure, void *data)`  
*Callback for Boltzmann sampling.*
- `typedef struct vrna_pbacktrack_memory_s * vrna_pbacktrack_mem_t`  
*Boltzmann sampling memory data structure.*

## Functions

- `char * vrna_pbacktrack5 (vrna_fold_compound_t *fc, unsigned int length)`  
*Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.*
- `char ** vrna_pbacktrack5_num (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int length, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack5_cb (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int length, vrna_boltzmann_sampling_callback *cb, void *data, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `char ** vrna_pbacktrack5_resume (vrna_fold_compound_t *vc, unsigned int num_samples, unsigned int length, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack5_resume_cb (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int length, vrna_boltzmann_sampling_callback *cb, void *data, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `char * vrna_pbacktrack (vrna_fold_compound_t *fc)`  
*Sample a secondary structure from the Boltzmann ensemble according its probability.*
- `char ** vrna_pbacktrack_num (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int options)`  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack_cb (vrna_fold_compound_t *fc, unsigned int num_samples, vrna_boltzmann_sampling_callback *cb, void *data, unsigned int options)`  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- `char ** vrna_pbacktrack_resume (vrna_fold_compound_t *fc, unsigned int num_samples, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack_resume_cb (vrna_fold_compound_t *fc, unsigned int num_samples, vrna_boltzmann_sampling_callback *cb, void *data, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- `char * vrna_pbacktrack_sub (vrna_fold_compound_t *fc, unsigned int start, unsigned int end)`  
*Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.*
- `char ** vrna_pbacktrack_sub_num (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int start, unsigned int end, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack_sub_cb (vrna_fold_compound_t *fc, unsigned int num_samples, unsigned int start, unsigned int end, vrna_boltzmann_sampling_callback *cb, void *data, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `char ** vrna_pbacktrack_sub_resume (vrna_fold_compound_t *vc, unsigned int num_samples, unsigned int start, unsigned int end, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `unsigned int vrna_pbacktrack_sub_resume_cb (vrna_fold_compound_t *fc, unsigned int num_↵ samples, unsigned int start, unsigned int end, vrna_boltzmann_sampling_callback *bs_cb, void *data, vrna_pbacktrack_mem_t *nr_mem, unsigned int options)`  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- `void vrna_pbacktrack_mem_free (vrna_pbacktrack_mem_t s)`  
*Release memory occupied by a Boltzmann sampling memory data structure.*



## 16.25.2 Macro Definition Documentation

### 16.25.2.1 VRNA\_PBACKTRACK\_DEFAULT

```
#define VRNA_PBACKTRACK_DEFAULT 0
#include <ViennaRNA/boltzmann_sampling.h>
Boltzmann sampling flag indicating default backtracing mode.
```

See also

[vrna\\_pbacktrack5\\_num\(\)](#), [vrna\\_pbacktrack5\\_cb\(\)](#), [vrna\\_pbacktrack5\\_resume\(\)](#), [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_num\(\)](#), [vrna\\_pbacktrack\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#)

### 16.25.2.2 VRNA\_PBACKTRACK\_NON\_REDUNDANT

```
#define VRNA_PBACKTRACK_NON_REDUNDANT 1
#include <ViennaRNA/boltzmann_sampling.h>
Boltzmann sampling flag indicating non-redundant backtracing mode.
This flag will turn the Boltzmann sampling into non-redundant backtracing mode along the lines of Michalik et al. 2017 [19]
```

See also

[vrna\\_pbacktrack5\\_num\(\)](#), [vrna\\_pbacktrack5\\_cb\(\)](#), [vrna\\_pbacktrack5\\_resume\(\)](#), [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_num\(\)](#), [vrna\\_pbacktrack\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#)

## 16.25.3 Typedef Documentation

### 16.25.3.1 vrna\_boltzmann\_sampling\_callback

```
typedef void() vrna_boltzmann_sampling_callback(const char *structure, void *data)
#include <ViennaRNA/boltzmann_sampling.h>
Callback for Boltzmann sampling.
```

**Notes on Callback Functions** This function will be called for each secondary structure that has been successfully backtraced from the partition function DP matrices.

See also

[vrna\\_pbacktrack5\\_cb\(\)](#), [vrna\\_pbacktrack\\_cb\(\)](#), [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#)

Parameters

|                  |                                                                            |
|------------------|----------------------------------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation                            |
| <i>data</i>      | Some arbitrary, auxiliary data address as provided to the calling function |

### 16.25.3.2 vrna\_pbacktrack\_mem\_t

```
typedef struct vrna_pbacktrack_memory_s* vrna_pbacktrack_mem_t
#include <ViennaRNA/boltzmann_sampling.h>
Boltzmann sampling memory data structure.
```

This structure is required for properly resuming a previous sampling round in specialized Boltzmann sampling, such

as non-redundant backtracking.

Initialize with `NULL` and pass its address to the corresponding functions [vrna\\_pbacktrack5\\_resume\(\)](#), etc.

#### Note

Do not forget to release memory occupied by this data structure before losing its context! Use [vrna\\_pbacktrack\\_mem\\_free\(\)](#).

#### See also

[vrna\\_pbacktrack5\\_resume\(\)](#), [vrna\\_pbacktrack\\_resume\(\)](#), [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_mem\\_free\(\)](#)

## 16.25.4 Function Documentation

### 16.25.4.1 vrna\_pbacktrack5()

```
char * vrna_pbacktrack5 (
    vrna_fold_compound_t * fc,
    unsigned int length )
#include <ViennaRNA/boltzmann_sampling.h>
```

Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a secondary structure.

The parameter `length` specifies the length of the substructure starting from the 5' end.

The structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

#### Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with [vrna\\_fold\\_compound\(\)](#) or similar. This can be done easily by passing [vrna\\_fold\\_compound\(\)](#) a model details parameter with `vrna_md_t.uniq_ML = 1`.

[vrna\\_pf\(\)](#) has to be called first to fill the partition function matrices

#### Note

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

#### See also

[vrna\\_pbacktrack5\\_num\(\)](#), [vrna\\_pbacktrack5\\_cb\(\)](#), [vrna\\_pbacktrack\(\)](#)

#### Parameters

|                     |                                                                  |
|---------------------|------------------------------------------------------------------|
| <code>fc</code>     | The fold compound data structure                                 |
| <code>length</code> | The length of the subsequence to consider (starting with 5' end) |

#### Returns

A sampled secondary structure in dot-bracket notation (or `NULL` on error)

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack5\(\)](#) to objects of type `fold_compound`. See also [Python Examples - Boltzmann Sampling](#)

16.25.4.2 `vrna_pbacktrack5_num()`

```
char ** vrna_pbacktrack5_num (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int length,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according to their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack5()`, `vrna_pbacktrack5_cb()`, `vrna_pbacktrack_num()`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`

**Parameters**

|                          |                                                                  |
|--------------------------|------------------------------------------------------------------|
| <code>fc</code>          | The fold compound data structure                                 |
| <code>num_samples</code> | The size of the sample set, i.e. number of structures            |
| <code>length</code>      | The length of the subsequence to consider (starting with 5' end) |
| <code>options</code>     | A bitwise OR-flag indicating the backtracing mode.               |

**Returns**

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack5\(\)](#) to objects of type *fold\_compound* where the last argument *options* is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.3 vrna\_pbacktrack5\_cb()**

```
unsigned int vrna_pbacktrack5_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int length,
    vrna_boltzmann_sampling_callback * cb,
    void * data,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according to their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to [vrna\\_pbacktrack5\(\)](#) and [vrna\\_pbacktrack5\\_num\(\)](#) this function yields the structure samples through a callback mechanism.

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with [vrna\\_fold\\_compound\(\)](#) or similar. This can be done easily by passing [vrna\\_fold\\_compound\(\)](#) a model details parameter with `vrna_md_t.uniq_ML = 1`.

[vrna\\_pf\(\)](#) has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

[vrna\\_pbacktrack5\(\)](#), [vrna\\_pbacktrack5\\_num\(\)](#), [vrna\\_pbacktrack\\_cb\(\)](#), `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`

## Parameters

|                    |                                                                  |
|--------------------|------------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                                 |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures            |
| <i>length</i>      | The length of the subsequence to consider (starting with 5' end) |
| <i>cb</i>          | The callback that receives the sampled structure                 |
| <i>data</i>        | A data structure passed through to the callback <i>cb</i>        |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.               |

## Returns

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack5\(\)](#) to objects of type *fold\_compound* where the last argument *options* is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

16.25.4.4 *vrna\_pbacktrack5\_resume()*

```
char ** vrna_pbacktrack5_resume (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int length,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according to their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular ([VRNA\\_PBACKTRACK\\_DEFAULT](#)) backtracing mode, and non-redundant sampling ([VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#)) along the lines of Michalik et al. 2017 [19].

In contrast to [vrna\\_pbacktrack5\\_cb\(\)](#) this function allows for resuming a previous sampling round in specialized Boltzmann sampling, such as non-redundant backtracking. For that purpose, the user passes the address of a Boltzmann sampling data structure ([vrna\\_pbacktrack\\_mem\\_t](#)) which will be re-used in each round of sampling, i.e. each successive call to [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#) or [vrna\\_pbacktrack5\\_resume\(\)](#).

A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack5_resume(fc,
    100,
    fc->length,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack5_resume(fc,
    500,
    fc->length,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack5_resume_cb()`, `vrna_pbacktrack5_cb()`, `vrna_pbacktrack_resume()`, `vrna_pbacktrack_mem_t`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`, `vrna_pbacktrack_mem_free`

**Parameters**

|                          |                                                                  |
|--------------------------|------------------------------------------------------------------|
| <code>fc</code>          | The fold compound data structure                                 |
| <code>num_samples</code> | The size of the sample set, i.e. number of structures            |
| <code>length</code>      | The length of the subsequence to consider (starting with 5' end) |
| <code>nr_mem</code>      | The address of the Boltzmann sampling memory data structure      |
| <code>options</code>     | A bitwise OR-flag indicating the backtracing mode.               |

**Returns**

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack5()` to objects of type `fold_compound`. In addition to the list of structures, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.5 vrna\_pbacktrack5\_resume\_cb()**

```
unsigned int vrna_pbacktrack5_resume_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int length,
    vrna_boltzmann_sampling_callback * cb,
    void * data,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ . Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracking mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack5_resume()` this function yields the structure samples through a callback mechanism. A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack5_resume_cb(fc,
    100,
    fc->length,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack5_resume_cb(fc,
    500,
    fc->length,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

#### Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

#### Note

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

#### Warning

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

#### See also

`vrna_pbacktrack5_resume()`, `vrna_pbacktrack5_cb()`, `vrna_pbacktrack_resume_cb()`, `vrna_pbacktrack_mem_t`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`, `vrna_pbacktrack_mem_free`

#### Parameters

|                          |                                                                  |
|--------------------------|------------------------------------------------------------------|
| <code>fc</code>          | The fold compound data structure                                 |
| <code>num_samples</code> | The size of the sample set, i.e. number of structures            |
| <code>length</code>      | The length of the subsequence to consider (starting with 5' end) |
| <code>cb</code>          | The callback that receives the sampled structure                 |
| <code>data</code>        | A data structure passed through to the callback <code>cb</code>  |
| <code>nr_mem</code>      | The address of the Boltzmann sampling memory data structure      |
| <code>options</code>     | A bitwise OR-flag indicating the backtracking mode.              |

**Returns**

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack5\(\)](#) to objects of type *fold\_compound*. In addition to the number of structures backtraced, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.6 vrna\_pbacktrack()**

```
char * vrna_pbacktrack (
    vrna_fold_compound_t * fc )
#include <ViennaRNA/boltzmann_sampling.h>
```

Sample a secondary structure from the Boltzmann ensemble according its probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a secondary structure.

The structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with [vrna\\_fold\\_compound\(\)](#) or similar. This can be done easily by passing [vrna\\_fold\\_compound\(\)](#) a model details parameter with `vrna_md_t.uniq_ML = 1`.

[vrna\\_pf\(\)](#) has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**See also**

[vrna\\_pbacktrack5\(\)](#), [vrna\\_pbacktrack\\_num](#), [vrna\\_pbacktrack\\_cb\(\)](#)

**Parameters**

|                 |                                  |
|-----------------|----------------------------------|
| <code>fc</code> | The fold compound data structure |
|-----------------|----------------------------------|

**Returns**

A sampled secondary structure in dot-bracket notation (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack\(\)](#) to objects of type *fold\_compound*. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.7 vrna\_pbacktrack\_num()**

```
char ** vrna_pbacktrack_num (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.



Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular ([VRNA\\_PBACKTRACK\\_DEFAULT](#)) backtracing mode, and non-redundant sampling ([VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#)) along the lines of Michalik et al. 2017 [19].

#### Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with [vrna\\_fold\\_compound\(\)](#) or similar. This can be done easily by passing [vrna\\_fold\\_compound\(\)](#) a model details parameter with [vrna\\_md\\_t.uniq\\_ML](#) = 1.

[vrna\\_pf\(\)](#) has to be called first to fill the partition function matrices

#### Note

This function is polymorphic. It accepts [vrna\\_fold\\_compound\\_t](#) of type [VRNA\\_FC\\_TYPE\\_SINGLE](#), and [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#).

#### Warning

In non-redundant sampling mode ([VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#)), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

#### See also

[vrna\\_pbacktrack\(\)](#), [vrna\\_pbacktrack\\_cb\(\)](#), [vrna\\_pbacktrack5\\_num\(\)](#), [VRNA\\_PBACKTRACK\\_DEFAULT](#), [VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#)

#### Parameters

|                    |                                                       |
|--------------------|-------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                      |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.    |

#### Returns

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack\(\)](#) to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

#### 16.25.4.8 vrna\_pbacktrack\_cb()

```
unsigned int vrna_pbacktrack_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    vrna_boltzmann_sampling_callback * cb,
```

```

    void * data,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>

```

Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack()` and `vrna_pbacktrack_num()` this function yields the structure samples through a callback mechanism.

#### Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

#### Note

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

#### Warning

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

#### See also

`vrna_pbacktrack()`, `vrna_pbacktrack_num()`, `vrna_pbacktrack5_cb()`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`

#### Parameters

|                          |                                                                 |
|--------------------------|-----------------------------------------------------------------|
| <code>fc</code>          | The fold compound data structure                                |
| <code>num_samples</code> | The size of the sample set, i.e. number of structures           |
| <code>cb</code>          | The callback that receives the sampled structure                |
| <code>data</code>        | A data structure passed through to the callback <code>cb</code> |
| <code>options</code>     | A bitwise OR-flag indicating the backtracing mode.              |

#### Returns

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack()` to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

16.25.4.9 `vrna_pbacktrack_resume()`

```
char ** vrna_pbacktrack_resume (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples from the Boltzmann ensemble according to their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack_cb()` this function allows for resuming a previous sampling round in specialized Boltzmann sampling, such as non-redundant backtracking. For that purpose, the user passes the address of a Boltzmann sampling data structure (`vrna_pbacktrack_mem_t`) which will be re-used in each round of sampling, i.e. each successive call to `vrna_pbacktrack_resume_cb()` or `vrna_pbacktrack_resume()`.

A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack_resume(fc,
    100,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack_resume(fc,
    500,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack_resume_cb()`, `vrna_pbacktrack_cb()`, `vrna_pbacktrack5_resume()`, `vrna_pbacktrack_mem_t`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`, `vrna_pbacktrack_mem_free`

## Parameters

|                    |                                                             |
|--------------------|-------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                            |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures       |
| <i>nr_mem</i>      | The address of the Boltzmann sampling memory data structure |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.          |

## Returns

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method **pbacktrack()** to objects of type *fold\_compound*. In addition to the list of structures, this function also returns the *nr\_mem* data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

16.25.4.10 `vrna_pbacktrack_resume_cb()`

```
unsigned int vrna_pbacktrack_resume_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    vrna_boltzmann_sampling_callback * cb,
    void * data,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of *num\_samples* secondary structures.

Any structure *s* with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant *k* and thermodynamic temperature *T*.

Using the *options* flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack5_resume()` this function yields the structure samples through a callback mechanism.

A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack5_resume_cb(fc,
    100,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack5_resume_cb(fc,
    500,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

## Precondition

Unique multiloop decomposition has to be active upon creation of *fc* with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack_resume()`, `vrna_pbacktrack_cb()`, `vrna_pbacktrack5_resume_cb()`, `vrna_pbacktrack_mem_t`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`, `vrna_pbacktrack_mem_free`

**Parameters**

|                    |                                                             |
|--------------------|-------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                            |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures       |
| <i>cb</i>          | The callback that receives the sampled structure            |
| <i>data</i>        | A data structure passed through to the callback <i>cb</i>   |
| <i>nr_mem</i>      | The address of the Boltzmann sampling memory data structure |
| <i>options</i>     | A bitwise OR-flag indicating the backtracking mode.         |

**Returns**

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack()` to objects of type `fold_compound`. In addition to the number of structures backtraced, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.11 vrna\_pbacktrack\_sub()**

```
char * vrna_pbacktrack_sub (
    vrna_fold_compound_t * fc,
    unsigned int start,
    unsigned int end )
#include <ViennaRNA/boltzmann_sampling.h>
```

Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a secondary structure. The parameters *start* and *end* specify the interval  $[start : end]$  of the subsequence with  $1 \leq start < end \leq n$  for sequence length *n*, the structure  $s_{start,end}$  should be drawn from.

The resulting substructure  $s_{start,end}$  with free energy  $E(s_{start,end})$  is picked from the Boltzmann distributed sub ensemble of all structures within the interval  $[start : end]$  according to its probability

$$p(s_{start,end}) = \frac{\exp(-E(s_{start,end})/kT)}{Z_{start,end}}$$

with partition function  $Z_{start,end} = \sum_{s_{start,end}} \exp(-E(s_{start,end})/kT)$ , Boltzmann constant *k* and thermodynamic temperature *T*.

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**See also**

`vrna_pbacktrack_sub_num()`, `vrna_pbacktrack_sub_cb()`, `vrna_pbacktrack()`

**Parameters**

|                    |                                                                         |
|--------------------|-------------------------------------------------------------------------|
| <code>fc</code>    | The fold compound data structure                                        |
| <code>start</code> | The start of the subsequence to consider, i.e. 5'-end position(1-based) |
| <code>end</code>   | The end of the subsequence to consider, i.e. 3'-end position (1-based)  |

**Returns**

A sampled secondary structure in dot-bracket notation (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack_sub()` to objects of type `fold_compound`. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.12 vrna\_pbacktrack\_sub\_num()**

```
char ** vrna_pbacktrack_sub_num (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int start,
    unsigned int end,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.

Perform a probabilistic (stochastic) backtracking in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracking mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack_sub()`, `vrna_pbacktrack_sub_cb()`, `vrna_pbacktrack_num()`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`

**Parameters**

|                    |                                                                          |
|--------------------|--------------------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                                         |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures                    |
| <i>start</i>       | The start of the subsequence to consider, i.e. 5'-end position (1-based) |
| <i>end</i>         | The end of the subsequence to consider, i.e. 3'-end position (1-based)   |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.                       |

**Returns**

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack_sub()` to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.13 vrna\_pbacktrack\_sub\_cb()**

```
unsigned int vrna_pbacktrack_sub_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int start,
    unsigned int end,
    vrna_boltzmann_sampling_callback * cb,
    void * data,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according to its probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end. Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack5()` and `vrna_pbacktrack5_num()` this function yields the structure samples through a callback mechanism.

**Precondition**

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

**Note**

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

`vrna_pbacktrack5()`, `vrna_pbacktrack5_num()`, `vrna_pbacktrack_cb()`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`

**Parameters**

|                    |                                                                          |
|--------------------|--------------------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                                         |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures                    |
| <i>start</i>       | The start of the subsequence to consider, i.e. 5'-end position (1-based) |
| <i>end</i>         | The end of the subsequence to consider, i.e. 3'-end position (1-based)   |
| <i>cb</i>          | The callback that receives the sampled structure                         |
| <i>data</i>        | A data structure passed through to the callback <i>cb</i>                |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.                       |

**Returns**

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack()` to objects of type `fold_compound` where the last argument `options` is optional with default value `options = VRNA_PBACKTRACK_DEFAULT`. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.14 vrna\_pbacktrack\_sub\_resume()**

```
char ** vrna_pbacktrack_sub_resume (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int start,
    unsigned int end,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according to their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.



Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack5_cb()` this function allows for resuming a previous sampling round in specialized Boltzmann sampling, such as non-redundant backtracking. For that purpose, the user passes the address of a Boltzmann sampling data structure (`vrna_pbacktrack_mem_t`) which will be re-used in each round of sampling, i.e. each successive call to `vrna_pbacktrack5_resume_cb()` or `vrna_pbacktrack5_resume()`.

A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack5_resume(fc,
    100,
    fc->length,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack5_resume(fc,
    500,
    fc->length,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

#### Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniq_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

#### Note

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

#### Warning

In non-redundant sampling mode (`VRNA_PBACKTRACK_NON_REDUNDANT`), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

#### See also

`vrna_pbacktrack5_resume_cb()`, `vrna_pbacktrack5_cb()`, `vrna_pbacktrack_resume()`, `vrna_pbacktrack_mem_t`, `VRNA_PBACKTRACK_DEFAULT`, `VRNA_PBACKTRACK_NON_REDUNDANT`, `vrna_pbacktrack_mem_free`

#### Parameters

|                          |                                                                          |
|--------------------------|--------------------------------------------------------------------------|
| <code>fc</code>          | The fold compound data structure                                         |
| <code>num_samples</code> | The size of the sample set, i.e. number of structures                    |
| <code>start</code>       | The start of the subsequence to consider, i.e. 5'-end position (1-based) |
| <code>end</code>         | The end of the subsequence to consider, i.e. 3'-end position (1-based)   |
| <code>nr_mem</code>      | The address of the Boltzmann sampling memory data structure              |
| <code>options</code>     | A bitwise OR-flag indicating the backtracing mode.                       |

## Returns

A set of secondary structure samples in dot-bracket notation terminated by NULL (or NULL on error)

**SWIG Wrapper Notes** This function is attached as overloaded method `pbacktrack()` to objects of type `fold_compound`. In addition to the list of structures, this function also returns the `nr_mem` data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

16.25.4.15 `vrna_pbacktrack_sub_resume_cb()`

```
unsigned int vrna_pbacktrack_sub_resume_cb (
    vrna_fold_compound_t * fc,
    unsigned int num_samples,
    unsigned int start,
    unsigned int end,
    vrna_boltzmann_sampling_callback * cb,
    void * data,
    vrna_pbacktrack_mem_t * nr_mem,
    unsigned int options )
```

```
#include <ViennaRNA/boltzmann_sampling.h>
```

Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.

Perform a probabilistic (stochastic) backtracing in the partition function DP arrays to obtain a set of `num_samples` secondary structures. The parameter `length` specifies the length of the substructure starting from the 5' end.

Any structure  $s$  with free energy  $E(s)$  is picked from the Boltzmann distributed ensemble according to its probability

$$p(s) = \frac{\exp(-E(s)/kT)}{Z}$$

with partition function  $Z = \sum_s \exp(-E(s)/kT)$ , Boltzmann constant  $k$  and thermodynamic temperature  $T$ .

Using the `options` flag one can switch between regular (`VRNA_PBACKTRACK_DEFAULT`) backtracing mode, and non-redundant sampling (`VRNA_PBACKTRACK_NON_REDUNDANT`) along the lines of Michalik et al. 2017 [19].

In contrast to `vrna_pbacktrack5_resume()` this function yields the structure samples through a callback mechanism.

A successive sample call to this function may look like:

```
vrna_pbacktrack_mem_t nonredundant_memory = NULL;
// sample the first 100 structures
vrna_pbacktrack5_resume_cb(fc,
    100,
    fc->length,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// sample another 500 structures
vrna_pbacktrack5_resume_cb(fc,
    500,
    fc->length,
    &callback_function,
    (void *)&callback_data,
    &nonredundant_memory,
    options);
// release memory occupied by the non-redundant memory data structure
vrna_pbacktrack_mem_free(nonredundant_memory);
```

## Precondition

Unique multiloop decomposition has to be active upon creation of `fc` with `vrna_fold_compound()` or similar. This can be done easily by passing `vrna_fold_compound()` a model details parameter with `vrna_md_t.uniql_ML = 1`.

`vrna_pf()` has to be called first to fill the partition function matrices

## Note

This function is polymorphic. It accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE`, and `VRNA_FC_TYPE_COMPARATIVE`.

**Warning**

In non-redundant sampling mode ([VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#)), this function may not yield the full number of requested samples. This may happen if a) the number of requested structures is larger than the total number of structures in the ensemble, b) numeric instabilities prevent the backtracking function to enumerate structures with high free energies, or c) any other error occurs.

**See also**

[vrna\\_pbacktrack5\\_resume\(\)](#), [vrna\\_pbacktrack5\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_mem\\_t](#), [VRNA\\_PBACKTRACK\\_DEFAULT](#), [VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#), [vrna\\_pbacktrack\\_mem\\_free](#)

**Parameters**

|                    |                                                                          |
|--------------------|--------------------------------------------------------------------------|
| <i>fc</i>          | The fold compound data structure                                         |
| <i>num_samples</i> | The size of the sample set, i.e. number of structures                    |
| <i>start</i>       | The start of the subsequence to consider, i.e. 5'-end position (1-based) |
| <i>end</i>         | The end of the subsequence to consider, i.e. 3'-end position (1-based)   |
| <i>cb</i>          | The callback that receives the sampled structure                         |
| <i>data</i>        | A data structure passed through to the callback <i>cb</i>                |
| <i>nr_mem</i>      | The address of the Boltzmann sampling memory data structure              |
| <i>options</i>     | A bitwise OR-flag indicating the backtracing mode.                       |

**Returns**

The number of structures actually backtraced

**SWIG Wrapper Notes** This function is attached as overloaded method [pbacktrack\(\)](#) to objects of type *fold* ↔ *compound*. In addition to the number of structures backtraced, this function also returns the *nr\_mem* data structure as first element. See also [Python Examples - Boltzmann Sampling](#)

**16.25.4.16 vrna\_pbacktrack\_mem\_free()**

```
void vrna_pbacktrack_mem_free (
    vrna_pbacktrack_mem_t s )
#include <ViennaRNA/boltzmann_sampling.h>
Release memory occupied by a Boltzmann sampling memory data structure.
```

**See also**

[vrna\\_pbacktrack\\_mem\\_t](#), [vrna\\_pbacktrack5\\_resume\(\)](#), [vrna\\_pbacktrack5\\_resume\\_cb\(\)](#), [vrna\\_pbacktrack\\_resume\(\)](#), [vrna\\_pbacktrack\\_resume\\_cb\(\)](#)

**Parameters**

|          |                                          |
|----------|------------------------------------------|
| <i>s</i> | The non-redundancy memory data structure |
|----------|------------------------------------------|

**16.26 Compute the Structure with Maximum Expected Accuracy (MEA)****16.26.1 Detailed Description**

Collaboration diagram for Compute the Structure with Maximum Expected Accuracy (MEA):

## Functions

- char \* `vrna_MEA` (`vrna_fold_compound_t` \*fc, double gamma, float \*mea)  
Compute a MEA (maximum expected accuracy) structure.
- char \* `vrna_MEA_from_plist` (`vrna_ep_t` \*plist, const char \*sequence, double gamma, `vrna_md_t` \*md, float \*mea)  
Compute a MEA (maximum expected accuracy) structure from a list of probabilities.
- float `MEA` (plist \*p, char \*structure, double gamma)  
Computes a MEA (maximum expected accuracy) structure.

## 16.26.2 Function Documentation

### 16.26.2.1 vrna\_MEA()

```
char * vrna_MEA (
    vrna_fold_compound_t * fc,
    double gamma,
    float * mea )
#include <ViennaRNA/MEA.h>
Compute a MEA (maximum expected accuracy) structure.
The algorithm maximizes the expected accuracy
```

$$A(S) = \sum_{(i,j) \in S} 2\gamma p_{ij} + \sum_{i \notin S} p_i^u$$

Higher values of  $\gamma$  result in more base pairs of lower probability and thus higher sensitivity. Low values of  $\gamma$  result in structures containing only highly likely pairs (high specificity). The code of the MEA function also demonstrates the use of sparse dynamic programming scheme to reduce the time and memory complexity of folding.

#### Precondition

`vrna_pf()` must be executed on input parameter `fc`

#### Parameters

|                    |                                                                               |
|--------------------|-------------------------------------------------------------------------------|
| <code>fc</code>    | The fold compound data structure with pre-filled base pair probability matrix |
| <code>gamma</code> | The weighting factor for base pairs vs. unpaired nucleotides                  |
| <code>mea</code>   | A pointer to a variable where the MEA value will be written to                |

#### Returns

An MEA structure (or NULL on any error)

**SWIG Wrapper Notes** This function is attached as overloaded method **MEA**(gamma = 1.) to objects of type `fold_compound`. Note, that it returns the MEA structure and MEA value as a tuple (MEA\_↵ structure, MEA)

### 16.26.2.2 vrna\_MEA\_from\_plist()

```
char * vrna_MEA_from_plist (
    vrna_ep_t * plist,
    const char * sequence,
    double gamma,
    vrna_md_t * md,
    float * mea )
```

```
#include <ViennaRNA/MEA.h>
```

Compute a MEA (maximum expected accuracy) structure from a list of probabilities.

The algorithm maximizes the expected accuracy

$$A(S) = \sum_{(i,j) \in S} 2\gamma p_{ij} + \sum_{i \notin S} p_i^u$$

Higher values of  $\gamma$  result in more base pairs of lower probability and thus higher sensitivity. Low values of  $\gamma$  result in structures containing only highly likely pairs (high specificity). The code of the MEA function also demonstrates the use of sparse dynamic programming scheme to reduce the time and memory complexity of folding.

#### Note

The unpaired probabilities  $p_i^u = 1 - \sum_{j \neq i} p_{ij}$  are usually computed from the supplied pairing probabilities  $p_{ij}$  as stored in `plist` entries of type `VRNA_PLIST_TYPE_BASEPAIR`. To overwrite individual  $p_o^u$  values simply add entries with type `VRNA_PLIST_TYPE_UNPAIRED`

To include G-Quadruplex support, the corresponding field in `md` must be set.

#### Parameters

|                 |                                                                      |
|-----------------|----------------------------------------------------------------------|
| <i>plist</i>    | A list of base pair probabilities the MEA structure is computed from |
| <i>sequence</i> | The RNA sequence that corresponds to the list of probability values  |
| <i>gamma</i>    | The weighting factor for base pairs vs. unpaired nucleotides         |
| <i>md</i>       | A model details data structure (maybe NULL)                          |
| <i>mea</i>      | A pointer to a variable where the MEA value will be written to       |

#### Returns

An MEA structure (or NULL on any error)

**SWIG Wrapper Notes** This function is available as overloaded function `MEA_from_plist(gamma = 1., md = NULL)`. Note, that it returns the MEA structure and MEA value as a tuple (MEA\_structure, MEA)

### 16.26.2.3 MEA()

```
float MEA (
    plist * p,
    char * structure,
    double gamma )
```

```
#include <ViennaRNA/MEA.h>
```

Computes a MEA (maximum expected accuracy) structure.

The algorithm maximizes the expected accuracy

$$A(S) = \sum_{(i,j) \in S} 2\gamma p_{ij} + \sum_{i \notin S} p_i^u$$

Higher values of  $\gamma$  result in more base pairs of lower probability and thus higher sensitivity. Low values of  $\gamma$  result in structures containing only highly likely pairs (high specificity). The code of the MEA function also demonstrates the use of sparse dynamic programming scheme to reduce the time and memory complexity of folding.

**Deprecated** Use `vrna_MEA()` or `vrna_MEA_from_plist()` instead!

## 16.27 Compute the Centroid Structure

### 16.27.1 Detailed Description

Collaboration diagram for Compute the Centroid Structure:

## Functions

- char \* [vrna\\_centroid](#) (vrna\_fold\_compound\_t \*vc, double \*dist)  
*Get the centroid structure of the ensemble.*
- char \* [vrna\\_centroid\\_from\\_plist](#) (int length, double \*dist, vrna\_ep\_t \*pl)  
*Get the centroid structure of the ensemble.*
- char \* [vrna\\_centroid\\_from\\_probs](#) (int length, double \*dist, FLT\_OR\_DBL \*probs)  
*Get the centroid structure of the ensemble.*

## 16.27.2 Function Documentation

### 16.27.2.1 vrna\_centroid()

```
char * vrna_centroid (
    vrna_fold_compound_t * vc,
    double * dist )
#include <ViennaRNA/centroid.h>
```

Get the centroid structure of the ensemble.

The centroid is the structure with the minimal average distance to all other structures

$$< d(S) > = \sum_{(i,j) \in S} (1 - p_{ij}) + \sum_{(i,j) \notin S} p_{ij}$$

Thus, the centroid is simply the structure containing all pairs with  $p_{ij} > 0.5$  The distance of the centroid to the ensemble is written to the memory addressed by *dist*.

#### Parameters

|     |      |                                                                                   |
|-----|------|-----------------------------------------------------------------------------------|
| in  | vc   | The fold compound data structure                                                  |
| out | dist | A pointer to the distance variable where the centroid distance will be written to |

#### Returns

The centroid structure of the ensemble in dot-bracket notation (NULL on error)

### 16.27.2.2 vrna\_centroid\_from\_plist()

```
char * vrna_centroid_from_plist (
    int length,
    double * dist,
    vrna_ep_t * pl )
#include <ViennaRNA/centroid.h>
```

Get the centroid structure of the ensemble.

This function is a threadsafe replacement for [centroid\(\)](#) with a [vrna\\_ep\\_t](#) input

The centroid is the structure with the minimal average distance to all other structures

$$< d(S) > = \sum_{(i,j) \in S} (1 - p_{ij}) + \sum_{(i,j) \notin S} p_{ij}$$

Thus, the centroid is simply the structure containing all pairs with  $p_{ij} > 0.5$  The distance of the centroid to the ensemble is written to the memory addressed by *dist*.

#### Parameters

|     |        |                                                                                   |
|-----|--------|-----------------------------------------------------------------------------------|
| in  | length | The length of the sequence                                                        |
| out | dist   | A pointer to the distance variable where the centroid distance will be written to |
| in  | pl     | A pair list containing base pair probability information about the ensemble       |

**Returns**

The centroid structure of the ensemble in dot-bracket notation (NULL on error)

**16.27.2.3 vrna\_centroid\_from\_probs()**

```
char * vrna_centroid_from_probs (
    int length,
    double * dist,
    FLT_OR_DBL * probs )
#include <ViennaRNA/centroid.h>
```

Get the centroid structure of the ensemble.

This function is a threadsafe replacement for [centroid\(\)](#) with a probability array input

The centroid is the structure with the minimal average distance to all other structures

$$< d(S) > = \sum_{(i,j) \in S} (1 - p_{ij}) + \sum_{(i,j) \notin S} p_{ij}$$

Thus, the centroid is simply the structure containing all pairs with  $p_{ij} > 0.5$  The distance of the centroid to the ensemble is written to the memory addressed by *dist*.

**Parameters**

|     |               |                                                                                                                    |
|-----|---------------|--------------------------------------------------------------------------------------------------------------------|
| in  | <i>length</i> | The length of the sequence                                                                                         |
| out | <i>dist</i>   | A pointer to the distance variable where the centroid distance will be written to                                  |
| in  | <i>probs</i>  | An upper triangular matrix containing base pair probabilities (access via <code>iindx vrna_idx_row_wise()</code> ) |

**Returns**

The centroid structure of the ensemble in dot-bracket notation (NULL on error)

**16.28 RNA-RNA Interaction****16.28.1 Detailed Description**

Collaboration diagram for RNA-RNA Interaction:

**Modules**

- [Partition Function for Two Hybridized Sequences](#)  
*Partition Function Cofolding.*
- [Partition Function for two Hybridized Sequences as a Stepwise Process](#)  
*RNA-RNA interaction as a stepwise process.*

**Files**

- file [concentrations.h](#)  
*Concentration computations for RNA-RNA interactions.*
- file [duplex.h](#)  
*Functions for simple RNA-RNA duplex interactions.*
- file [part\\_func\\_up.h](#)  
*Implementations for accessibility and RNA-RNA interaction as a stepwise process.*

**16.29 Classified Dynamic Programming Variants****16.29.1 Detailed Description**

Collaboration diagram for Classified Dynamic Programming Variants:

## Modules

- [Distance Based Partitioning of the Secondary Structure Space](#)
- [Compute the Density of States](#)

## 16.30 Distance Based Partitioning of the Secondary Structure Space

### 16.30.1 Detailed Description

Collaboration diagram for Distance Based Partitioning of the Secondary Structure Space:

## Modules

- [Computing MFE representatives of a Distance Based Partitioning](#)  
*Compute the minimum free energy (MFE) and secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures basepair distance to two fixed reference structures.*
- [Computing Partition Functions of a Distance Based Partitioning](#)  
*Compute the partition function and stochastically sample secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures.*
- [Stochastic Backtracking of Structures from Distance Based Partitioning](#)  
*Contains functions related to stochastic backtracking from a specified distance class.*

## Files

- file [2Dfold.h](#)  
*MFE structures for base pair distance classes.*
- file [2Dpfold.h](#)  
*Partition function implementations for base pair distance classes.*

## 16.31 Computing MFE representatives of a Distance Based Partitioning

Compute the minimum free energy (MFE) and secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures basepair distance to two fixed reference structures.

### 16.31.1 Detailed Description

Compute the minimum free energy (MFE) and secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures basepair distance to two fixed reference structures.

See also

For further details, we refer to Lorenz et al. 2009 [[15](#)]

Collaboration diagram for Computing MFE representatives of a Distance Based Partitioning:

## Data Structures

- struct [vrna\\_sol\\_TwoD\\_t](#)  
*Solution element returned from [vrna\\_mfe\\_TwoD\(\)](#) [More...](#)*
- struct [TwoDfold\\_vars](#)  
*Variables compound for 2Dfold MFE folding. [More...](#)*



## Typedefs

- typedef struct [vrna\\_sol\\_TwoD\\_t](#) [vrna\\_sol\\_TwoD\\_t](#)  
*Solution element returned from [vrna\\_mfe\\_TwoD\(\)](#)*
- typedef struct [TwoDfold\\_vars](#) [TwoDfold\\_vars](#)  
*Variables compound for 2Dfold MFE folding.*

## Functions

- [vrna\\_sol\\_TwoD\\_t](#) \* [vrna\\_mfe\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int distance1, int distance2)  
*Compute MFE's and representative for distance partitioning.*
- char \* [vrna\\_backtrack5\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int k, int l, unsigned int j)  
*Backtrack a minimum free energy structure from a 5' section of specified length.*
- [TwoDfold\\_vars](#) \* [get\\_TwoDfold\\_variables](#) (const char \*seq, const char \*structure1, const char \*structure2, int circ)  
*Get a structure of type [TwoDfold\\_vars](#) prefilled with current global settings.*
- void [destroy\\_TwoDfold\\_variables](#) ([TwoDfold\\_vars](#) \*our\_variables)  
*Destroy a [TwoDfold\\_vars](#) datastructure without memory loss.*
- [vrna\\_sol\\_TwoD\\_t](#) \* [TwoDfoldList](#) ([TwoDfold\\_vars](#) \*vars, int distance1, int distance2)  
*Compute MFE's and representative for distance partitioning.*
- char \* [TwoDfold\\_backtrack\\_f5](#) (unsigned int j, int k, int l, [TwoDfold\\_vars](#) \*vars)  
*Backtrack a minimum free energy structure from a 5' section of specified length.*

## 16.31.2 Data Structure Documentation

### 16.31.2.1 struct [vrna\\_sol\\_TwoD\\_t](#)

Solution element returned from [vrna\\_mfe\\_TwoD\(\)](#)

This element contains free energy and structure for the appropriate kappa (k), lambda (l) neighborhood. The datastructure contains two integer attributes 'k' and 'l' as well as an attribute 'en' of type float representing the free energy in kcal/mol and an attribute 's' of type char\* containing the secondary structure representative. A value of [INF](#) in k denotes the end of a list.

See also

[vrna\\_mfe\\_TwoD\(\)](#)

### Data Fields

- int **k**  
*Distance to first reference.*
- int **l**  
*Distance to second reference.*
- float **en**  
*Free energy in kcal/mol.*
- char \* **s**  
*MFE representative structure in dot-bracket notation.*

### 16.31.2.2 struct [TwoDfold\\_vars](#)

Variables compound for 2Dfold MFE folding.

**Deprecated** This data structure will be removed from the library soon! Use [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_mfe\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

Collaboration diagram for [TwoDfold\\_vars](#):

## Data Fields

- `vrna_param_t * P`  
*Precomputed energy parameters and model details.*
- `int do_backtrack`  
*Flag whether to do backtracing of the structure(s) or not.*
- `char * ptype`  
*Precomputed array of pair types.*
- `char * sequence`  
*The input sequence*
- `short * S1`  
*The input sequences in numeric form.*
- `unsigned int maxD1`  
*Maximum allowed base pair distance to first reference.*
- `unsigned int maxD2`  
*Maximum allowed base pair distance to second reference.*
- `unsigned int * mm1`  
*Maximum matching matrix, reference struct 1 disallowed.*
- `unsigned int * mm2`  
*Maximum matching matrix, reference struct 2 disallowed.*
- `int * my_iindx`  
*Index for moving in quadratic distance dimensions.*
- `unsigned int * referenceBPs1`  
*Matrix containing number of basepairs of reference structure1 in interval [i,j].*
- `unsigned int * referenceBPs2`  
*Matrix containing number of basepairs of reference structure2 in interval [i,j].*
- `unsigned int * bpdist`  
*Matrix containing base pair distance of reference structure 1 and 2 on interval [i,j].*

## 16.31.3 Typedef Documentation

### 16.31.3.1 vrna\_sol\_TwoD\_t

```
typedef struct vrna_sol_TwoD_t vrna_sol_TwoD_t
#include <ViennaRNA/2Dfold.h>
```

Solution element returned from `vrna_mfe_TwoD()`

This element contains free energy and structure for the appropriate kappa (k), lambda (l) neighborhood. The data-structure contains two integer attributes 'k' and 'l' as well as an attribute 'en' of type float representing the free energy in kcal/mol and an attribute 's' of type char\* containing the secondary structure representative. A value of `INF` in k denotes the end of a list.

See also

`vrna_mfe_TwoD()`

### 16.31.3.2 TwoDfold\_vars

```
typedef struct TwoDfold_vars TwoDfold_vars
#include <ViennaRNA/2Dfold.h>
```

Variables compound for 2Dfold MFE folding.

**Deprecated** This data structure will be removed from the library soon! Use `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

## 16.31.4 Function Documentation

### 16.31.4.1 `vrna_mfe_TwoD()`

```
vrna_sol_TwoD_t * vrna_mfe_TwoD (
    vrna_fold_compound_t * vc,
    int distance1,
    int distance2 )
#include <ViennaRNA/2Dfold.h>
```

Compute MFE's and representative for distance partitioning.

This function computes the minimum free energies and a representative secondary structure for each distance class according to the two references specified in the datastructure 'vars'. The maximum basepair distance to each of both references may be set by the arguments 'distance1' and 'distance2', respectively. If both distance arguments are set to '-1', no restriction is assumed and the calculation is performed for each distance class possible.

The returned list contains an entry for each distance class. If a maximum basepair distance to either of the references was passed, an entry with  $k=l-1$  will be appended in the list, denoting the class where all structures exceeding the maximum will be thrown into. The end of the list is denoted by an attribute value of `INF` in the  $k$ -attribute of the list entry.

See also

`vrna_fold_compound_TwoD()`, `vrna_fold_compound_free()`, `vrna_pf_TwoD()` `vrna_backtrack5_TwoD()`,  
[vrna\\_sol\\_TwoD\\_t](#), [vrna\\_fold\\_compound\\_t](#)

#### Parameters

|                        |                                                                 |
|------------------------|-----------------------------------------------------------------|
| <code>vc</code>        | The datastructure containing all precomputed folding attributes |
| <code>distance1</code> | maximum distance to reference1 (-1 means no restriction)        |
| <code>distance2</code> | maximum distance to reference2 (-1 means no restriction)        |

#### Returns

A list of minimum free energies (and corresponding structures) for each distance class

### 16.31.4.2 `vrna_backtrack5_TwoD()`

```
char * vrna_backtrack5_TwoD (
    vrna_fold_compound_t * vc,
    int k,
    int l,
    unsigned int j )
#include <ViennaRNA/2Dfold.h>
```

Backtrack a minimum free energy structure from a 5' section of specified length.

This function allows one to backtrack a secondary structure beginning at the 5' end, a specified length and residing in a specific distance class. If the argument 'k' gets a value of -1, the structure that is backtracked is assumed to reside in the distance class where all structures exceeding the maximum basepair distance specified in `vrna_mfe_TwoD()` belong to.

#### Note

The argument 'vars' must contain precalculated energy values in the energy matrices, i.e. a call to `vrna_mfe_TwoD()` preceding this function is mandatory!

See also

[vrna\\_mfe\\_TwoD\(\)](#)

## Parameters

|           |                                                                 |
|-----------|-----------------------------------------------------------------|
| <i>vc</i> | The datastructure containing all precomputed folding attributes |
| <i>j</i>  | The length in nucleotides beginning from the 5' end             |
| <i>k</i>  | distance to reference1 (may be -1)                              |
| <i>l</i>  | distance to reference2                                          |

**16.31.4.3 get\_TwoDfold\_variables()**

```
TwoDfold_vars * get_TwoDfold_variables (
    const char * seq,
    const char * structure1,
    const char * structure2,
    int circ )
```

```
#include <ViennaRNA/2Dfold.h>
```

Get a structure of type `TwoDfold_vars` prefilled with current global settings.

This function returns a datastructure of type `TwoDfold_vars`. The data fields inside the `TwoDfold_vars` are prefilled by global settings and all memory allocations necessary to start a computation are already done for the convenience of the user

**Note**

Make sure that the reference structures are compatible with the sequence according to Watson-Crick- and Wobble-base pairing

**Deprecated** Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

## Parameters

|                   |                                                                                            |
|-------------------|--------------------------------------------------------------------------------------------|
| <i>seq</i>        | The RNA sequence                                                                           |
| <i>structure1</i> | The first reference structure in dot-bracket notation                                      |
| <i>structure2</i> | The second reference structure in dot-bracket notation                                     |
| <i>circ</i>       | A switch to indicate the assumption to fold a circular instead of linear RNA (0=OFF, 1=ON) |

## Returns

A datastructure prefilled with folding options and allocated memory

**16.31.4.4 destroy\_TwoDfold\_variables()**

```
void destroy_TwoDfold_variables (
    TwoDfold_vars * our_variables )
```

```
#include <ViennaRNA/2Dfold.h>
```

Destroy a `TwoDfold_vars` datastructure without memory loss.

This function free's all allocated memory that depends on the datastructure given.

**Deprecated** Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

## Parameters

|                      |                                                |
|----------------------|------------------------------------------------|
| <i>our_variables</i> | A pointer to the datastructure to be destroyed |
|----------------------|------------------------------------------------|

#### 16.31.4.5 TwoDfoldList()

```
vrna_sol_TwoD_t * TwoDfoldList (
    TwoDfold_vars * vars,
    int distance1,
    int distance2 )
#include <ViennaRNA/2Dfold.h>
```

Compute MFE's and representative for distance partitioning.

This function computes the minimum free energies and a representative secondary structure for each distance class according to the two references specified in the datastructure 'vars'. The maximum basepair distance to each of both references may be set by the arguments 'distance1' and 'distance2', respectively. If both distance arguments are set to '-1', no restriction is assumed and the calculation is performed for each distance class possible.

The returned list contains an entry for each distance class. If a maximum basepair distance to either of the references was passed, an entry with  $k=-1$  will be appended in the list, denoting the class where all structures exceeding the maximum will be thrown into. The end of the list is denoted by an attribute value of **INF** in the  $k$ -attribute of the list entry.

**Deprecated** Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, and `vrna_fold_compound_free()` instead!

##### Parameters

|                  |                                                                |
|------------------|----------------------------------------------------------------|
| <i>vars</i>      | the datastructure containing all predefined folding attributes |
| <i>distance1</i> | maximum distance to reference1 (-1 means no restriction)       |
| <i>distance2</i> | maximum distance to reference2 (-1 means no restriction)       |

#### 16.31.4.6 TwoDfold\_backtrack\_f5()

```
char * TwoDfold_backtrack_f5 (
    unsigned int j,
    int k,
    int l,
    TwoDfold_vars * vars )
#include <ViennaRNA/2Dfold.h>
```

Backtrack a minimum free energy structure from a 5' section of specified length.

This function allows one to backtrack a secondary structure beginning at the 5' end, a specified length and residing in a specific distance class. If the argument 'k' gets a value of -1, the structure that is backtracked is assumed to reside in the distance class where all structures exceeding the maximum basepair distance specified in `TwoDfold()` belong to.

##### Note

The argument 'vars' must contain precalculated energy values in the energy matrices, i.e. a call to `TwoDfold()` preceding this function is mandatory!

**Deprecated** Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_mfe_TwoD()`, `vrna_backtrack5_TwoD()`, and `vrna_fold_compound_free()` instead!

##### Parameters

|             |                                                                |
|-------------|----------------------------------------------------------------|
| <i>j</i>    | The length in nucleotides beginning from the 5' end            |
| <i>k</i>    | distance to reference1 (may be -1)                             |
| <i>l</i>    | distance to reference2                                         |
| <i>vars</i> | the datastructure containing all predefined folding attributes |

## 16.32 Computing Partition Functions of a Distance Based Partitioning

Compute the partition function and stochastically sample secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures.

### 16.32.1 Detailed Description

Compute the partition function and stochastically sample secondary structures for a partitioning of the secondary structure space according to the base pair distance to two fixed reference structures.

Collaboration diagram for Computing Partition Functions of a Distance Based Partitioning:

### Data Structures

- struct [vrna\\_sol\\_TwoD\\_pf\\_t](#)  
*Solution element returned from [vrna\\_pf\\_TwoD\(\)](#) [More...](#)*

### Typedefs

- typedef struct [vrna\\_sol\\_TwoD\\_pf\\_t](#) [vrna\\_sol\\_TwoD\\_pf\\_t](#)  
*Solution element returned from [vrna\\_pf\\_TwoD\(\)](#)*

### Functions

- [vrna\\_sol\\_TwoD\\_pf\\_t \\* vrna\\_pf\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int maxDistance1, int maxDistance2)  
*Compute the partition function for all distance classes.*

## 16.32.2 Data Structure Documentation

### 16.32.2.1 struct vrna\_sol\_TwoD\_pf\_t

Solution element returned from [vrna\\_pf\\_TwoD\(\)](#)

This element contains the partition function for the appropriate kappa (k), lambda (l) neighborhood The datastructure contains two integer attributes 'k' and 'l' as well as an attribute 'q' of type [FLT\\_OR\\_DBL](#)

A value of [INF](#) in k denotes the end of a list

See also

[vrna\\_pf\\_TwoD\(\)](#)

### Data Fields

- int k  
*Distance to first reference.*
- int l  
*Distance to second reference.*
- [FLT\\_OR\\_DBL](#) q  
*partition function*

## 16.32.3 Typedef Documentation

### 16.32.3.1 vrna\_sol\_TwoD\_pf\_t

```
typedef struct vrna\_sol\_TwoD\_pf\_t vrna\_sol\_TwoD\_pf\_t
#include <ViennaRNA/2Dpfold.h>
```

Solution element returned from [vrna\\_pf\\_TwoD\(\)](#)

This element contains the partition function for the appropriate kappa (k), lambda (l) neighborhood The datastructure contains two integer attributes 'k' and 'l' as well as an attribute 'q' of type [FLT\\_OR\\_DBL](#)

A value of [INF](#) in k denotes the end of a list

See also

[vrna\\_pf\\_TwoD\(\)](#)

## 16.32.4 Function Documentation

### 16.32.4.1 vrna\_pf\_TwoD()

```
vrna_sol_TwoD_pf_t * vrna_pf_TwoD (
    vrna_fold_compound_t * vc,
    int maxDistance1,
    int maxDistance2 )
```

```
#include <ViennaRNA/2Dpfold.h>
```

Compute the partition function for all distance classes.

This function computes the partition functions for all distance classes according the two reference structures specified in the datastructure 'vars'. Similar to [vrna\\_mfe\\_TwoD\(\)](#) the arguments maxDistance1 and maxDistance2 specify the maximum distance to both reference structures. A value of '-1' in either of them makes the appropriate distance restrictionless, i.e. all basepair distances to the reference are taken into account during computation. In case there is a restriction, the returned solution contains an entry where the attribute k!= -1 contains the partition function for all structures exceeding the restriction. A value of [INF](#) in the attribute 'k' of the returned list denotes the end of the list

See also

[vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_fold\\_compound](#) [vrna\\_sol\\_TwoD\\_pf\\_t](#)

#### Parameters

|                     |                                                                            |
|---------------------|----------------------------------------------------------------------------|
| <i>vc</i>           | The datastructure containing all necessary folding attributes and matrices |
| <i>maxDistance1</i> | The maximum basepair distance to reference1 (may be -1)                    |
| <i>maxDistance2</i> | The maximum basepair distance to reference2 (may be -1)                    |

#### Returns

A list of partition funtions for the corresponding distance classes

## 16.33 Stochastic Backtracking of Structures from Distance Based Partitioning

Contains functions related to stochastic backtracking from a specified distance class.

### 16.33.1 Detailed Description

Contains functions related to stochastic backtracking from a specified distance class.

Collaboration diagram for Stochastic Backtracking of Structures from Distance Based Partitioning:

#### Functions

- char \* [vrna\\_pbacktrack\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int d1, int d2)  
*Sample secondary structure representatives from a set of distance classes according to their Boltzmann probability.*
- char \* [vrna\\_pbacktrack5\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int d1, int d2, unsigned int length)  
*Sample secondary structure representatives with a specified length from a set of distance classes according to their Boltzmann probability.*

## 16.33.2 Function Documentation

### 16.33.2.1 `vrna_pbacktrack_TwoD()`

```
char * vrna_pbacktrack_TwoD (
    vrna_fold_compound_t * vc,
    int d1,
    int d2 )
#include <ViennaRNA/2Dpfold.h>
```

Sample secondary structure representatives from a set of distance classes according to their Boltzmann probability. If the argument 'd1' is set to '-1', the structure will be backtracked in the distance class where all structures exceeding the maximum basepair distance to either of the references reside.

#### Precondition

The argument 'vars' must contain precalculated partition function matrices, i.e. a call to `vrna_pf_TwoD()` preceding this function is mandatory!

#### See also

[vrna\\_pf\\_TwoD\(\)](#)

#### Parameters

|         |    |                                                                                                              |
|---------|----|--------------------------------------------------------------------------------------------------------------|
| in, out | vc | The <code>vrna_fold_compound_t</code> datastructure containing all necessary folding attributes and matrices |
| in      | d1 | The distance to reference1 (may be -1)                                                                       |
| in      | d2 | The distance to reference2                                                                                   |

#### Returns

A sampled secondary structure in dot-bracket notation

### 16.33.2.2 `vrna_pbacktrack5_TwoD()`

```
char * vrna_pbacktrack5_TwoD (
    vrna_fold_compound_t * vc,
    int d1,
    int d2,
    unsigned int length )
#include <ViennaRNA/2Dpfold.h>
```

Sample secondary structure representatives with a specified length from a set of distance classes according to their Boltzmann probability.

This function does essentially the same as `vrna_pbacktrack_TwoD()` with the only difference that partial structures, i.e. structures beginning from the 5' end with a specified length of the sequence, are backtracked

#### Note

This function does not work (since it makes no sense) for circular RNA sequences!

#### Precondition

The argument 'vars' must contain precalculated partition function matrices, i.e. a call to `vrna_pf_TwoD()` preceding this function is mandatory!



See also

[vrna\\_pbacktrack\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#)

#### Parameters

|                      |                     |                                                                                                                 |
|----------------------|---------------------|-----------------------------------------------------------------------------------------------------------------|
| <code>in, out</code> | <code>vc</code>     | The <a href="#">vrna_fold_compound_t</a> datastructure containing all necessary folding attributes and matrices |
| <code>in</code>      | <code>d1</code>     | The distance to reference1 (may be -1)                                                                          |
| <code>in</code>      | <code>d2</code>     | The distance to reference2                                                                                      |
| <code>in</code>      | <code>length</code> | The length of the structure beginning from the 5' end                                                           |

#### Returns

A sampled secondary structure in dot-bracket notation

## 16.34 Predicting various thermodynamic properties

Compute various thermodynamic properties using the partition function.

### 16.34.1 Detailed Description

Compute various thermodynamic properties using the partition function.  
Many thermodynamic properties can be derived from the partition function

$$Q = \sum_{s \in \omega} e^{\frac{-E(s)}{kT}}.$$

In particular, for nucleic acids in equilibrium the probability  $p(F)$  of a particular structural feature  $F$  follows Boltzmann's law, i.e.

$$p(F) \propto \sum_{s|F \in s} e^{\frac{-E(s)}{kT}}.$$

The actual probabilities can then be obtained from the ratio of those structures containing  $F$  and *all* structures, i.e.

$$p(F) = \frac{1}{Q} \sum_{s|F \in s} e^{\frac{-E(s)}{kT}}.$$

Consequently, a particular secondary structure  $s$  has equilibrium probability

$$p(s) = \frac{1}{Q} e^{\frac{-E(s)}{kT}}$$

which can be easily computed once  $Q$  and  $E(s)$  are known.

On the other hand, efficient dynamic programming algorithms exist to compute the equilibrium probabilities

$$p_{ij} = \frac{1}{Q} \sum_{s|(i,j) \in s} e^{\frac{-E(s)}{kT}}$$

of base pairs  $(i, j)$  without the need for exhaustive enumeration of  $s$ .

This interface provides the functions for all thermodynamic property computations implemented in *RNAlib*. Collaboration diagram for Predicting various thermodynamic properties:

#### Files

- file [equilibrium\\_probs.h](#)  
*Equilibrium Probability implementations.*
- file [heat\\_capacity.h](#)  
*Compute heat capacity for an RNA.*

## Data Structures

- struct [vrna\\_heat\\_capacity\\_s](#)  
A single result from heat capacity computations. [More...](#)

## Typedefs

- typedef void() [vrna\\_heat\\_capacity\\_callback](#)(float temp, float heat\_capacity, void \*data)  
The callback for heat capacity predictions.
- typedef struct [vrna\\_heat\\_capacity\\_s](#) [vrna\\_heat\\_capacity\\_t](#)  
A single result from heat capacity computations.

## Base pair probabilities and derived computations

- int [vrna\\_pairing\\_probs](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)
- double [vrna\\_mean\\_bp\\_distance\\_pr](#) (int length, [FLT\\_OR\\_DBL](#) \*pr)  
Get the mean base pair distance in the thermodynamic ensemble from a probability matrix.
- double [vrna\\_mean\\_bp\\_distance](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
Get the mean base pair distance in the thermodynamic ensemble.
- double [vrna\\_ensemble\\_defect\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt)  
Compute the Ensemble Defect for a given target structure provided as a [vrna\\_ptable](#).
- double [vrna\\_ensemble\\_defect](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
Compute the Ensemble Defect for a given target structure.
- double \* [vrna\\_positional\\_entropy](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)  
Compute a vector of positional entropies.
- [vrna\\_ep\\_t](#) \* [vrna\\_stack\\_prob](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double cutoff)  
Compute stacking probabilities.

## Multimer probabilities computations

- void [vrna\\_pf\\_dimer\\_probs](#) (double FAB, double FA, double FB, [vrna\\_ep\\_t](#) \*prAB, const [vrna\\_ep\\_t](#) \*prA, const [vrna\\_ep\\_t](#) \*prB, int Alength, const [vrna\\_exp\\_param\\_t](#) \*exp\_params)  
Compute Boltzmann probabilities of dimerization without homodimers.

## Structure probability computations

- double [vrna\\_pr\\_structure](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
Compute the equilibrium probability of a particular secondary structure.
- double [vrna\\_pr\\_energy](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double e)

## Basic heat capacity function interface

- [vrna\\_heat\\_capacity\\_t](#) \* [vrna\\_heat\\_capacity](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, float T\_min, float T\_max, float T\_increment, unsigned int mpoints)  
Compute the specific heat for an RNA.
- int [vrna\\_heat\\_capacity\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, float T\_min, float T\_max, float T\_increment, unsigned int mpoints, [vrna\\_heat\\_capacity\\_callback](#) \*cb, void \*data)  
Compute the specific heat for an RNA (callback variant)

## Simplified heat capacity computation

- [vrna\\_heat\\_capacity\\_t](#) \* [vrna\\_heat\\_capacity\\_simple](#) (const char \*sequence, float T\_min, float T\_max, float T\_increment, unsigned int mpoints)  
Compute the specific heat for an RNA (simplified variant)

## 16.34.2 Data Structure Documentation

### 16.34.2.1 struct vrna\_heat\_capacity\_s

A single result from heat capacity computations.

See also

[vrna\\_heat\\_capacity\(\)](#)

#### Data Fields

- float **temperature**  
*The temperature in °C.*
- float **heat\_capacity**  
*The specific heat at this temperature in Kcal/(Mol \* K)*

## 16.34.3 Typedef Documentation

### 16.34.3.1 vrna\_heat\_capacity\_callback

```
typedef void() vrna_heat_capacity_callback(float temp, float heat_capacity, void *data)
#include <ViennaRNA/heat_capacity.h>
```

The callback for heat capacity predictions.

**Notes on Callback Functions** This function will be called for each evaluated temperature in the heat capacity prediction.

See also

[vrna\\_heat\\_capacity\\_cb\(\)](#)

#### Parameters

|                      |                                                                                   |
|----------------------|-----------------------------------------------------------------------------------|
| <i>temp</i>          | The current temperature this results corresponds to in °C                         |
| <i>heat_capacity</i> | The heat capacity in Kcal/(Mol * K)                                               |
| <i>data</i>          | Some arbitrary data pointer passed through by the function executing the callback |

### 16.34.3.2 vrna\_heat\_capacity\_t

```
typedef struct vrna_heat_capacity_s vrna_heat_capacity_t
#include <ViennaRNA/heat_capacity.h>
```

A single result from heat capacity computations.

This is a convenience typedef for [vrna\\_heat\\_capacity\\_s](#), i.e. results as obtained from [vrna\\_heat\\_capacity\(\)](#)

## 16.34.4 Function Documentation

### 16.34.4.1 vrna\_mean\_bp\_distance\_pr()

```
double vrna_mean_bp_distance_pr (
    int length,
    FLT_OR_DBL * pr )
#include <ViennaRNA/equilibrium_probs.h>
```

Get the mean base pair distance in the thermodynamic ensemble from a probability matrix.

$$\langle d \rangle = \sum_{a,b} p_a p_b d(S_a, S_b)$$

this can be computed from the pair probs  $p_{ij}$  as

$$\langle d \rangle = \sum_{ij} p_{ij} (1 - p_{ij})$$

#### Parameters

|               |                                                   |
|---------------|---------------------------------------------------|
| <i>length</i> | The length of the sequence                        |
| <i>pr</i>     | The matrix containing the base pair probabilities |

#### Returns

The mean pair distance of the structure ensemble

#### 16.34.4.2 vrna\_mean\_bp\_distance()

```
double vrna_mean_bp_distance (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/equilibrium_probs.h>
```

Get the mean base pair distance in the thermodynamic ensemble.

$$\langle d \rangle = \sum_{a,b} p_a p_b d(S_a, S_b)$$

this can be computed from the pair probs  $p_{ij}$  as

$$\langle d \rangle = \sum_{ij} p_{ij} (1 - p_{ij})$$

#### Parameters

|           |                                  |
|-----------|----------------------------------|
| <i>vc</i> | The fold compound data structure |
|-----------|----------------------------------|

#### Returns

The mean pair distance of the structure ensemble

**SWIG Wrapper Notes** This function is attached as method **mean\_bp\_distance()** to objects of type *fold\_compound*

#### 16.34.4.3 vrna\_ensemble\_defect\_pt()

```
double vrna_ensemble_defect_pt (
    vrna_fold_compound_t * fc,
    const short * pt )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute the Ensemble Defect for a given target structure provided as a **vrna\_ptable**.

Given a target structure  $s$ , compute the average dissimilarity of a randomly drawn structure from the ensemble, i.e.:

$$ED(s) = 1 - \frac{1}{n} \sum_{ij, (i,j) \in s} p_{ij} - \frac{1}{n} \sum_i (1 - s_i) q_i$$

with sequence length  $n$ , the probability  $p_{ij}$  of a base pair  $(i, j)$ , the probability  $q_i = 1 - \sum_j p_{ij}$  of nucleotide  $i$  being unpaired, and the indicator variable  $s_i = 1$  if  $\exists (i, j) \in s$ , and  $s_i = 0$  otherwise.

#### Precondition

The `vrna_fold_compound_t` input parameter `fc` must contain a valid base pair probability matrix. This means that partition function and base pair probabilities must have been computed using `fc` before execution of this function!

#### See also

`vrna_pf()`, `vrna_pairing_probs()`, `vrna_ensemble_defect()`

#### Parameters

|                 |                                                           |
|-----------------|-----------------------------------------------------------|
| <code>fc</code> | A fold_compound with pre-computed base pair probabilities |
| <code>pt</code> | A pair table representing a target structure              |

#### Returns

The ensemble defect with respect to the target structure, or -1. upon failure, e.g. pre-conditions are not met

**SWIG Wrapper Notes** This function is attached as overloaded method `ensemble_defect()` to objects of type `fold_compound`.

#### 16.34.4.4 vrna\_ensemble\_defect()

```
double vrna_ensemble_defect (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute the Ensemble Defect for a given target structure.

This is a wrapper around `vrna_ensemble_defect_pt()`. Given a target structure  $s$ , compute the average dissimilarity of a randomly drawn structure from the ensemble, i.e.:

$$ED(s) = 1 - \frac{1}{n} \sum_{ij, (i,j) \in s} p_{ij} - \frac{1}{n} \sum_i (1 - s_i) q_i$$

with sequence length  $n$ , the probability  $p_{ij}$  of a base pair  $(i, j)$ , the probability  $q_i = 1 - \sum_j p_{ij}$  of nucleotide  $i$  being unpaired, and the indicator variable  $s_i = 1$  if  $\exists (i, j) \in s$ , and  $s_i = 0$  otherwise.

#### Precondition

The `vrna_fold_compound_t` input parameter `fc` must contain a valid base pair probability matrix. This means that partition function and base pair probabilities must have been computed using `fc` before execution of this function!

#### See also

`vrna_pf()`, `vrna_pairing_probs()`, `vrna_ensemble_defect_pt()`

#### Parameters

|                        |                                                           |
|------------------------|-----------------------------------------------------------|
| <code>fc</code>        | A fold_compound with pre-computed base pair probabilities |
| <code>structure</code> | A target structure in dot-bracket notation                |

## Returns

The ensemble defect with respect to the target structure, or -1. upon failure, e.g. pre-conditions are not met

**SWIG Wrapper Notes** This function is attached as method **ensemble\_defect()** to objects of type *fold\_compound*. Note that the SWIG wrapper takes a structure in dot-bracket notation and converts it into a pair table using [vrna\\_ptable\\_from\\_string\(\)](#). The resulting pair table is then internally passed to [vrna\\_ensemble\\_defect\\_pt\(\)](#). To control which kind of matching brackets will be used during conversion, the optional argument `options` can be used. See also the description of [vrna\\_ptable\\_from\\_string\(\)](#) for available options. (default: **VRNA\_BRACKETS\_RND**).

#### 16.34.4.5 vrna\_positional\_entropy()

```
double * vrna_positional_entropy (
    vrna_fold_compound_t * fc )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute a vector of positional entropies.

This function computes the positional entropies from base pair probabilities as

$$S(i) = - \sum_j p_{ij} \log(p_{ij}) - q_i \log(q_i)$$

with unpaired probabilities  $q_i = 1 - \sum_j p_{ij}$ .

Low entropy regions have little structural flexibility and the reliability of the predicted structure is high. High entropy implies many structural alternatives. While these alternatives may be functionally important, they make structure prediction more difficult and thus less reliable.

## Precondition

This function requires pre-computed base pair probabilities! Thus, [vrna\\_pf\(\)](#) must be called beforehand.

## Parameters

|           |                                                           |
|-----------|-----------------------------------------------------------|
| <i>fc</i> | A fold_compound with pre-computed base pair probabilities |
|-----------|-----------------------------------------------------------|

## Returns

A 1-based vector of positional entropies  $S(i)$ . (position 0 contains the sequence length)

**SWIG Wrapper Notes** This function is attached as method **positional\_entropy()** to objects of type *fold\_compound*

#### 16.34.4.6 vrna\_stack\_prob()

```
vrna_ep_t * vrna_stack_prob (
    vrna_fold_compound_t * vc,
    double cutoff )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute stacking probabilities.

For each possible base pair  $(i, j)$ , compute the probability of a stack  $(i, j)$ ,  $(i + 1, j - 1)$ .

## Parameters

|               |                                                                            |
|---------------|----------------------------------------------------------------------------|
| <i>vc</i>     | The fold compound data structure with precomputed base pair probabilities  |
| <i>cutoff</i> | A cutoff value that limits the output to stacks with $p > \text{cutoff}$ . |

**Returns**

A list of stacks with enclosing base pair  $(i, j)$  and probability  $p$

**16.34.4.7 vrna\_pf\_dimer\_probs()**

```
void vrna_pf_dimer_probs (
    double FAB,
    double FA,
    double FB,
    vrna_ep_t * prAB,
    const vrna_ep_t * prA,
    const vrna_ep_t * prB,
    int Alength,
    const vrna_exp_param_t * exp_params )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute Boltzmann probabilities of dimerization without homodimers.

Given the pair probabilities and free energies (in the null model) for a dimer AB and the two constituent monomers A and B, compute the conditional pair probabilities given that a dimer AB actually forms. Null model pair probabilities are given as a list as produced by [vrna\\_plist\\_from\\_probs\(\)](#), the dimer probabilities 'prAB' are modified in place.

**Parameters**

|                   |                                   |
|-------------------|-----------------------------------|
| <i>FAB</i>        | free energy of dimer AB           |
| <i>FA</i>         | free energy of monomer A          |
| <i>FB</i>         | free energy of monomer B          |
| <i>prAB</i>       | pair probabilities for dimer      |
| <i>prA</i>        | pair probabilities monomer        |
| <i>prB</i>        | pair probabilities monomer        |
| <i>Alength</i>    | Length of molecule A              |
| <i>exp_params</i> | The precomputed Boltzmann factors |

**16.34.4.8 vrna\_pr\_structure()**

```
double vrna_pr_structure (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/equilibrium_probs.h>
```

Compute the equilibrium probability of a particular secondary structure.

The probability  $p(s)$  of a particular secondary structure  $s$  can be computed as

$$p(s) = \frac{\exp(-\beta E(s))}{Z}$$

from the structures free energy  $E(s)$  and the partition function

$$Z = \sum_s \exp(-\beta E(s)), \quad \text{with} \quad \beta = \frac{1}{RT}$$

where  $R$  is the gas constant and  $T$  the thermodynamic temperature.

**Precondition**

The fold compound `fc` must have went through a call to [vrna\\_pf\(\)](#) to fill the dynamic programming matrices with the corresponding partition function.

## Parameters

|                  |                                                                                |
|------------------|--------------------------------------------------------------------------------|
| <i>fc</i>        | The fold compound data structure with precomputed partition function           |
| <i>structure</i> | The secondary structure to compute the probability for in dot-bracket notation |

## Returns

The probability of the input structure (range [0 : 1])

**SWIG Wrapper Notes** This function is attached as method **pr\_structure()** to objects of type *fold\_compound*

## 16.34.4.9 vrna\_pr\_energy()

```
double vrna_pr_energy (
    vrna_fold_compound_t * fc,
    double e )
#include <ViennaRNA/equilibrium_probs.h>
```

**SWIG Wrapper Notes** This function is attached as method **pr\_energy()** to objects of type *fold\_compound*

## 16.34.4.10 vrna\_heat\_capacity()

```
vrna_heat_capacity_t * vrna_heat_capacity (
    vrna_fold_compound_t * fc,
    float T_min,
    float T_max,
    float T_increment,
    unsigned int mpoints )
#include <ViennaRNA/heat_capacity.h>
```

Compute the specific heat for an RNA.

This function computes an RNAs specific heat in a given temperature range from the partition function by numeric differentiation. The result is returned as a list of pairs of temperature in °C and specific heat in Kcal/(Mol\*K). Users can specify the temperature range for the computation from T\_min to T\_max, as well as the increment step size T\_increment. The latter also determines how many times the partition function is computed. Finally, the parameter mpoints determines how smooth the curve should be. The algorithm itself fits a parabola to  $2 \cdot mpoints + 1$  data points to calculate 2nd derivatives. Increasing this parameter produces a smoother curve.

## See also

[vrna\\_heat\\_capacity\\_cb\(\)](#), [vrna\\_heat\\_capacity\\_t](#), [vrna\\_heat\\_capacity\\_s](#)

## Parameters

|                    |                                                                                                                   |
|--------------------|-------------------------------------------------------------------------------------------------------------------|
| <i>fc</i>          | The <a href="#">vrna_fold_compound_t</a> with the RNA sequence to analyze                                         |
| <i>T_min</i>       | Lowest temperature in °C                                                                                          |
| <i>T_max</i>       | Highest temperature in °C                                                                                         |
| <i>T_increment</i> | Stepsize for temperature incrementation in °C (a reasonable choice might be 1 °C)                                 |
| <i>mpoints</i>     | The number of interpolation points to calculate 2nd derivative (a reasonable choice might be 2, min: 1, max: 100) |

## Returns

A list of pairs of temperatures and corresponding heat capacity or *NULL* upon any failure. The last entry of the list is indicated by a **temperature** field set to a value smaller than T\_min



**SWIG Wrapper Notes** This function is attached as overloaded method **heat\_capacity()** to objects of type *fold\_compound*. If the optional function arguments *T\_min*, *T\_max*, *T\_increment*, and *mpoints* are omitted, they default to 0.0, 100.0, 1.0 and 2, respectively.

#### 16.34.4.11 vrna\_heat\_capacity\_cb()

```
int vrna_heat_capacity_cb (
    vrna_fold_compound_t * fc,
    float T_min,
    float T_max,
    float T_increment,
    unsigned int mpoints,
    vrna_heat_capacity_callback * cb,
    void * data )
```

```
#include <ViennaRNA/heat_capacity.h>
```

Compute the specific heat for an RNA (callback variant)

Similar to [vrna\\_heat\\_capacity\(\)](#), this function computes an RNA's specific heat in a given temperature range from the partition function by numeric differentiation. Instead of returning a list of temperature/specific heat pairs, however, this function returns the individual results through a callback mechanism. The provided function will be called for each result and passed the corresponding temperature and specific heat values along with the arbitrary data as provided through the *data* pointer argument.

Users can specify the temperature range for the computation from *T\_min* to *T\_max*, as well as the increment step size *T\_increment*. The latter also determines how many times the partition function is computed. Finally, the parameter *mpoints* determines how smooth the curve should be. The algorithm itself fits a parabola to  $2 \cdot mpoints + 1$  data points to calculate 2nd derivatives. Increasing this parameter produces a smoother curve.

See also

[vrna\\_heat\\_capacity\(\)](#), [vrna\\_heat\\_capacity\\_callback](#)

#### Parameters

|                    |                                                                                                                   |
|--------------------|-------------------------------------------------------------------------------------------------------------------|
| <i>fc</i>          | The <a href="#">vrna_fold_compound_t</a> with the RNA sequence to analyze                                         |
| <i>T_min</i>       | Lowest temperature in °C                                                                                          |
| <i>T_max</i>       | Highest temperature in °C                                                                                         |
| <i>T_increment</i> | Stepsize for temperature incrementation in °C (a reasonable choice might be 1 °C)                                 |
| <i>mpoints</i>     | The number of interpolation points to calculate 2nd derivative (a reasonable choice might be 2, min: 1, max: 100) |
| <i>cb</i>          | The user-defined callback function that receives the individual results                                           |
| <i>data</i>        | An arbitrary data structure that will be passed to the callback in conjunction with the results                   |

#### Returns

Returns 0 upon failure, and non-zero otherwise

**SWIG Wrapper Notes** This function is attached as method **heat\_capacity\_cb()** to objects of type *fold\_compound*

#### 16.34.4.12 vrna\_heat\_capacity\_simple()

```
vrna_heat_capacity_t * vrna_heat_capacity_simple (
    const char * sequence,
    float T_min,
    float T_max,
    float T_increment,
    unsigned int mpoints )
```

```
#include <ViennaRNA/heat_capacity.h>
```

Compute the specific heat for an RNA (simplified variant)

Similar to [vrna\\_heat\\_capacity\(\)](#), this function computes an RNAs specific heat in a given temperature range from the partition function by numeric differentiation. This simplified version, however, only requires the RNA sequence as input instead of a `vrna_fold_compound_t` data structure. The result is returned as a list of pairs of temperature in °C and specific heat in Kcal/(Mol\*K).

Users can specify the temperature range for the computation from `T_min` to `T_max`, as well as the increment step size `T_increment`. The latter also determines how many times the partition function is computed. Finally, the parameter `mpoints` determines how smooth the curve should be. The algorithm itself fits a parabola to  $2 \cdot mpoints + 1$  data points to calculate 2nd derivatives. Increasing this parameter produces a smoother curve.

See also

[vrna\\_heat\\_capacity\(\)](#), [vrna\\_heat\\_capacity\\_cb\(\)](#), [vrna\\_heat\\_capacity\\_t](#), [vrna\\_heat\\_capacity\\_s](#)

#### Parameters

|                    |                                                                                                                   |
|--------------------|-------------------------------------------------------------------------------------------------------------------|
| <i>sequence</i>    | The RNA sequence input (must be uppercase)                                                                        |
| <i>T_min</i>       | Lowest temperature in °C                                                                                          |
| <i>T_max</i>       | Highest temperature in °C                                                                                         |
| <i>T_increment</i> | Stepsize for temperature incrementation in °C (a reasonable choice might be 1 °C)                                 |
| <i>mpoints</i>     | The number of interpolation points to calculate 2nd derivative (a reasonable choice might be 2, min: 1, max: 100) |

#### Returns

A list of pairs of temperatures and corresponding heat capacity or *NULL* upon any failure. The last entry of the list is indicated by a **temperature** field set to a value smaller than `T_min`

**SWIG Wrapper Notes** This function is available as overloaded function **heat\_capacity()**. If the optional function arguments `T_min`, `T_max`, `T_increment`, and `mpoints` are omitted, they default to 0.0, 100.0, 1.0 and 2, respectively.

## 16.35 Compute the Density of States

### 16.35.1 Detailed Description

Collaboration diagram for Compute the Density of States:

#### Variables

- int [density\\_of\\_states](#) [MAXDOS+1]

*The Density of States.*

### 16.35.2 Variable Documentation

#### 16.35.2.1 density\_of\_states

```
int density_of_states[MAXDOS+1] [extern]
```

```
#include <ViennaRNA/subopt.h>
```

The Density of States.

This array contains the density of states for an RNA sequences after a call to [subopt\\_par\(\)](#), [subopt\(\)](#) or [subopt\\_circ\(\)](#).

**Precondition**

Call one of the functions [subopt\\_par\(\)](#), [subopt\(\)](#) or [subopt\\_circ\(\)](#) prior accessing the contents of this array

**See also**

[subopt\\_par\(\)](#), [subopt\(\)](#), [subopt\\_circ\(\)](#)

## 16.36 Inverse Folding (Design)

RNA sequence design.

### 16.36.1 Detailed Description

RNA sequence design.

**Files**

- file [inverse.h](#)  
*Inverse folding routines.*

**Functions**

- float [inverse\\_fold](#) (char \*start, const char \*target)  
*Find sequences with predefined structure.*
- float [inverse\\_pf\\_fold](#) (char \*start, const char \*target)  
*Find sequence that maximizes probability of a predefined structure.*

**Variables**

- char \* **symbolset**  
*This global variable points to the allowed bases, initially "AUGC". It can be used to design sequences from reduced alphabets.*
- float [final\\_cost](#)
- int [give\\_up](#)
- int [inv\\_verbose](#)

### 16.36.2 Function Documentation

#### 16.36.2.1 [inverse\\_fold\(\)](#)

```
float inverse_fold (  
    char * start,  
    const char * target )  
#include <ViennaRNA/inverse.h>
```

Find sequences with predefined structure.

This function searches for a sequence with minimum free energy structure provided in the parameter 'target', starting with sequence 'start'. It returns 0 if the search was successful, otherwise a structure distance in terms of the energy difference between the search result and the actual target 'target' is returned. The found sequence is returned in 'start'. If [give\\_up](#) is set to 1, the function will return as soon as it is clear that the search will be unsuccessful, this speeds up the algorithm if you are only interested in exact solutions.

**Parameters**

|               |                                                        |
|---------------|--------------------------------------------------------|
| <i>start</i>  | The start sequence                                     |
| <i>target</i> | The target secondary structure in dot-bracket notation |

**Returns**

The distance to the target in case a search was unsuccessful, 0 otherwise

**16.36.2.2 inverse\_pf\_fold()**

```
float inverse_pf_fold (
    char * start,
    const char * target )
#include <ViennaRNA/inverse.h>
```

Find sequence that maximizes probability of a predefined structure.

This function searches for a sequence with maximum probability to fold into the provided structure 'target' using the partition function algorithm. It returns  $-kT \cdot \log(p)$  where  $p$  is the frequency of 'target' in the ensemble of possible structures. This is usually much slower than [inverse\\_fold\(\)](#).

**Parameters**

|               |                                                        |
|---------------|--------------------------------------------------------|
| <i>start</i>  | The start sequence                                     |
| <i>target</i> | The target secondary structure in dot-bracket notation |

**Returns**

The distance to the target in case a search was unsuccessful, 0 otherwise

**16.36.3 Variable Documentation****16.36.3.1 final\_cost**

```
float final_cost [extern]
#include <ViennaRNA/inverse.h>
when to stop inverse\_pf\_fold\(\)
```

**16.36.3.2 give\_up**

```
int give_up [extern]
#include <ViennaRNA/inverse.h>
default 0: try to minimize structure distance even if no exact solution can be found
```

**16.36.3.3 inv\_verbose**

```
int inv_verbose [extern]
#include <ViennaRNA/inverse.h>
print out substructure on which inverse\_fold\(\) fails
```

**16.37 Neighborhood Relation and Move Sets for Secondary Structures**

Different functions to generate structural neighbors of a secondary structure according to a particular Move Set.

**16.37.1 Detailed Description**

Different functions to generate structural neighbors of a secondary structure according to a particular Move Set.

This module contains methods to compute the neighbors of an RNA secondary structure. Neighbors of a given structure are all structures that differ in exactly one base pair. That means one can insert an delete base pairs in the given structure. These insertions and deletions of base pairs are usually called moves. A third move which is considered in these methods is a shift move. A shifted base pair has one stable position and one position that

changes. These moves are encoded as follows:

- insertion:  $(i, j)$  where  $i, j > 0$
  - deletion:  $(i, j)$  where  $i, j < 0$
  - shift:  $(i, j)$  where either  $i > 0, j < 0$  or  $i < 0, j > 0$
- The negative position of a shift indicates the position that has changed.

Example:

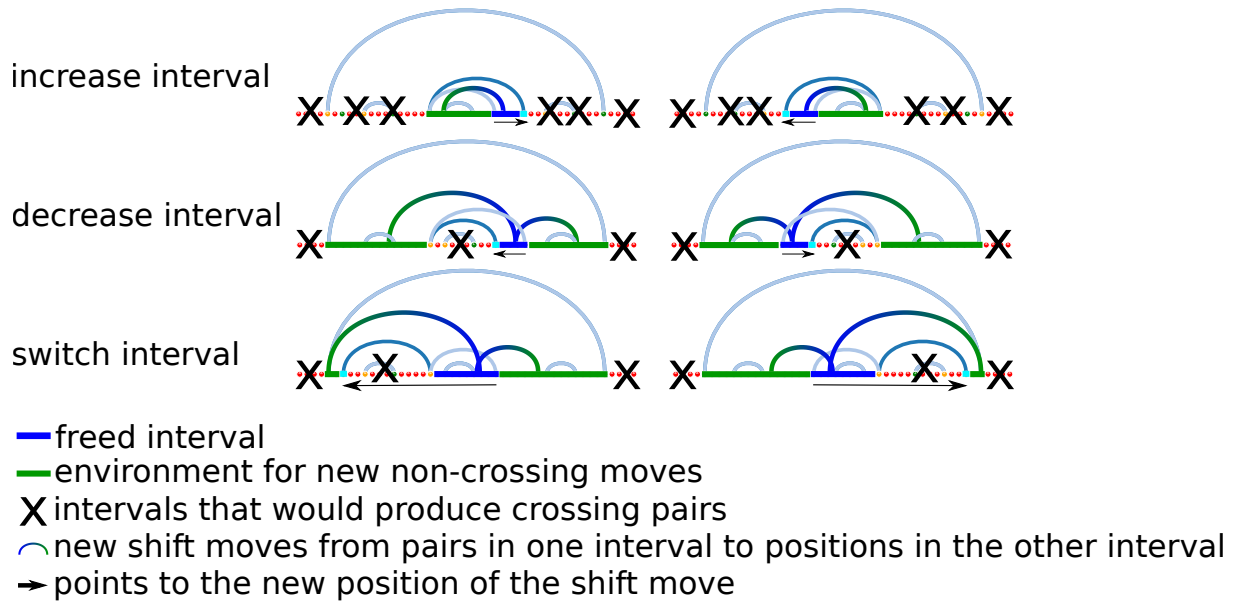
```
We have given a sequence and a structure.
Sequence  AAGGAAACC
Structure ..(.....)
Indices   123456789
The given base pair is (3,9) and the neighbors are the insertion (4, 8), the deletion (-3,-9), the
shift (3,-8)
and the shift (-4, 9).
This leads to the neighbored structures:
... (....)
.....
... (....)
.... (....)
```

A simple method to construct all insertions is to iterate over the positions of a sequence twice. The first iteration has the index  $i$  in  $[1, \text{sequence length}]$ , the second iteration has the index  $j$  in  $[i+1, \text{sequence length}]$ . All pairs  $(i, j)$  with compatible letters and which are non-crossing with present base pairs are valid neighbored insertion moves. Valid deletion moves are all present base pairs with negative sign. Valid shift moves are constructed by taking all paired positions as fix position of a shift move and iterating over all positions of the sequence. If the letters of a position are compatible and if it the move is non-crossing with existing base pairs, we have a valid shift move. The method of generating shift moves can be accelerated by skipping neighbored base pairs.

If we need to construct all neighbors several times for subsequent moves, we can speed up the task by using the move set of the previous structure. The previous move set has to be filtered, such that all moves that would cross the next selected move are non-crossing. Next, the selected move has to be removed. Then one has to only to generate all moves that were not possible before. One move is the inverted selected move (if it was an insertion, simply make the indices negative). The generation of all other new moves is different and depends on the selected move. It is easy for an insertion move, because we have only to include all non-crossing shift moves, that are possible with the new base pair. For that we can either iterate over the sequence or we can select all crossing shift moves in the filter procedure and convert them into shifts.

The generation of new moves given a deletion is a little bit more complex, because we can create more moves. At first we can insert the deleted pair as insertion move. Then we generate all insertions that would have crossed the deleted base pair. Finally we construct all crossing shift moves.

If the given move is a shift, we can save much time by specifying the intervals for the generation of new moves. The interval which was enclosed by the positive position of the shift move and the previous paired position is the freed interval after applying the move. This freed interval includes all positions and base pairs that we need to construct new insertions and shifts. All these new moves have one position in the freed interval and the other position in the environment of the freed interval. The environment are all position which are outside the freed interval, but within the same enclosing loop of the shift move. The environment for valid base pairs can be divided into one or more intervals, depending on the shift move. The following examples describe a few scenarios to specify the intervals of the environment.



Given the intervals of the environment and the freed interval, the new shift moves can be constructed quickly. One has to take all positions of pairs from the environment in order to create valid pairs with positions in the freed interval. The same procedure can be applied for the other direction. This is taking all paired positions within the freed interval in order to look for pairs with valid positions in the intervals of the environment. Collaboration diagram for Neighborhood Relation and Move Sets for Secondary Structures:

## Files

- file [move.h](#)  
*Methods to operate with structural neighbors of RNA secondary structures.*
- file [neighbor.h](#)  
*Methods to compute the neighbors of an RNA secondary structure.*

## Data Structures

- struct [vrna\\_move\\_s](#)  
*An atomic representation of the transition / move from one structure to its neighbor. [More...](#)*

## Macros

- `#define VRNA_MOVESET_INSERTION 4`  
*Option flag indicating insertion move.*
- `#define VRNA_MOVESET_DELETION 8`  
*Option flag indicating deletion move.*
- `#define VRNA_MOVESET_SHIFT 16`  
*Option flag indicating shift move.*
- `#define VRNA_MOVESET_NO_LP 32`  
*Option flag indicating moves without lonely base pairs.*
- `#define VRNA_MOVESET_DEFAULT (VRNA_MOVESET_INSERTION | VRNA_MOVESET_DELETION)`  
*Option flag indicating default move set, i.e. insertions/deletion of a base pair.*
- `#define VRNA_NEIGHBOR_CHANGE 1`  
*State indicator for a neighbor that has been changed.*
- `#define VRNA_NEIGHBOR_INVALID 2`  
*State indicator for a neighbor that has been invalidated.*
- `#define VRNA_NEIGHBOR_NEW 3`  
*State indicator for a neighbor that has become newly available.*

## Typedefs

- typedef struct `vrna_move_s` `vrna_move_t`  
*A single move that transforms a secondary structure into one of its neighbors.*
- typedef void() `vrna_callback_move_update`(`vrna_fold_compound_t` \*fc, `vrna_move_t` neighbor, unsigned int state, void \*data)  
*Prototype of the neighborhood update callback.*

## Functions

- `vrna_move_t` `vrna_move_init` (int pos\_5, int pos\_3)  
*Create an atomic move.*
- void `vrna_move_list_free` (`vrna_move_t` \*moves)
- void `vrna_move_apply` (short \*pt, const `vrna_move_t` \*m)  
*Apply a particular move / transition to a secondary structure, i.e. transform a structure.*
- int `vrna_move_is_removal` (const `vrna_move_t` \*m)  
*Test whether a move is a base pair removal.*
- int `vrna_move_is_insertion` (const `vrna_move_t` \*m)  
*Test whether a move is a base pair insertion.*
- int `vrna_move_is_shift` (const `vrna_move_t` \*m)  
*Test whether a move is a base pair shift.*
- int `vrna_move_compare` (const `vrna_move_t` \*a, const `vrna_move_t` \*b, const short \*pt)  
*Compare two moves.*
- void `vrna_loopidx_update` (int \*loopidx, const short \*pt, int length, const `vrna_move_t` \*m)  
*Alters the loopIndices array that was constructed with `vrna_loopidx_from_ptable()`.*
- `vrna_move_t` \* `vrna_neighbors` (`vrna_fold_compound_t` \*vc, const short \*pt, unsigned int options)  
*Generate neighbors of a secondary structure.*
- `vrna_move_t` \* `vrna_neighbors_successive` (const `vrna_fold_compound_t` \*vc, const `vrna_move_t` \*curr↔\_move, const short \*prev\_pt, const `vrna_move_t` \*prev\_neighbors, int size\_prev\_neighbors, int \*size\_↔neighbors, unsigned int options)  
*Generate neighbors of a secondary structure (the fast way)*
- int `vrna_move_neighbor_diff_cb` (`vrna_fold_compound_t` \*fc, short \*ptable, `vrna_move_t` move, `vrna_callback_move_update` \*cb, void \*data, unsigned int options)  
*Apply a move to a secondary structure and indicate which neighbors have changed consequentially.*
- `vrna_move_t` \* `vrna_move_neighbor_diff` (`vrna_fold_compound_t` \*fc, short \*ptable, `vrna_move_t` move, `vrna_move_t` \*\*invalid\_moves, unsigned int options)  
*Apply a move to a secondary structure and indicate which neighbors have changed consequentially.*

## 16.37.2 Data Structure Documentation

### 16.37.2.1 struct `vrna_move_s`

An atomic representation of the transition / move from one structure to its neighbor.

An atomic transition / move may be one of the following:

- a **base pair insertion**,
- a **base pair removal**, or
- a **base pair shift** where an existing base pair changes one of its pairing partner.

These moves are encoded by two integer values that represent the affected 5' and 3' nucleotide positions. Furthermore, we use the following convention on the signedness of these encodings:

- both values are positive for *insertion moves*
- both values are negative for *base pair removals*
- both values have different signedness for *shift moves*, where the positive value indicates the nucleotide that stays constant, and the others absolute value is the new pairing partner

**Note**

A value of 0 in either field is used as list-end indicator and doesn't represent any valid move.

Collaboration diagram for `vrna_move_s`:

**Data Fields**

- `int pos_5`  
*The (absolute value of the) 5' position of a base pair, or any position of a shifted pair.*
- `int pos_3`  
*The (absolute value of the) 3' position of a base pair, or any position of a shifted pair.*
- `vrna_move_t * next`  
*The next base pair (if an elementary move changes more than one base pair), or `NULL` Has to be terminated with move 0,0.*

**16.37.3 Macro Definition Documentation****16.37.3.1 VRNA\_MOVESET\_INSERTION**

```
#define VRNA_MOVESET_INSERTION 4
#include <ViennaRNA/landscape/move.h>
```

Option flag indicating insertion move.

See also

[vrna\\_neighbors\(\)](#), [vrna\\_neighbors\\_successive](#), [vrna\\_path\(\)](#)

**16.37.3.2 VRNA\_MOVESET\_DELETION**

```
#define VRNA_MOVESET_DELETION 8
#include <ViennaRNA/landscape/move.h>
```

Option flag indicating deletion move.

See also

[vrna\\_neighbors\(\)](#), [vrna\\_neighbors\\_successive](#), [vrna\\_path\(\)](#)

**16.37.3.3 VRNA\_MOVESET\_SHIFT**

```
#define VRNA_MOVESET_SHIFT 16
#include <ViennaRNA/landscape/move.h>
```

Option flag indicating shift move.

See also

[vrna\\_neighbors\(\)](#), [vrna\\_neighbors\\_successive](#), [vrna\\_path\(\)](#)

**16.37.3.4 VRNA\_MOVESET\_NO\_LP**

```
#define VRNA_MOVESET_NO_LP 32
#include <ViennaRNA/landscape/move.h>
```

Option flag indicating moves without lonely base pairs.

See also

[vrna\\_neighbors\(\)](#), [vrna\\_neighbors\\_successive](#), [vrna\\_path\(\)](#)



**16.37.3.5 VRNA\_MOVESET\_DEFAULT**

```
#define VRNA_MOVESET_DEFAULT (VRNA_MOVESET_INSERTION | VRNA_MOVESET_DELETION)
#include <ViennaRNA/landscape/move.h>
```

Option flag indicating default move set, i.e. insertions/deletion of a base pair.

See also

[vrna\\_neighbors\(\)](#), [vrna\\_neighbors\\_successive](#), [vrna\\_path\(\)](#)

**16.37.3.6 VRNA\_NEIGHBOR\_CHANGE**

```
#define VRNA_NEIGHBOR_CHANGE 1
#include <ViennaRNA/landscape/neighbor.h>
```

State indicator for a neighbor that has been changed.

See also

[vrna\\_move\\_neighbor\\_diff\\_cb\(\)](#)

**16.37.3.7 VRNA\_NEIGHBOR\_INVALID**

```
#define VRNA_NEIGHBOR_INVALID 2
#include <ViennaRNA/landscape/neighbor.h>
```

State indicator for a neighbor that has been invalidated.

See also

[vrna\\_move\\_neighbor\\_diff\\_cb\(\)](#)

**16.37.3.8 VRNA\_NEIGHBOR\_NEW**

```
#define VRNA_NEIGHBOR_NEW 3
#include <ViennaRNA/landscape/neighbor.h>
```

State indicator for a neighbor that has become newly available.

See also

[vrna\\_move\\_neighbor\\_diff\\_cb\(\)](#)

**16.37.4 Typedef Documentation****16.37.4.1 vrna\_callback\_move\_update**

```
typedef void() vrna_callback_move_update(vrna_fold_compound_t *fc, vrna_move_t neighbor, unsigned
int state, void *data)
#include <ViennaRNA/landscape/neighbor.h>
```

Prototype of the neighborhood update callback.

See also

[vrna\\_move\\_neighbor\\_diff\\_cb\(\)](#), [VRNA\\_NEIGHBOR\\_CHANGE](#), [VRNA\\_NEIGHBOR\\_INVALID](#), [VRNA\\_NEIGHBOR\\_NEW](#)

**Parameters**

|                 |                                                                                       |
|-----------------|---------------------------------------------------------------------------------------|
| <i>fc</i>       | The fold compound the calling function is working on                                  |
| <i>neighbor</i> | The move that generates the (changed or new) neighbor                                 |
| <i>state</i>    | The state of the neighbor (move) as supplied by argument <i>neighbor</i>              |
| <i>data</i>     | Some arbitrary data pointer as passed to <a href="#">vrna_move_neighbor_diff_cb()</a> |

## 16.37.5 Function Documentation

### 16.37.5.1 `vrna_move_init()`

```
vrna_move_t vrna_move_init (
    int pos_5,
    int pos_3 )
#include <ViennaRNA/landscape/move.h>
Create an atomic move.
```

See also

[vrna\\_move\\_s](#)

#### Parameters

|                    |                                                                                                        |
|--------------------|--------------------------------------------------------------------------------------------------------|
| <code>pos_5</code> | The 5' position of the move (positive for insertions, negative for removal, any value for shift moves) |
| <code>pos_3</code> | The 3' position of the move (positive for insertions, negative for removal, any value for shift moves) |

#### Returns

An atomic move as specified by `pos_5` and `pos_3`

### 16.37.5.2 `vrna_move_list_free()`

```
void vrna_move_list_free (
    vrna_move_t * moves )
#include <ViennaRNA/landscape/move.h>
delete all moves in a zero terminated list.
```

### 16.37.5.3 `vrna_move_apply()`

```
void vrna_move_apply (
    short * pt,
    const vrna_move_t * m )
#include <ViennaRNA/landscape/move.h>
Apply a particular move / transition to a secondary structure, i.e. transform a structure.
```

#### Parameters

|                      |                 |                                                          |
|----------------------|-----------------|----------------------------------------------------------|
| <code>in, out</code> | <code>pt</code> | The pair table representation of the secondary structure |
| <code>in</code>      | <code>m</code>  | The move to apply                                        |

### 16.37.5.4 `vrna_move_is_removal()`

```
int vrna_move_is_removal (
    const vrna_move_t * m )
#include <ViennaRNA/landscape/move.h>
Test whether a move is a base pair removal.
```

## Parameters

|          |                          |
|----------|--------------------------|
| <i>m</i> | The move to test against |
|----------|--------------------------|

## Returns

Non-zero if the move is a base pair removal, 0 otherwise

**16.37.5.5 vrna\_move\_is\_insertion()**

```
int vrna_move_is_insertion (
    const vrna_move_t * m )
#include <ViennaRNA/landscape/move.h>
Test whether a move is a base pair insertion.
```

## Parameters

|          |                          |
|----------|--------------------------|
| <i>m</i> | The move to test against |
|----------|--------------------------|

## Returns

Non-zero if the move is a base pair insertion, 0 otherwise

**16.37.5.6 vrna\_move\_is\_shift()**

```
int vrna_move_is_shift (
    const vrna_move_t * m )
#include <ViennaRNA/landscape/move.h>
Test whether a move is a base pair shift.
```

## Parameters

|          |                          |
|----------|--------------------------|
| <i>m</i> | The move to test against |
|----------|--------------------------|

## Returns

Non-zero if the move is a base pair shift, 0 otherwise

**16.37.5.7 vrna\_move\_compare()**

```
int vrna_move_compare (
    const vrna_move_t * a,
    const vrna_move_t * b,
    const short * pt )
#include <ViennaRNA/landscape/move.h>
```

Compare two moves.

The function compares two moves *a* and *b* and returns whether move *a* is lexicographically smaller (-1), larger (1) or equal to move *b*.

If any of the moves *a* or *b* is a shift move, this comparison only makes sense in a structure context. Thus, the third argument with the current structure must be provided.

**Note**

This function returns 0 (equality) upon any error, e.g. missing input

**Warning**

Currently, shift moves are not supported!

**Parameters**

|           |                                                                                                                                 |
|-----------|---------------------------------------------------------------------------------------------------------------------------------|
| <i>a</i>  | The first move of the comparison                                                                                                |
| <i>b</i>  | The second move of the comparison                                                                                               |
| <i>pt</i> | The pair table of the current structure that is compatible with both moves (maybe NULL if moves are guaranteed to be no shifts) |

**Returns**

-1 if  $a < b$ , 1 if  $a > b$ , 0 otherwise

**16.37.5.8 vrna\_loopidx\_update()**

```
void vrna_loopidx_update (
    int * loopidx,
    const short * pt,
    int length,
    const vrna_move_t * m )
```

#include <ViennaRNA/landscape/neighbor.h>

Alters the loopIndices array that was constructed with [vrna\\_loopidx\\_from\\_ptable\(\)](#).

The loopIndex of the current move will be inserted. The correctness of the input will not be checked because the speed should be optimized.

**Parameters**

|         |                |                                                    |
|---------|----------------|----------------------------------------------------|
| in, out | <i>loopidx</i> | The loop index data structure that needs an update |
| in      | <i>pt</i>      | A pair table on which the move will be executed    |
|         | <i>length</i>  | The length of the structure                        |
| in      | <i>m</i>       | The move that is applied to the current structure  |

**16.37.5.9 vrna\_neighbors()**

```
vrna_move_t * vrna_neighbors (
    vrna_fold_compound_t * vc,
    const short * pt,
    unsigned int options )
```

#include <ViennaRNA/landscape/neighbor.h>

Generate neighbors of a secondary structure.

This function allows one to generate all structural neighbors (according to a particular move set) of an RNA secondary structure. The neighborhood is then returned as a list of transitions / moves required to transform the current structure into the actual neighbor.

**See also**

[vrna\\_neighbors\\_successive\(\)](#), [vrna\\_move\\_apply\(\)](#), [VRNA\\_MOVESET\\_INSERTION](#), [VRNA\\_MOVESET\\_DELETION](#), [VRNA\\_MOVESET\\_SHIFT](#), [VRNA\\_MOVESET\\_DEFAULT](#)

## Parameters

|    |                |                                                                                        |
|----|----------------|----------------------------------------------------------------------------------------|
| in | <i>vc</i>      | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details |
| in | <i>pt</i>      | The pair table representation of the structure                                         |
|    | <i>options</i> | Options to modify the behavior of this function, e.g. available move set               |

## Returns

Neighbors as a list of moves / transitions (the last element in the list has both of its fields set to 0)

**SWIG Wrapper Notes** This function is attached as an overloaded method `neighbors()` to objects of type `fold_compound`. The optional parameter `options` defaults to `VRNA_MOVESET_DEFAULT` if it is omitted.

16.37.5.10 `vrna_neighbors_successive()`

```
vrna_move_t * vrna_neighbors_successive (
    const vrna_fold_compound_t * vc,
    const vrna_move_t * curr_move,
    const short * prev_pt,
    const vrna_move_t * prev_neighbors,
    int size_prev_neighbors,
    int * size_neighbors,
    unsigned int options )
#include <ViennaRNA/landscape/neighbor.h>
```

Generate neighbors of a secondary structure (the fast way)

This function implements a fast way to generate all neighbors of a secondary structure that results from successive applications of individual moves. The speed-up results from updating an already known list of valid neighbors before the individual move towards the current structure took place. In essence, this function removes neighbors that are not accessible anymore and inserts neighbors emerging after a move took place.

## See also

`vrna_neighbors()`, `vrna_move_apply()`, `VRNA_MOVESET_INSERTION`, `VRNA_MOVESET_DELETION`, `VRNA_MOVESET_SHIFT`, `VRNA_MOVESET_DEFAULT`

## Parameters

|     |                            |                                                                                           |
|-----|----------------------------|-------------------------------------------------------------------------------------------|
| in  | <i>vc</i>                  | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details    |
| in  | <i>curr_move</i>           | The move that was/will be applied to <code>prev_pt</code>                                 |
| in  | <i>prev_pt</i>             | A pair table representation of the structure before <code>curr_move</code> is/was applied |
| in  | <i>prev_neighbors</i>      | The list of neighbors of <code>prev_pt</code>                                             |
|     | <i>size_prev_neighbors</i> | The size of <code>prev_neighbors</code> , i.e. the lists length                           |
| out | <i>size_neighbors</i>      | A pointer to store the size / length of the new neighbor list                             |
|     | <i>options</i>             | Options to modify the behavior of this function, e.g. available move set                  |

## Returns

Neighbors as a list of moves / transitions (the last element in the list has both of its fields set to 0)

16.37.5.11 `vrna_move_neighbor_diff_cb()`

```
int vrna_move_neighbor_diff_cb (
    vrna_fold_compound_t * fc,
```

```

short * ptable,
vrna_move_t move,
vrna_callback_move_update * cb,
void * data,
unsigned int options )

```

```
#include <ViennaRNA/landscape/neighbor.h>
```

Apply a move to a secondary structure and indicate which neighbors have changed consequentially.

This function applies a move to a secondary structure and explores the local neighborhood of the affected loop. Any changes to previously compatible neighbors that have been affected by this loop will be reported through a callback function. In particular, any of the three cases might appear:

- A previously available neighbor move has changed, usually the free energy change of the move ([VRNA\\_NEIGHBOR\\_CHANGE](#))
- A previously available neighbor move became invalid ([VRNA\\_NEIGHBOR\\_INVALID](#))
- A new neighbor move becomes available ([VRNA\\_NEIGHBOR\\_NEW](#))

See also

[vrna\\_move\\_neighbor\\_diff\(\)](#), [VRNA\\_NEIGHBOR\\_CHANGE](#), [VRNA\\_NEIGHBOR\\_INVALID](#), [VRNA\\_NEIGHBOR\\_NEW](#), [vrna\\_callback\\_move\\_update](#)

#### Parameters

|                |                                                                                          |
|----------------|------------------------------------------------------------------------------------------|
| <i>fc</i>      | A fold compound for the RNA sequence(s) that this function operates on                   |
| <i>ptable</i>  | The current structure as pair table                                                      |
| <i>move</i>    | The move to apply                                                                        |
| <i>cb</i>      | The address of the callback function that is passed the neighborhood changes             |
| <i>data</i>    | An arbitrary data pointer that will be passed through to the callback function <i>cb</i> |
| <i>options</i> | Options to modify the behavior of this function, .e.g available move set                 |

#### Returns

Non-zero on success, 0 otherwise

#### 16.37.5.12 vrna\_move\_neighbor\_diff()

```

vrna_move_t * vrna_move_neighbor_diff (
    vrna_fold_compound_t * fc,
    short * ptable,
    vrna_move_t move,
    vrna_move_t ** invalid_moves,
    unsigned int options )

```

```
#include <ViennaRNA/landscape/neighbor.h>
```

Apply a move to a secondary structure and indicate which neighbors have changed consequentially.

Similar to [vrna\\_move\\_neighbor\\_diff\\_cb\(\)](#), this function applies a move to a secondary structure and reports back the neighbors of the current structure become affected by this move. Instead of executing a callback for each of the affected neighbors, this function compiles two lists of neighbor moves, one that is returned and consists of all moves that are novel or may have changed in energy, and a second, *invalid\_moves*, that consists of all the neighbor moves that become invalid, respectively.

#### Parameters

|               |                                                                        |
|---------------|------------------------------------------------------------------------|
| <i>fc</i>     | A fold compound for the RNA sequence(s) that this function operates on |
| <i>ptable</i> | The current structure as pair table                                    |

## Parameters

|                      |                                                                                      |
|----------------------|--------------------------------------------------------------------------------------|
| <i>move</i>          | The move to apply                                                                    |
| <i>invalid_moves</i> | The address of a move list where the function stores those moves that become invalid |
| <i>options</i>       | Options to modify the behavior of this function, .e.g available move set             |

## Returns

A list of moves that might have changed in energy or are novel compared to the structure before application of the move

## 16.38 (Re-)folding Paths, Saddle Points, Energy Barriers, and Local Minima

API for various RNA folding path algorithms.

### 16.38.1 Detailed Description

API for various RNA folding path algorithms.

This part of our API allows for generating RNA secondary structure (re-)folding paths between two secondary structures or simply starting from a single structure. This is most important if an estimate of the refolding energy barrier between two structures is required, or a structure's corresponding local minimum needs to be determined, e.g. through a gradient-descent walk.

This part of the interface is further split into the following sections:

- [Direct Refolding Paths between two Secondary Structures](#), and
- [Folding Paths that start at a single Secondary Structure](#)

Collaboration diagram for (Re-)folding Paths, Saddle Points, Energy Barriers, and Local Minima:

### Modules

- [Direct Refolding Paths between two Secondary Structures](#)  
*Heuristics to explore direct, optimal (re-)folding paths between two secondary structures.*
- [Folding Paths that start at a single Secondary Structure](#)  
*Implementation of gradient- and random walks starting from a single secondary structure.*
- [Deprecated Interface for \(Re-\)folding Paths, Saddle Points, and Energy Barriers](#)

### Files

- file [findpath.h](#)  
*A breadth-first search heuristic for optimal direct folding paths.*
- file [paths.h](#)  
*API for computing (optimal) (re-)folding paths between secondary structures.*
- file [walk.h](#)  
*Methods to generate particular paths such as gradient or random walks through the energy landscape of an RNA sequence.*

### Data Structures

- struct [vrna\\_path\\_s](#)  
*An element of a refolding path list. [More...](#)*

## Macros

- `#define VRNA_PATH_TYPE_DOT_BRACKET 1U`  
*Flag to indicate producing a (re-)folding path as list of dot-bracket structures.*
- `#define VRNA_PATH_TYPE_MOVES 2U`  
*Flag to indicate producing a (re-)folding path as list of transition moves.*

## Typedefs

- `typedef struct vrna_path_s vrna_path_t`  
*Typename for the refolding path data structure `vrna_path_s`.*
- `typedef struct vrna_path_options_s * vrna_path_options_t`  
*Options data structure for (re-)folding path implementations.*

## Functions

- `void vrna_path_free (vrna_path_t *path)`  
*Release (free) memory occupied by a (re-)folding path.*
- `void vrna_path_options_free (vrna_path_options_t options)`  
*Release (free) memory occupied by an options data structure for (re-)folding path implementations.*

## 16.38.2 Data Structure Documentation

### 16.38.2.1 struct vrna\_path\_s

An element of a refolding path list.

Usually, one has to deal with an array of `vrna_path_s`, e.g. returned from one of the refolding-path algorithms. Since in most cases the length of the list is not known in advance, such lists have an *end-of-list* marker, which is either:

- a value of `NULL` for `vrna_path_s::s` if `vrna_path_s::type = VRNA_PATH_TYPE_DOT_BRACKET`, or
- a `vrna_path_s::move` with zero in both fields `vrna_move_t::pos_5` and `vrna_move_t::pos_3` if `vrna_path_s::type = VRNA_PATH_TYPE_MOVES`.

In the following we show an example for how to cover both cases of iteration:

```
vrna_path_t *ptr = path; // path was returned from one of the refolding path functions, e.g.
    vrna_path_direct()
if (ptr) {
    if (ptr->type == VRNA_PATH_TYPE_DOT_BRACKET) {
        for (; ptr->s; ptr++)
            printf("%s [%6.2f]\n", ptr->s, ptr->en);
    } else if (ptr->type == VRNA_PATH_TYPE_MOVES) {
        for (; ptr->move.pos_5 != 0; ptr++)
            printf("move %d:%d, dG = %6.2f\n", ptr->move.pos_5, ptr->move.pos_3, ptr->en);
    }
}
```

See also

[vrna\\_path\\_free\(\)](#)

Collaboration diagram for `vrna_path_s`:

## Data Fields

- unsigned int `type`  
*The type of the path element.*
- double `en`  
*Free energy of current structure.*
- char \* `s`  
*Secondary structure in dot-bracket notation.*
- `vrna_move_t` `move`  
*Move that transforms the previous structure into it's next neighbor along the path.*



### 16.38.2.1.1 Field Documentation

#### 16.38.2.1.1.1 `type` `unsigned int vrna_path_s::type`

The type of the path element.

A value of `VRNA_PATH_TYPE_DOT_BRACKET` indicates that `vrna_path_s::s` consists of the secondary structure in dot-bracket notation, and `vrna_path_s::en` the corresponding free energy.

On the other hand, if the value is `VRNA_PATH_TYPE_MOVES`, `vrna_path_s::s` is `NULL` and `vrna_path_s::move` is set to the transition move that transforms a previous structure into it's neighbor along the path. In this case, the attribute `vrna_path_s::en` states the change in free energy with respect to the structure before application of `vrna_path_s::move`.

## 16.38.3 Macro Definition Documentation

### 16.38.3.1 `VRNA_PATH_TYPE_DOT_BRACKET`

```
#define VRNA_PATH_TYPE_DOT_BRACKET 1U
#include <ViennaRNA/landscape/paths.h>
```

Flag to indicate producing a (re-)folding path as list of dot-bracket structures.

See also

[vrna\\_path\\_t](#), [vrna\\_path\\_options\\_findpath\(\)](#), [vrna\\_path\\_direct\(\)](#), [vrna\\_path\\_direct\\_ub\(\)](#)

### 16.38.3.2 `VRNA_PATH_TYPE_MOVES`

```
#define VRNA_PATH_TYPE_MOVES 2U
#include <ViennaRNA/landscape/paths.h>
```

Flag to indicate producing a (re-)folding path as list of transition moves.

See also

[vrna\\_path\\_t](#), [vrna\\_path\\_options\\_findpath\(\)](#), [vrna\\_path\\_direct\(\)](#), [vrna\\_path\\_direct\\_ub\(\)](#)

## 16.38.4 Function Documentation

### 16.38.4.1 `vrna_path_free()`

```
void vrna_path_free (
    vrna_path_t * path )
#include <ViennaRNA/landscape/paths.h>
```

Release (free) memory occupied by a (re-)folding path.

See also

[vrna\\_path\\_direct\(\)](#), [vrna\\_path\\_direct\\_ub\(\)](#), [vrna\\_path\\_findpath\(\)](#), [vrna\\_path\\_findpath\\_ub\(\)](#)

Parameters

|             |                                 |
|-------------|---------------------------------|
| <i>path</i> | The refolding path to be free'd |
|-------------|---------------------------------|

### 16.38.4.2 vrna\_path\_options\_free()

```
void vrna_path_options_free (
    vrna_path_options_t options )
#include <ViennaRNA/landscape/paths.h>
```

Release (free) memory occupied by an options data structure for (re-)folding path implementations.

See also

[vrna\\_path\\_options\\_findpath\(\)](#), [vrna\\_path\\_direct\(\)](#), [vrna\\_path\\_direct\\_ub\(\)](#)

#### Parameters

|                |                                         |
|----------------|-----------------------------------------|
| <i>options</i> | The options data structure to be free'd |
|----------------|-----------------------------------------|

## 16.39 Direct Refolding Paths between two Secondary Structures

Heuristics to explore direct, optimal (re-)folding paths between two secondary structures.

### 16.39.1 Detailed Description

Heuristics to explore direct, optimal (re-)folding paths between two secondary structures.

Collaboration diagram for Direct Refolding Paths between two Secondary Structures:

#### Functions

- [int vrna\\_path\\_findpath\\_saddle](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int width)  
*Find energy of a saddle point between 2 structures (search only direct path)*
- [int vrna\\_path\\_findpath\\_saddle\\_ub](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int width, int maxE)  
*Find energy of a saddle point between 2 structures (search only direct path)*
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_findpath](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int width)  
*Find refolding path between 2 structures (search only direct path)*
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_findpath\\_ub](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int width, int maxE)  
*Find refolding path between 2 structures (search only direct path)*
- [vrna\\_path\\_options\\_t](#) [vrna\\_path\\_options\\_findpath](#) (int width, unsigned int type)  
*Create options data structure for findpath direct (re-)folding path heuristic.*
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_direct](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, [vrna\\_path\\_options\\_t](#) options)  
*Determine an optimal direct (re-)folding path between two secondary structures.*
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_direct\\_ub](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int maxE, [vrna\\_path\\_options\\_t](#) options)  
*Determine an optimal direct (re-)folding path between two secondary structures.*

### 16.39.2 Function Documentation

#### 16.39.2.1 vrna\_path\_findpath\_saddle()

```
int vrna_path_findpath_saddle (
    vrna_fold_compound_t * fc,
    const char * s1,
```

```

    const char * s2,
    int width )
#include <ViennaRNA/landscape/findpath.h>

```

Find energy of a saddle point between 2 structures (search only direct path)

This function uses an implementation of the *findpath* algorithm [7] for near-optimal direct refolding path prediction. Model details, and energy parameters are used as provided via the parameter 'fc'. The `vrna_fold_compound_t` does not require memory for any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_DEFAULT);
```

See also

[vrna\\_path\\_findpath\\_saddle\\_ub\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#), [vrna\\_path\\_findpath\(\)](#)

#### Parameters

|              |                                                                                               |
|--------------|-----------------------------------------------------------------------------------------------|
| <i>fc</i>    | The <a href="#">vrna_fold_compound_t</a> with precomputed sequence encoding and model details |
| <i>s1</i>    | The start structure in dot-bracket notation                                                   |
| <i>s2</i>    | The target structure in dot-bracket notation                                                  |
| <i>width</i> | A number specifying how many strutures are being kept at each step during the search          |

#### Returns

The saddle energy in 10cal/mol

**SWIG Wrapper Notes** This function is attached as an overloaded method *path\_findpath\_saddle()* to objects of type *fold\_compound*. The optional parameter *width* defaults to 1 if it is omitted.

#### 16.39.2.2 vrna\_path\_findpath\_saddle\_ub()

```

int vrna_path_findpath_saddle_ub (
    vrna_fold_compound_t * fc,
    const char * s1,
    const char * s2,
    int width,
    int maxE )
#include <ViennaRNA/landscape/findpath.h>

```

Find energy of a saddle point between 2 structures (search only direct path)

This function uses an implementation of the *findpath* algorithm [7] for near-optimal direct refolding path prediction. Model details, and energy parameters are used as provided via the parameter 'fc'. The `vrna_fold_compound_t` does not require memory for any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_DEFAULT);
```

#### Warning

The argument `maxE` ( $E_{max}$ ) enables one to specify an upper bound, or maximum free energy for the saddle point between the two input structures. If no path with  $E_{saddle} < E_{max}$  is found, the function simply returns `maxE`

See also

[vrna\\_path\\_findpath\\_saddle\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#), [vrna\\_path\\_findpath\(\)](#)

#### Parameters

|              |                                                                                               |
|--------------|-----------------------------------------------------------------------------------------------|
| <i>fc</i>    | The <a href="#">vrna_fold_compound_t</a> with precomputed sequence encoding and model details |
| <i>s1</i>    | The start structure in dot-bracket notation                                                   |
| <i>s2</i>    | The target structure in dot-bracket notation                                                  |
| <i>width</i> | A number specifying how many strutures are being kept at each step during the search          |
| <i>maxE</i>  | An upper bound for the saddle point energy in 10cal/mol                                       |

## Returns

The saddle energy in 10cal/mol

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_findpath_saddle()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted, while the optional parameter `maxE` defaults to `INF`. In case the function did not find a path with  $E_{saddle} < E_{max}$  the function returns a `NULL` object, i.e. `undef` for Perl and `None` for Python.

### 16.39.2.3 vrna\_path\_findpath()

```
vrna_path_t * vrna_path_findpath (
    vrna_fold_compound_t * fc,
    const char * s1,
    const char * s2,
    int width )
#include <ViennaRNA/landscape/findpath.h>
```

Find refolding path between 2 structures (search only direct path)

This function uses an implementation of the *findpath* algorithm [7] for near-optimal direct refolding path prediction. Model details, and energy parameters are used as provided via the parameter 'fc'. The `vrna_fold_compound_t` does not require memory for any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_DEFAULT);
```

## See also

[vrna\\_path\\_findpath\\_ub\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#), [vrna\\_path\\_findpath\\_saddle\(\)](#)

## Parameters

|              |                                                                                               |
|--------------|-----------------------------------------------------------------------------------------------|
| <i>fc</i>    | The <a href="#">vrna_fold_compound_t</a> with precomputed sequence encoding and model details |
| <i>s1</i>    | The start structure in dot-bracket notation                                                   |
| <i>s2</i>    | The target structure in dot-bracket notation                                                  |
| <i>width</i> | A number specifying how many strutures are being kept at each step during the search          |

## Returns

The saddle energy in 10cal/mol

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_findpath()` to objects of type `fold_compound`. The optional parameter `width` defaults to 1 if it is omitted.

### 16.39.2.4 vrna\_path\_findpath\_ub()

```
vrna_path_t * vrna_path_findpath_ub (
    vrna_fold_compound_t * fc,
    const char * s1,
    const char * s2,
    int width,
    int maxE )
#include <ViennaRNA/landscape/findpath.h>
```

Find refolding path between 2 structures (search only direct path)

This function uses an implementation of the *findpath* algorithm [7] for near-optimal direct refolding path prediction. Model details, and energy parameters are used as provided via the parameter 'fc'. The `vrna_fold_compound_t` does not require memory for any DP matrices, but requires all most basic init values as one would get from a call like this:

```
fc = vrna_fold_compound(sequence, NULL, VRNA_OPTION_DEFAULT);
```

**Warning**

The argument `maxE` enables one to specify an upper bound, or maximum free energy for the saddle point between the two input structures. If no path with  $E_{saddle} < E_{max}$  is found, the function simply returns `NULL`

**See also**

[vrna\\_path\\_findpath\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_t](#), [vrna\\_path\\_findpath\\_saddle\(\)](#)

**Parameters**

|              |                                                                                               |
|--------------|-----------------------------------------------------------------------------------------------|
| <i>fc</i>    | The <a href="#">vrna_fold_compound_t</a> with precomputed sequence encoding and model details |
| <i>s1</i>    | The start structure in dot-bracket notation                                                   |
| <i>s2</i>    | The target structure in dot-bracket notation                                                  |
| <i>width</i> | A number specifying how many strutures are being kept at each step during the search          |
| <i>maxE</i>  | An upper bound for the saddle point energy in 10cal/mol                                       |

**Returns**

The saddle energy in 10cal/mol

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_findpath()` to objects of type `fold↔_compound`. The optional parameter `width` defaults to 1 if it is omitted, while the optional parameter `maxE` defaults to `INF`. In case the function did not find a path with  $E_{saddle} < E_{max}$  the function returns an empty list.

**16.39.2.5 vrna\_path\_options\_findpath()**

```
vrna_path_options_t vrna_path_options_findpath (
    int width,
    unsigned int type )
```

```
#include <ViennaRNA/landscape/paths.h>
```

Create options data structure for findpath direct (re-)folding path heuristic.

This function returns an options data structure that switches the [vrna\\_path\\_direct\(\)](#) and [vrna\\_path\\_direct\\_ub\(\)](#) API functions to use the *findpath* [7] heuristic. The parameter `width` specifies the width of the breadth-first search while the second parameter `type` allows one to set the type of the returned (re-)folding path.

Currently, the following return types are available:

- A list of dot-bracket structures and corresponding free energy (flag: [VRNA\\_PATH\\_TYPE\\_DOT\\_BRACKET](#))
- A list of transition moves and corresponding free energy changes (flag: [VRNA\\_PATH\\_TYPE\\_MOVES](#))

**See also**

[VRNA\\_PATH\\_TYPE\\_DOT\\_BRACKET](#), [VRNA\\_PATH\\_TYPE\\_MOVES](#), [vrna\\_path\\_options\\_free\(\)](#), [vrna\\_path\\_direct\(\)](#), [vrna\\_path\\_direct\\_ub\(\)](#)

**Parameters**

|              |                                                                           |
|--------------|---------------------------------------------------------------------------|
| <i>width</i> | Width of the breath-first search strategy                                 |
| <i>type</i>  | Setting that specifies how the return (re-)folding path should be encoded |

## Returns

An options data structure with settings for the findpath direct path heuristic

**SWIG Wrapper Notes** This function is available as overloaded function `path_options_findpath()`. The optional parameter `width` defaults to 10 if omitted, while the optional parameter `type` defaults to `VRNA_PATH_TYPE_DOT_BRACKET`.

16.39.2.6 `vrna_path_direct()`

```
vrna_path_t * vrna_path_direct (
    vrna_fold_compound_t * fc,
    const char * s1,
    const char * s2,
    vrna_path_options_t options )
#include <ViennaRNA/landscape/paths.h>
```

Determine an optimal direct (re-)folding path between two secondary structures.

This is the generic wrapper function to retrieve (an optimal) (re-)folding path between two secondary structures `s1` and `s2`. The actual algorithm that is used to generate the (re-)folding path is determined by the settings specified in the `options` data structure. This data structure also determines the return type, which might be either:

- a list of dot-bracket structures with corresponding free energy, or
- a list of transition moves with corresponding free energy change

If the `options` parameter is passed a `NULL` pointer, this function defaults to the *findpath heuristic* [7] with a breadth-first search width of 10, and the returned path consists of dot-bracket structures with corresponding free energies.

See also

[vrna\\_path\\_direct\\_ub\(\)](#), [vrna\\_path\\_options\\_findpath\(\)](#), [vrna\\_path\\_options\\_free\(\)](#), [vrna\\_path\\_free\(\)](#)

## Parameters

|                      |                                                                                                                   |
|----------------------|-------------------------------------------------------------------------------------------------------------------|
| <code>fc</code>      | The <code>vrna_fold_compound_t</code> with precomputed sequence encoding and model details                        |
| <code>s1</code>      | The start structure in dot-bracket notation                                                                       |
| <code>s2</code>      | The target structure in dot-bracket notation                                                                      |
| <code>options</code> | An options data structure that specifies the path heuristic and corresponding settings (maybe <code>NULL</code> ) |

## Returns

An optimal (re-)folding path between the two input structures

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_direct()` to objects of type `fold_compound`. The optional parameter `options` defaults to `NULL` if it is omitted.

16.39.2.7 `vrna_path_direct_ub()`

```
vrna_path_t * vrna_path_direct_ub (
    vrna_fold_compound_t * fc,
    const char * s1,
    const char * s2,
    int maxE,
    vrna_path_options_t options )
#include <ViennaRNA/landscape/paths.h>
```

Determine an optimal direct (re-)folding path between two secondary structures.

This function is similar to `vrna_path_direct()`, but allows to specify an *upper-bound* for the saddle point energy. The underlying algorithms will stop determining an (optimal) (re-)folding path, if none can be found that has a saddle point below the specified upper-bound threshold `maxE`.

#### Warning

The argument `maxE` enables one to specify an upper bound, or maximum free energy for the saddle point between the two input structures. If no path with  $E_{saddle} < E_{max}$  is found, the function simply returns `NULL`.

#### See also

`vrna_path_direct_ub()`, `vrna_path_options_findpath()`, `vrna_path_options_free()`, `vrna_path_free()`

#### Parameters

|                      |                                                                                                                   |
|----------------------|-------------------------------------------------------------------------------------------------------------------|
| <code>fc</code>      | The <code>vrna_fold_compound_t</code> with precomputed sequence encoding and model details                        |
| <code>s1</code>      | The start structure in dot-bracket notation                                                                       |
| <code>s2</code>      | The target structure in dot-bracket notation                                                                      |
| <code>maxE</code>    | Upper bound for the saddle point along the (re-)folding path                                                      |
| <code>options</code> | An options data structure that specifies the path heuristic and corresponding settings (maybe <code>NULL</code> ) |

#### Returns

An optimal (re-)folding path between the two input structures

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_direct()` to objects of type `fold_compound`. The optional parameter `maxE` defaults to `#INT_MAX - 1` if it is omitted, while the optional parameter `options` defaults to `NULL`. In case the function did not find a path with  $E_{saddle} < E_{max}$  it returns an empty list.

## 16.40 Folding Paths that start at a single Secondary Structure

Implementation of gradient- and random walks starting from a single secondary structure.

### 16.40.1 Detailed Description

Implementation of gradient- and random walks starting from a single secondary structure.

Collaboration diagram for Folding Paths that start at a single Secondary Structure:

#### Macros

- `#define VRNA_PATH_STEEPEST_DESCENT 128`  
*Option flag to request a steepest descent / gradient path.*
- `#define VRNA_PATH_RANDOM 256`  
*Option flag to request a random walk path.*
- `#define VRNA_PATH_NO_TRANSITION_OUTPUT 512`  
*Option flag to omit returning the transition path.*
- `#define VRNA_PATH_DEFAULT (VRNA_PATH_STEEPEST_DESCENT | VRNA_MOVESET_DEFAULT)`  
*Option flag to request defaults (steepest descent / default move set)*

#### Functions

- `vrna_move_t * vrna_path (vrna_fold_compound_t *vc, short *pt, unsigned int steps, unsigned int options)`  
*Compute a path, store the final structure, and return a list of transition moves from the start to the final structure.*
- `vrna_move_t * vrna_path_gradient (vrna_fold_compound_t *vc, short *pt, unsigned int options)`

*Compute a steepest descent / gradient path, store the final structure, and return a list of transition moves from the start to the final structure.*

- [vrna\\_move\\_t](#) \* [vrna\\_path\\_random](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, short \*pt, unsigned int steps, unsigned int options)

*Generate a random walk / path of a given length, store the final structure, and return a list of transition moves from the start to the final structure.*

## 16.40.2 Macro Definition Documentation

### 16.40.2.1 VRNA\_PATH\_STEEPEST\_DESCENT

```
#define VRNA_PATH_STEEPEST_DESCENT 128
#include <ViennaRNA/landscape/walk.h>
```

Option flag to request a steepest descent / gradient path.

See also

[vrna\\_path\(\)](#)

### 16.40.2.2 VRNA\_PATH\_RANDOM

```
#define VRNA_PATH_RANDOM 256
#include <ViennaRNA/landscape/walk.h>
```

Option flag to request a random walk path.

See also

[vrna\\_path\(\)](#)

### 16.40.2.3 VRNA\_PATH\_NO\_TRANSITION\_OUTPUT

```
#define VRNA_PATH_NO_TRANSITION_OUTPUT 512
#include <ViennaRNA/landscape/walk.h>
```

Option flag to omit returning the transition path.

See also

[vrna\\_path\(\)](#), [vrna\\_path\\_gradient\(\)](#), [vrna\\_path\\_random\(\)](#)

### 16.40.2.4 VRNA\_PATH\_DEFAULT

```
#define VRNA_PATH_DEFAULT (VRNA_PATH_STEEPEST_DESCENT | VRNA_MOVESET_DEFAULT)
#include <ViennaRNA/landscape/walk.h>
```

Option flag to request defaults (steepest descent / default move set)

See also

[vrna\\_path\(\)](#), [VRNA\\_PATH\\_STEEPEST\\_DESCENT](#), [VRNA\\_MOVESET\\_DEFAULT](#)

## 16.40.3 Function Documentation



### 16.40.3.1 vrna\_path()

```
vrna_move_t * vrna_path (
    vrna_fold_compound_t * vc,
    short * pt,
    unsigned int steps,
    unsigned int options )
#include <ViennaRNA/landscape/walk.h>
```

Compute a path, store the final structure, and return a list of transition moves from the start to the final structure. This function computes, given a start structure in pair table format, a transition path, updates the pair table to the final structure of the path. Finally, if not requested otherwise by using the [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#) flag in the `options` field, this function returns a list of individual transitions that lead from the start to the final structure if requested.

The currently available transition paths are

- Steepest Descent / Gradient walk (flag: [VRNA\\_PATH\\_STEEPEST\\_DESCENT](#))
- Random walk (flag: [VRNA\\_PATH\\_RANDOM](#))

The type of transitions must be set through the `options` parameter

#### Note

Since the result is written to the input structure you may want to use [vrna\\_ptable\\_copy\(\)](#) before calling this function to keep the initial structure

#### See also

[vrna\\_path\\_gradient\(\)](#), [vrna\\_path\\_random\(\)](#), [vrna\\_ptable\(\)](#), [vrna\\_ptable\\_copy\(\)](#), [vrna\\_fold\\_compound\(\)](#), [VRNA\\_PATH\\_STEEPEST\\_DESCENT](#), [VRNA\\_PATH\\_RANDOM](#), [VRNA\\_MOVESET\\_DEFAULT](#), [VRNA\\_MOVESET\\_SHIFT](#), [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#)

#### Parameters

|         |                |                                                                                                                       |
|---------|----------------|-----------------------------------------------------------------------------------------------------------------------|
| in      | <i>vc</i>      | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details                                |
| in, out | <i>pt</i>      | The pair table containing the start structure. Used to update to the final structure after execution of this function |
| in      | <i>options</i> | Options to modify the behavior of this function                                                                       |

#### Returns

A list of transition moves (default), or NULL (if options & [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#))

**SWIG Wrapper Notes** This function is attached as an overloaded method *path()* to objects of type *fold\_compound*. The optional parameter `options` defaults to [VRNA\\_PATH\\_DEFAULT](#) if it is omitted.

### 16.40.3.2 vrna\_path\_gradient()

```
vrna_move_t * vrna_path_gradient (
    vrna_fold_compound_t * vc,
    short * pt,
    unsigned int options )
#include <ViennaRNA/landscape/walk.h>
```

Compute a steepest descent / gradient path, store the final structure, and return a list of transition moves from the start to the final structure.

This function computes, given a start structure in pair table format, a steepest descent path, updates the pair table to the final structure of the path. Finally, if not requested otherwise by using the [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#) flag in the `options` field, this function returns a list of individual transitions that lead from the start to the final structure if requested.

**Note**

Since the result is written to the input structure you may want to use [vrna\\_ptable\\_copy\(\)](#) before calling this function to keep the initial structure

**See also**

[vrna\\_path\\_random\(\)](#), [vrna\\_path\(\)](#), [vrna\\_ptable\(\)](#), [vrna\\_ptable\\_copy\(\)](#), [vrna\\_fold\\_compound\(\)](#) [VRNA\\_MOVESET\\_DEFAULT](#), [VRNA\\_MOVESET\\_SHIFT](#), [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#)

**Parameters**

|                      |                      |                                                                                                                       |
|----------------------|----------------------|-----------------------------------------------------------------------------------------------------------------------|
| <code>in</code>      | <code>vc</code>      | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details                                |
| <code>in, out</code> | <code>pt</code>      | The pair table containing the start structure. Used to update to the final structure after execution of this function |
| <code>in</code>      | <code>options</code> | Options to modify the behavior of this function                                                                       |

**Returns**

A list of transition moves (default), or NULL (if options & [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#))

**SWIG Wrapper Notes** This function is attached as an overloaded method `path_gradient()` to objects of type `fold_compound`. The optional parameter `options` defaults to [VRNA\\_PATH\\_DEFAULT](#) if it is omitted.

**16.40.3.3 vrna\_path\_random()**

```
vrna_move_t * vrna_path_random (
    vrna_fold_compound_t * vc,
    short * pt,
    unsigned int steps,
    unsigned int options )
#include <ViennaRNA/landscape/walk.h>
```

Generate a random walk / path of a given length, store the final structure, and return a list of transition moves from the start to the final structure.

This function generates, given a start structure in pair table format, a random walk / path, updates the pair table to the final structure of the path. Finally, if not requested otherwise by using the [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#) flag in the `options` field, this function returns a list of individual transitions that lead from the start to the final structure if requested.

**Note**

Since the result is written to the input structure you may want to use [vrna\\_ptable\\_copy\(\)](#) before calling this function to keep the initial structure

**See also**

[vrna\\_path\\_gradient\(\)](#), [vrna\\_path\(\)](#), [vrna\\_ptable\(\)](#), [vrna\\_ptable\\_copy\(\)](#), [vrna\\_fold\\_compound\(\)](#) [VRNA\\_MOVESET\\_DEFAULT](#), [VRNA\\_MOVESET\\_SHIFT](#), [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#)

**Parameters**

|                      |                      |                                                                                                                       |
|----------------------|----------------------|-----------------------------------------------------------------------------------------------------------------------|
| <code>in</code>      | <code>vc</code>      | A <code>vrna_fold_compound_t</code> containing the energy parameters and model details                                |
| <code>in, out</code> | <code>pt</code>      | The pair table containing the start structure. Used to update to the final structure after execution of this function |
| <code>in</code>      | <code>steps</code>   | The length of the path, i.e. the total number of transitions / moves                                                  |
| <code>in</code>      | <code>options</code> | Options to modify the behavior of this function                                                                       |

## Returns

A list of transition moves (default), or NULL (if options & [VRNA\\_PATH\\_NO\\_TRANSITION\\_OUTPUT](#))

**SWIG Wrapper Notes** This function is attached as an overloaded method *path\_gradient()* to objects of type *fold\_compound*. The optional parameter *options* defaults to [VRNA\\_PATH\\_DEFAULT](#) if it is omitted.

## 16.41 Experimental Structure Probing Data

Include Experimental Structure Probing Data to Guide Structure Predictions.

### 16.41.1 Detailed Description

Include Experimental Structure Probing Data to Guide Structure Predictions.

Collaboration diagram for Experimental Structure Probing Data:

### Modules

- [SHAPE Reactivity Data](#)

*Incorporate SHAPE reactivity structure probing data into the folding recursions by means of soft constraints.*

- [Generate Soft Constraints from Data](#)

*Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.*

## 16.42 SHAPE Reactivity Data

Incorporate SHAPE reactivity structure probing data into the folding recursions by means of soft constraints.

### 16.42.1 Detailed Description

Incorporate SHAPE reactivity structure probing data into the folding recursions by means of soft constraints.

Details for our implementation to incorporate SHAPE reactivity data to guide secondary structure prediction can be found in [17] Collaboration diagram for SHAPE Reactivity Data:

### Files

- file [SHAPE.h](#)

*This module provides function to incorporate SHAPE reactivity data into the folding recursions by means of soft constraints.*

### Functions

- int [vrna\\_sc\\_add\\_SHAPE\\_deigan](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const double \*reactivities, double m, double b, unsigned int options)

*Add SHAPE reactivity data as soft constraints (Deigan et al. method)*

- int [vrna\\_sc\\_add\\_SHAPE\\_deigan\\_al](#)i ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*\*shape\_files, const int \*shape\_file\_association, double m, double b, unsigned int options)

*Add SHAPE reactivity data from files as soft constraints for consensus structure prediction (Deigan et al. method)*

- int [vrna\\_sc\\_add\\_SHAPE\\_zarringhalam](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const double \*reactivities, double b, double default\_value, const char \*shape\_conversion, unsigned int options)

*Add SHAPE reactivity data as soft constraints (Zarringhalam et al. method)*

- int [vrna\\_sc\\_SHAPE\\_to\\_pr](#) (const char \*shape\_conversion, double \*values, int length, double default\_value)

*Convert SHAPE reactivity values to probabilities for being unpaired.*

## 16.42.2 Function Documentation

### 16.42.2.1 `vrna_sc_add_SHAPE_deigan()`

```
int vrna_sc_add_SHAPE_deigan (
    vrna_fold_compound_t * vc,
    const double * reactivities,
    double m,
    double b,
    unsigned int options )
#include <ViennaRNA/constraints/SHAPE.h>
Add SHAPE reactivity data as soft constraints (Deigan et al. method)
This approach of SHAPE directed RNA folding uses the simple linear ansatz
```

$$\Delta G_{\text{SHAPE}}(i) = m \ln(\text{SHAPE reactivity}(i) + 1) + b$$

to convert SHAPE reactivity values to pseudo energies whenever a nucleotide  $i$  contributes to a stacked pair. A positive slope  $m$  penalizes high reactivities in paired regions, while a negative intercept  $b$  results in a confirmatory “bonus” free energy for correctly predicted base pairs. Since the energy evaluation of a base pair stack involves two pairs, the pseudo energies are added for all four contributing nucleotides. Consequently, the energy term is applied twice for pairs inside a helix and only once for pairs adjacent to other structures. For all other loop types the energy model remains unchanged even when the experimental data highly disagrees with a certain motif.

See also

For further details, we refer to [6].

[vrna\\_sc\\_remove\(\)](#), [vrna\\_sc\\_add\\_SHAPE\\_zarringhalam\(\)](#), [vrna\\_sc\\_minimize\\_pertubation\(\)](#)

#### Parameters

|                     |                                                                                   |
|---------------------|-----------------------------------------------------------------------------------|
| <i>vc</i>           | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>reactivities</i> | A vector of normalized SHAPE reactivities                                         |
| <i>m</i>            | The slope of the conversion function                                              |
| <i>b</i>            | The intercept of the conversion function                                          |
| <i>options</i>      | The options flag indicating how/where to store the soft constraints               |

#### Returns

1 on successful extraction of the method, 0 on errors

**SWIG Wrapper Notes** This function is attached as method `sc_add_SHAPE_deigan()` to objects of type `fold_compound`

### 16.42.2.2 `vrna_sc_add_SHAPE_deigan_aln()`

```
int vrna_sc_add_SHAPE_deigan_aln (
    vrna_fold_compound_t * vc,
    const char ** shape_files,
    const int * shape_file_association,
    double m,
    double b,
    unsigned int options )
#include <ViennaRNA/constraints/SHAPE.h>
Add SHAPE reactivity data from files as soft constraints for consensus structure prediction (Deigan et al. method)
```

## Parameters

|                               |                                                                                   |
|-------------------------------|-----------------------------------------------------------------------------------|
| <i>vc</i>                     | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>shape_files</i>            | A set of filenames that contain normalized SHAPE reactivity data                  |
| <i>shape_file_association</i> | An array of integers that associate the files with sequences in the alignment     |
| <i>m</i>                      | The slope of the conversion function                                              |
| <i>b</i>                      | The intercept of the conversion function                                          |
| <i>options</i>                | The options flag indicating how/where to store the soft constraints               |

## Returns

1 on successful extraction of the method, 0 on errors

**SWIG Wrapper Notes** This function is attached as method `sc_add_SHAPE_deigan_ali()` to objects of type `fold_compound`

16.42.2.3 `vrna_sc_add_SHAPE_zarringhalam()`

```
int vrna_sc_add_SHAPE_zarringhalam (
    vrna_fold_compound_t * vc,
    const double * reactivities,
    double b,
    double default_value,
    const char * shape_conversion,
    unsigned int options )
```

#include <[ViennaRNA/constraints/SHAPE.h](#)>

Add SHAPE reactivity data as soft constraints (Zarringhalam et al. method)

This method first converts the observed SHAPE reactivity of nucleotide  $i$  into a probability  $q_i$  that position  $i$  is unpaired by means of a non-linear map. Then pseudo-energies of the form

$$\Delta G_{\text{SHAPE}}(x, i) = \beta |x_i - q_i|$$

are computed, where  $x_i = 0$  if position  $i$  is unpaired and  $x_i = 1$  if  $i$  is paired in a given secondary structure. The parameter  $\beta$  serves as scaling factor. The magnitude of discrepancy between prediction and experimental observation is represented by  $|x_i - q_i|$ .

## See also

For further details, we refer to [26]

[vrna\\_sc\\_remove\(\)](#), [vrna\\_sc\\_add\\_SHAPE\\_deigan\(\)](#), [vrna\\_sc\\_minimize\\_pertubation\(\)](#)

## Parameters

|                         |                                                                                   |
|-------------------------|-----------------------------------------------------------------------------------|
| <i>vc</i>               | The <a href="#">vrna_fold_compound_t</a> the soft constraints are associated with |
| <i>reactivities</i>     | A vector of normalized SHAPE reactivities                                         |
| <i>b</i>                | The scaling factor $\beta$ of the conversion function                             |
| <i>default_value</i>    | The default value for a nucleotide where reactivity data is missing for           |
| <i>shape_conversion</i> | A flag that specifies how to convert reactivities to probabilities                |
| <i>options</i>          | The options flag indicating how/where to store the soft constraints               |

## Returns

1 on successful extraction of the method, 0 on errors

**SWIG Wrapper Notes** This function is attached as method `sc_add_SHAPE_zarringhalam()` to objects of type `fold_compound`

#### 16.42.2.4 vrna\_sc\_SHAPE\_to\_pr()

```
int vrna_sc_SHAPE_to_pr (
    const char * shape_conversion,
    double * values,
    int length,
    double default_value )
#include <ViennaRNA/constraints/SHAPE.h>
```

Convert SHAPE reactivity values to probabilities for being unpaired.

This function parses the informations from a given file and stores the result in the preallocated string sequence and the `FLT_OR_DBL` array values.

## See also

[vrna\\_file\\_SHAPE\\_read\(\)](#)

## Parameters

|                         |                                                                 |
|-------------------------|-----------------------------------------------------------------|
| <i>shape_conversion</i> | String defining the method used for the conversion process      |
| <i>values</i>           | Pointer to an array of SHAPE reactivities                       |
| <i>length</i>           | Length of the array of SHAPE reactivities                       |
| <i>default_value</i>    | Result used for position with invalid/missing reactivity values |

## 16.43 Generate Soft Constraints from Data

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

### 16.43.1 Detailed Description

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

Collaboration diagram for Generate Soft Constraints from Data:

## Files

- file [perturbation\\_fold.h](#)

*Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.*

## Macros

- `#define VRNA_OBJECTIVE_FUNCTION_QUADRATIC 0`  
*Use the sum of squared aberrations as objective function.*
- `#define VRNA_OBJECTIVE_FUNCTION_ABSOLUTE 1`  
*Use the sum of absolute aberrations as objective function.*
- `#define VRNA_MINIMIZER_DEFAULT 0`

*Use a custom implementation of the gradient descent algorithm to minimize the objective function.*

- `#define VRNA_MINIMIZER_CONJUGATE_FR 1`

*Use the GNU Scientific Library implementation of the Fletcher-Reeves conjugate gradient algorithm to minimize the objective function.*

- `#define VRNA_MINIMIZER_CONJUGATE_PR 2`

*Use the GNU Scientific Library implementation of the Polak-Ribiere conjugate gradient algorithm to minimize the objective function.*

- `#define VRNA_MINIMIZER_VECTOR_BFGS 3`

*Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.*

- `#define VRNA_MINIMIZER_VECTOR_BFGS2 4`

*Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.*

- `#define VRNA_MINIMIZER_STEEPEST_DESCENT 5`

*Use the GNU Scientific Library implementation of the steepest descent algorithm to minimize the objective function.*

## Typedefs

- `typedef void(* progress_callback) (int iteration, double score, double *epsilon)`

*Callback for following the progress of the minimization process.*

## Functions

- `void vrna_sc_minimize_pertubation (vrna_fold_compound_t *vc, const double *q_prob_unpaired, int objective_function, double sigma_squared, double tau_squared, int algorithm, int sample_size, double *epsilon, double initialStepSize, double minStepSize, double minImprovement, double minimizerTolerance, progress_callback callback)`

*Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.*

## 16.43.2 Macro Definition Documentation

### 16.43.2.1 VRNA\_OBJECTIVE\_FUNCTION\_QUADRATIC

```
#define VRNA_OBJECTIVE_FUNCTION_QUADRATIC 0
#include <ViennaRNA/perturbation_fold.h>
```

Use the sum of squared aberrations as objective function.

$$F(\vec{\epsilon}) = \sum_{i=1}^n \frac{\epsilon_i^2}{\tau^2} + \sum_{i=1}^n \frac{(p_i(\vec{\epsilon}) - q_i)^2}{\sigma^2} \rightarrow \min$$

### 16.43.2.2 VRNA\_OBJECTIVE\_FUNCTION\_ABSOLUTE

```
#define VRNA_OBJECTIVE_FUNCTION_ABSOLUTE 1
#include <ViennaRNA/perturbation_fold.h>
```

Use the sum of absolute aberrations as objective function.

$$F(\vec{\epsilon}) = \sum_{i=1}^n \frac{|\epsilon_i|}{\tau^2} + \sum_{i=1}^n \frac{|p_i(\vec{\epsilon}) - q_i|}{\sigma^2} \rightarrow \min$$

### 16.43.2.3 VRNA\_MINIMIZER\_CONJUGATE\_FR

```
#define VRNA_MINIMIZER_CONJUGATE_FR 1
#include <ViennaRNA/perturbation_fold.h>
```

Use the GNU Scientific Library implementation of the Fletcher-Reeves conjugate gradient algorithm to minimize the objective function.

Please note that this algorithm can only be used when the GNU Scientific Library is available on your system

### 16.43.2.4 VRNA\_MINIMIZER\_CONJUGATE\_PR

```
#define VRNA_MINIMIZER_CONJUGATE_PR 2
```

```
#include <ViennaRNA/perturbation_fold.h>
```

Use the GNU Scientific Library implementation of the Polak-Ribiere conjugate gradient algorithm to minimize the objective function.

Please note that this algorithm can only be used when the GNU Scientific Library is available on your system

### 16.43.2.5 VRNA\_MINIMIZER\_VECTOR\_BFGS

```
#define VRNA_MINIMIZER_VECTOR_BFGS 3
```

```
#include <ViennaRNA/perturbation_fold.h>
```

Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.

Please note that this algorithm can only be used when the GNU Scientific Library is available on your system

### 16.43.2.6 VRNA\_MINIMIZER\_VECTOR\_BFGS2

```
#define VRNA_MINIMIZER_VECTOR_BFGS2 4
```

```
#include <ViennaRNA/perturbation_fold.h>
```

Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.

Please note that this algorithm can only be used when the GNU Scientific Library is available on your system

### 16.43.2.7 VRNA\_MINIMIZER\_STEEPEST\_DESCENT

```
#define VRNA_MINIMIZER_STEEPEST_DESCENT 5
```

```
#include <ViennaRNA/perturbation_fold.h>
```

Use the GNU Scientific Library implementation of the steepest descent algorithm to minimize the objective function.

Please note that this algorithm can only be used when the GNU Scientific Library is available on your system

## 16.43.3 Typedef Documentation

### 16.43.3.1 progress\_callback

```
typedef void(* progress_callback) (int iteration, double score, double *epsilon)
```

```
#include <ViennaRNA/perturbation_fold.h>
```

Callback for following the progress of the minimization process.

#### Parameters

|                  |                                                     |
|------------------|-----------------------------------------------------|
| <i>iteration</i> | The number of the current iteration                 |
| <i>score</i>     | The score of the objective function                 |
| <i>epsilon</i>   | The perturbation vector yielding the reported score |

## 16.43.4 Function Documentation

### 16.43.4.1 vrna\_sc\_minimize\_pertubation()

```
void vrna_sc_minimize_pertubation (
    vrna_fold_compound_t * vc,
    const double * q_prob_unpaired,
    int objective_function,
    double sigma_squared,
```



```

double tau_squared,
int algorithm,
int sample_size,
double * epsilon,
double initialStepSize,
double minStepSize,
double minImprovement,
double minimizerTolerance,
progress_callback callback )
#include <ViennaRNA/perturbation_fold.h>

```

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

Use an iterative minimization algorithm to find a vector of perturbation energies whose incorporation as soft constraints shifts the predicted pairing probabilities closer to the experimentally observed probabilities. The algorithm aims to minimize an objective function that penalizes discrepancies between predicted and observed pairing probabilities and energy model adjustments, i.e. an appropriate vector of perturbation energies satisfies

$$F(\vec{\epsilon}) = \sum_{\mu} \frac{\epsilon_{\mu}^2}{\tau^2} + \sum_{i=1}^n \frac{(p_i(\vec{\epsilon}) - q_i)^2}{\sigma^2} \rightarrow \min.$$

An initialized fold compound and an array containing the observed probability for each nucleotide to be unbound are required as input data. The parameters `objective_function`, `sigma_squared` and `tau_squared` are responsible for adjusting the aim of the objective function. Dependend on which type of objective function is selected, either squared or absolute aberrations are contributing to the objective function. The ratio of the parameters `sigma_squared` and `tau_squared` can be used to adjust the algorithm to find a solution either close to the thermodynamic prediction (`sigma_squared >> tau_squared`) or close to the experimental data (`tau_squared >> sigma_squared`). The minimization can be performed by makeing use of a custom gradient descent implementation or using one of the minimizing algorithms provided by the GNU Scientific Library. All algorithms require the evaluation of the gradient of the objective function, which includes the evaluation of conditional pairing probabilities. Since an exact evaluation is expensive, the probabilities can also be estimated from sampling by setting an appropriate sample size. The found vector of perturbation energies will be stored in the array `epsilon`. The progress of the minimization process can be tracked by implementing and passing a callback function.

See also

For further details we refere to [23].

#### Parameters

|                                 |                                                                                                                                                                     |
|---------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>vc</code>                 | Pointer to a fold compound                                                                                                                                          |
| <code>q_prob_unpaired</code>    | Pointer to an array containing the probability to be unpaired for each nucleotide                                                                                   |
| <code>objective_function</code> | The type of objective function to be used (VRNA_OBJECTIVE_FUNCTION_QUADRATIC / VRNA_OBJECTIVE_FUNCTION_LINEAR)                                                      |
| <code>sigma_squared</code>      | A factor used for weighting the objective function. More weight on this factor will lead to a solution close to the null vector.                                    |
| <code>tau_squared</code>        | A factor used for weighting the objective function. More weight on this factor will lead to a solution close to the data provided in <code>q_prob_unpaired</code> . |
| <code>algorithm</code>          | The minimization algorithm (VRNA_MINIMIZER_*)                                                                                                                       |
| <code>sample_size</code>        | The number of sampled sequences used for estimating the pairing probabilities. A value $\leq 0$ will lead to an exact evaluation.                                   |
| <code>epsilon</code>            | A pointer to an array used for storing the calculated vector of perturbation energies                                                                               |
| <code>callback</code>           | A pointer to a callback function used for reporting the current minimization progress                                                                               |

## 16.44 Ligands Binding to RNA Structures

Simple Extensions to Model Ligand Binding to RNA Structures.

### 16.44.1 Detailed Description

Simple Extensions to Model Ligand Binding to RNA Structures.

Collaboration diagram for Ligands Binding to RNA Structures:

#### Modules

- [Ligands Binding to Unstructured Domains](#)  
*Add ligand binding to loop regions using the [Unstructured Domains](#) feature.*
- [Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints](#)  
*Ligand binding to specific hairpin/interior loop like motifs using the [Soft Constraints](#) feature.*

#### Files

- file [ligand.h](#)  
*Functions for incorporation of ligands binding to hairpin and interior loop motifs using the soft constraints framework.*

## 16.45 Ligands Binding to Unstructured Domains

Add ligand binding to loop regions using the [Unstructured Domains](#) feature.

Add ligand binding to loop regions using the [Unstructured Domains](#) feature.

Sometime, certain ligands, like single strand binding (SSB) proteins, compete with intramolecular base pairing of the RNA. In situations, where the dissociation constant of the ligand is known and the ligand binds to a consecutive stretch of single-stranded nucleotides we can use the [Unstructured Domains](#) functionality to extend the RNA folding grammar. This module provides a convenience default implementation that covers most of the application scenarios. The function `vrna_ud_add_motif()` attaches a ligands sequence motif and corresponding binding free energy to the list of known ligand motifs within a `vrna_fold_compound_t.domains_up` attribute. The first call to this function initializes the [Unstructured Domains](#) feature with our default implementation. Subsequent calls of secondary structure prediction algorithms with the modified `vrna_fold_compound_t` then directly include the competition of the ligand with regulas base pairing. Since we utilize the unstructured domain extension, The ligand binding model can be removed again using the `vrna_ud_remove()` function. Collaboration diagram for Ligands Binding to Unstructured Domains:

## 16.46 Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints

Ligand binding to specific hairpin/interior loop like motifs using the [Soft Constraints](#) feature.

### 16.46.1 Detailed Description

Ligand binding to specific hairpin/interior loop like motifs using the [Soft Constraints](#) feature.

Collaboration diagram for Incorporating Ligands Binding to Specific Sequence/Structure Motifs using Soft Constraints:

#### Data Structures

- struct [vrna\\_sc\\_motif\\_s](#)

#### Typedefs

- typedef struct [vrna\\_sc\\_motif\\_s](#) [vrna\\_sc\\_motif\\_t](#)  
*Type definition for soft constraint motif.*

## Functions

- int `vrna_sc_add_hi_motif` (`vrna_fold_compound_t` \*fc, const char \*seq, const char \*structure, FLT\_OR\_DBL energy, unsigned int options)

Add soft constraints for hairpin or interior loop binding motif.

### 16.46.2 Data Structure Documentation

#### 16.46.2.1 struct `vrna_sc_motif_s`

### 16.46.3 Function Documentation

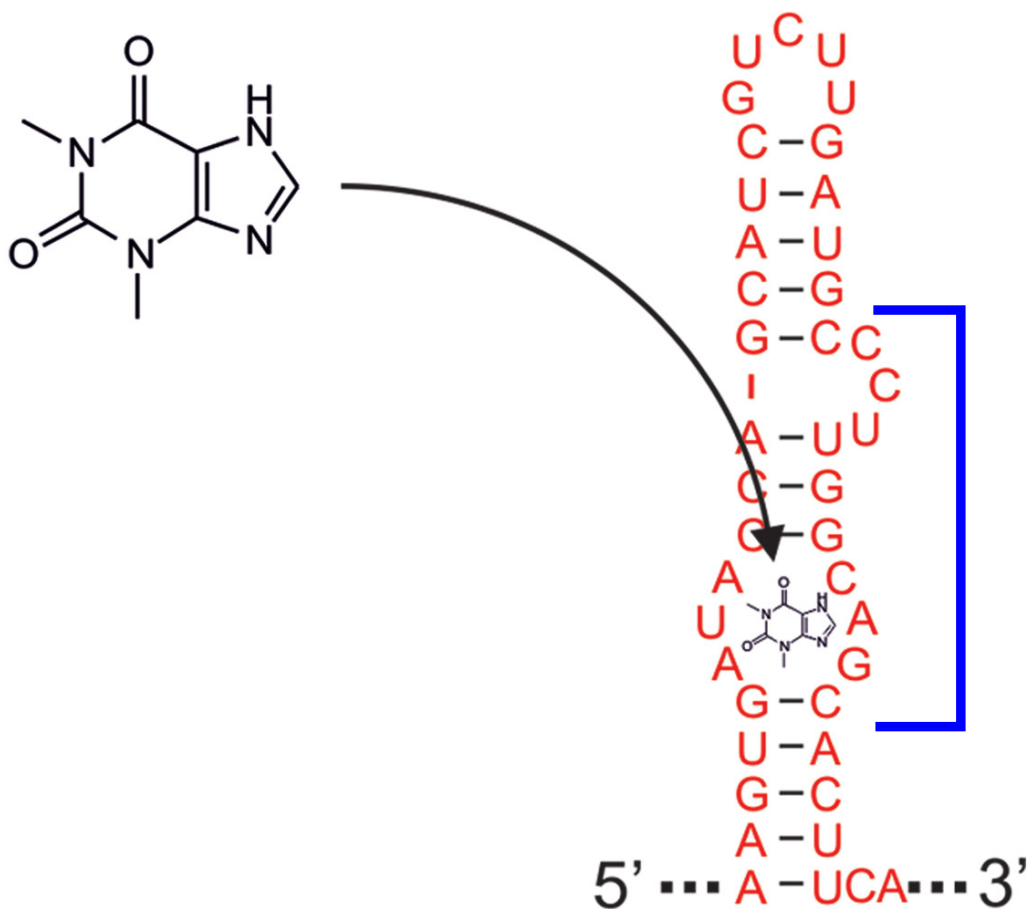
#### 16.46.3.1 `vrna_sc_add_hi_motif()`

```
int vrna_sc_add_hi_motif (
    vrna_fold_compound_t * fc,
    const char * seq,
    const char * structure,
    FLT_OR_DBL energy,
    unsigned int options )
```

#include <ViennaRNA/constraints/ligand.h>

Add soft constraints for hairpin or interior loop binding motif.

Here is an example that adds a theophylline binding motif. Free energy contribution is derived from  $k_d = 0.1\mu M$ , taken from Jenison et al. 1994. At  $1M$  concentration the corresponding binding free energy amounts to  $-9.93\text{ kcal/mol}$ .



```
vrna_sc_add_hi_motif(fc,
    "GAUACCAG&CCCUUGGCAGC",
```

```
" (... (( (&) ... )) ... )",
-9.93, VRNA_OPTION_DEFAULT);
```

#### Parameters

|                  |                                                                  |
|------------------|------------------------------------------------------------------|
| <i>fc</i>        | The <a href="#">vrna_fold_compound_t</a> the motif is applied to |
| <i>seq</i>       | The sequence motif (may be interspaced by '&' character          |
| <i>structure</i> | The structure motif (may be interspaced by '&' character         |
| <i>energy</i>    | The free energy of the motif (e.g. binding free energy)          |
| <i>options</i>   | Options                                                          |

#### Returns

non-zero value if application of the motif using soft constraints was successful

**SWIG Wrapper Notes** This function is attached as method `sc_add_hi_motif()` to objects of type *fold\_compound*

## 16.47 Structure Modules and Pseudoknots

### 16.47.1 Detailed Description

Collaboration diagram for Structure Modules and Pseudoknots:

#### Modules

- [Pseudoknots](#)  
*Implementations to predict pseudoknotted structures.*
- [G-Quadruplexes](#)  
*Various functions related to G-quadruplex computations.*

#### Files

- file [gquad.h](#)  
*G-quadruplexes.*

## 16.48 Pseudoknots

Implementations to predict pseudoknotted structures.

### 16.48.1 Detailed Description

Implementations to predict pseudoknotted structures.

Collaboration diagram for Pseudoknots:

#### Files

- file [pk\\_plex.h](#)  
*Heuristics for two-step pseudoknot forming interaction predictions.*

#### Data Structures

- struct [vrna\\_pk\\_plex\\_result\\_s](#)  
*A result of the RNA PKplex interaction prediction. [More...](#)*

## Typedefs

- typedef int() [vrna\\_callback\\_pk\\_plex\\_score](#)(const short \*pt, int start\_5, int end\_5, int start\_3, int end\_3, void \*data)  
*Pseudoknot loop scoring function prototype.*
- typedef struct vrna\_pk\_plex\_option\_s \* [vrna\\_pk\\_plex\\_opt\\_t](#)  
*RNA PKplex options object.*
- typedef struct [vrna\\_pk\\_plex\\_result\\_s](#) [vrna\\_pk\\_plex\\_t](#)  
*Convenience typedef for results of the RNA PKplex prediction.*

## Functions

- [vrna\\_pk\\_plex\\_t](#) \* [vrna\\_pk\\_plex](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const int \*\*accessibility, [vrna\\_pk\\_plex\\_opt\\_t](#) options)  
*Predict Pseudoknot interactions in terms of a two-step folding process.*
- int \*\* [vrna\\_pk\\_plex\\_accessibility](#) (const char \*sequence, unsigned int [unpaired](#), double cutoff)  
*Obtain a list of opening energies suitable for PKplex computations.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt\\_defaults](#) (void)  
*Default options for PKplex algorithm.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt](#) (unsigned int delta, unsigned int max\_interaction\_length, int pk\_↔ penalty)  
*Simple options for PKplex algorithm.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt\\_fun](#) (unsigned int delta, unsigned int max\_interaction\_length, [vrna\\_callback\\_pk\\_plex\\_score](#) \*scoring\_function, void \*scoring\_data)  
*Simple options for PKplex algorithm.*

## 16.48.2 Data Structure Documentation

### 16.48.2.1 struct vrna\_pk\_plex\_result\_s

A result of the RNA PKplex interaction prediction.

See also

[vrna\\_pk\\_plex\\_t](#)

### Data Fields

- char \* **structure**  
*Secondary Structure in dot-bracket notation.*
- double **energy**  
*Net free energy in kcal/mol.*
- double **dGpk**  
*Free energy of PK loop in kcal/mol.*
- double **dGint**  
*Free energy of PK forming duplex interaction.*
- double **dG1**  
*Opening energy for the 5' interaction site used in the heuristic.*
- double **dG2**  
*Opening energy for the 3' interaction site used in the heuristic.*
- unsigned int **start\_5**  
*Start coordinate of the 5' interaction site.*
- unsigned int **end\_5**  
*End coordinate of the 5' interaction site.*
- unsigned int **start\_3**  
*Start coordinate of the 3' interaction site.*
- unsigned int **end\_3**  
*End coordinate of the 3' interaction site.*

## 16.48.3 Typedef Documentation

### 16.48.3.1 `vrna_callback_pk_plex_score`

```
typedef int() vrna_callback_pk_plex_score(const short *pt, int start_5, int end_5, int start_↵
3, int end_3, void *data)
#include <ViennaRNA/pk_plex.h>
```

Pseudoknot loop scoring function prototype.

This function is used to evaluate a formed pseudoknot (PK) interaction in `vrna_pk_plex()`. It is supposed to take a PK-free secondary structure as input and coordinates of an additional interaction site. From this data, the energy (penalty) to score the PK loop is derived and returned in decakal/mol. Upon passing zero in any of the interaction site coordinates (`start_5`, `end_5`, `start_3`, `end_3`) or a *NULL* pointer in `pt`, the function must return a PK loop score. This minimum PK loop score is used in the first phase of the heuristic implemented in `vrna_pk_plex()` to assess whether a particular interaction is further taken into account in a later, more thorough evaluation step.

The simplest scoring function would simply return a constant score for any PK loop, no matter what type of loop is formed and how large the loop is. This is the default if `vrna_pk_plex_opt_defaults()` or `vrna_pk_plex_opt()` is used to generate options for `vrna_pk_plex()`.

See also

[vrna\\_pk\\_plex\\_opt\\_fun\(\)](#), [vrna\\_pk\\_plex\(\)](#)

#### Parameters

|                  |                                                                     |
|------------------|---------------------------------------------------------------------|
| <i>pt</i>        | The secondary structure (without pseudoknot) in pair table notation |
| <i>start_↵_5</i> | The start coordinate of the 5' site of the pseudoknot interaction   |
| <i>end_↵_5</i>   | The end coordinate of the 5' site of the pseudoknot interaction     |
| <i>start_↵_3</i> | The start coordinate of the 3' site of the pseudoknot interaction   |
| <i>end_↵_3</i>   | The end coordinate of the 3' site of the pseudoknot interaction     |
| <i>data</i>      | An arbitrary data structure passed from the calling function        |

#### Returns

The energy (penalty) of the resulting pseudoknot

### 16.48.3.2 `vrna_pk_plex_opt_t`

```
typedef struct vrna_pk_plex_option_s* vrna_pk_plex_opt_t
#include <ViennaRNA/pk_plex.h>
RNA PKplex options object.
```

See also

[vrna\\_pk\\_plex\\_opt\\_defaults\(\)](#), [vrna\\_pk\\_plex\\_opt\(\)](#), [vrna\\_pk\\_plex\\_opt\\_fun\(\)](#), [vrna\\_pk\\_plex\(\)](#), [vrna\\_callback\\_pk\\_plex\\_score](#)

### 16.48.3.3 `vrna_pk_plex_t`

```
typedef struct vrna_pk_plex_result_s vrna_pk_plex_t
#include <ViennaRNA/pk_plex.h>
Convenience typedef for results of the RNA PKplex prediction.
```

See also

[#vrna\\_pk\\_plex\\_results\\_s](#), [vrna\\_pk\\_plex\(\)](#)

## 16.48.4 Function Documentation

### 16.48.4.1 vrna\_pk\_plex()

```
vrna_pk_plex_t * vrna_pk_plex (
    vrna_fold_compound_t * fc,
    const int ** accessibility,
    vrna_pk_plex_opt_t options )
#include <ViennaRNA/pk_plex.h>
```

Predict Pseudoknot interactions in terms of a two-step folding process.

Computes simple pseudoknot interactions according to the PKplex algorithm. This simple heuristic first compiles a list of potential interaction sites that may form a pseudoknot. The resulting candidate interactions are then fixed and an PK-free MFE structure for the remainder of the sequence is computed.

The `accessibility` argument is a list of opening energies for potential interaction sites. It is used in the first step of the algorithm to identify potential interactions. Upon passing `NULL`, the opening energies are determined automatically based on the current model settings.

Depending on the `options`, the function can return the MFE (incl. PK loops) or suboptimal structures within an energy band around the MFE. The PK loop is internally scored by a scoring function that in the simplest cases assigns a constant value for each PK loop. More complicated scoring functions can be passed as well, see [vrna\\_callback\\_pk\\_plex\\_score](#) and [vrna\\_pk\\_plex\\_opt\\_fun\(\)](#).

The function returns `NULL` on any error. Otherwise, a list of structures and interaction coordinates with corresponding energy contributions is returned. If no PK-interaction that satisfies the options is found, the list only consists of the PK-free MFE structure.

#### Parameters

|                            |                                                                                                       |
|----------------------------|-------------------------------------------------------------------------------------------------------|
| <code>fc</code>            | fold compound with the input sequence and model settings                                              |
| <code>accessibility</code> | An array of opening energies for the implemented heuristic (maybe <code>NULL</code> )                 |
| <code>options</code>       | An <a href="#">vrna_pk_plex_opt_t</a> options data structure that determines the algorithm parameters |

#### Returns

A list of potentially pseudoknotted structures (Last element in the list indicated by `NULL` value in [vrna\\_pk\\_plex\\_result\\_s.structure](#))

### 16.48.4.2 vrna\_pk\_plex\_accessibility()

```
int ** vrna_pk_plex_accessibility (
    const char * sequence,
    unsigned int unpaired,
    double cutoff )
#include <ViennaRNA/pk_plex.h>
```

Obtain a list of opening energies suitable for PKplex computations.

See also

[vrna\\_pk\\_plex\(\)](#)

#### Parameters

|                       |                                                                        |
|-----------------------|------------------------------------------------------------------------|
| <code>sequence</code> | The RNA sequence                                                       |
| <code>unpaired</code> | The maximum number of unpaired nucleotides, i.e. length of interaction |
| <code>cutoff</code>   | A cutoff value for unpaired probabilities                              |

**Returns**

Opening energies as required for [vrna\\_pk\\_plex\(\)](#)

**16.48.4.3 vrna\_pk\_plex\_opt\_defaults()**

```
vrna_pk_plex_opt_t vrna_pk_plex_opt_defaults (
    void )
#include <ViennaRNA/pk_plex.h>
Default options for PKplex algorithm.
```

**See also**

[vrna\\_pk\\_plex\(\)](#), [vrna\\_pk\\_plex\\_opt\(\)](#), [vrna\\_pk\\_plex\\_opt\\_fun\(\)](#)

**Returns**

An options data structure suitable for PKplex computations

**16.48.4.4 vrna\_pk\_plex\_opt()**

```
vrna_pk_plex_opt_t vrna_pk_plex_opt (
    unsigned int delta,
    unsigned int max_interaction_length,
    int pk_penalty )
#include <ViennaRNA/pk_plex.h>
Simple options for PKplex algorithm.
```

**See also**

[vrna\\_pk\\_plex\(\)](#), [vrna\\_pk\\_plex\\_opt\\_defaults\(\)](#), [vrna\\_pk\\_plex\\_opt\\_fun\(\)](#)

**Parameters**

|                               |                                                                    |
|-------------------------------|--------------------------------------------------------------------|
| <i>delta</i>                  | Size of energy band around MFE for suboptimal results in dekal/mol |
| <i>max_interaction_length</i> | Maximum length of interaction                                      |
| <i>pk_penalty</i>             | Energy constant to score the PK forming loop                       |

**Returns**

An options data structure suitable for PKplex computations

**16.48.4.5 vrna\_pk\_plex\_opt\_fun()**

```
vrna_pk_plex_opt_t vrna_pk_plex_opt_fun (
    unsigned int delta,
    unsigned int max_interaction_length,
    vrna_callback_pk_plex_score * scoring_function,
    void * scoring_data )
#include <ViennaRNA/pk_plex.h>
Simple options for PKplex algorithm.
```

**See also**

[vrna\\_pk\\_plex\(\)](#), [vrna\\_pk\\_plex\\_opt\\_defaults\(\)](#), [vrna\\_pk\\_plex\\_opt\(\)](#), [vrna\\_callback\\_pk\\_plex\\_score](#)



## Parameters

|                               |                                                                                |
|-------------------------------|--------------------------------------------------------------------------------|
| <i>delta</i>                  | Size of energy band around MFE for suboptimal results in dekal/mol             |
| <i>max_interaction_length</i> | Maximum length of interaction                                                  |
| <i>scoring_function</i>       | Energy evaluating function to score the PK forming loop                        |
| <i>scoring_data</i>           | An arbitrary data structure passed to the scoring function (maybe <i>NUL</i> ) |

## Returns

An options data structure suitable for PKplex computations

## 16.49 G-Quadruplexes

Various functions related to G-quadruplex computations.

### 16.49.1 Detailed Description

Various functions related to G-quadruplex computations.

Collaboration diagram for G-Quadruplexes:

### Functions

- int \* [get\\_gquad\\_matrix](#) (short \*S, [vrna\\_param\\_t](#) \*P)  
*Get a triangular matrix prefilled with minimum free energy contributions of G-quadruplexes.*
- int [parse\\_gquad](#) (const char \*struc, int \*L, int l[3])
- PRIVATE int [backtrack\\_GQuad\\_IntLoop](#) (int c, int i, int j, int type, short \*S, int \*ggg, int \*index, int \*p, int \*q, [vrna\\_param\\_t](#) \*P)
- PRIVATE int [backtrack\\_GQuad\\_IntLoop\\_L](#) (int c, int i, int j, int type, short \*S, int \*\*ggg, int maxdist, int \*p, int \*q, [vrna\\_param\\_t](#) \*P)

### 16.49.2 Function Documentation

#### 16.49.2.1 [get\\_gquad\\_matrix\(\)](#)

```
int * get_gquad_matrix (
    short * S,
    vrna\_param\_t * P )
#include <ViennaRNA/gquad.h>
```

Get a triangular matrix prefilled with minimum free energy contributions of G-quadruplexes.

At each position ij in the matrix, the minimum free energy of any G-quadruplex delimited by i and j is stored. If no G-quadruplex formation is possible, the matrix element is set to INF. Access the elements in the matrix via matrix[indx[j]+i]. To get the integer array indx see [get\\_jindx\(\)](#).

#### See also

[get\\_jindx\(\)](#), [encode\\_sequence\(\)](#)

## Parameters

|          |                                                                                 |
|----------|---------------------------------------------------------------------------------|
| <i>S</i> | The encoded sequence                                                            |
| <i>P</i> | A pointer to the data structure containing the precomputed energy contributions |

**Returns**

A pointer to the G-quadruplex contribution matrix

**16.49.2.2 parse\_gquad()**

```
int parse_gquad (
    const char * struc,
    int * L,
    int l[3] )
#include <ViennaRNA/gquad.h>
given a dot-bracket structure (possibly) containing gquads encoded by '+' signs, find first gquad, return end position
or 0 if none found Upon return L and l[] contain the number of stacked layers, as well as the lengths of the linker
regions. To parse a string with many gquads, call parse_gquad repeatedly e.g. end1 = parse_gquad(struc, &L, l); ...
; end2 = parse_gquad(struc+end1, &L, l); end2+=end1; ... ; end3 = parse_gquad(struc+end2, &L, l); end3+=end2;
... ;
```

**16.49.2.3 backtrack\_GQuad\_IntLoop()**

```
PRIVATE int backtrack_GQuad_IntLoop (
    int c,
    int i,
    int j,
    int type,
    short * S,
    int * ggg,
    int * index,
    int * p,
    int * q,
    vrna_param_t * P )
#include <ViennaRNA/gquad.h>
backtrack an interior loop like enclosed g-quadruplex with closing pair (i,j)
```

**Parameters**

|              |                                                              |
|--------------|--------------------------------------------------------------|
| <i>c</i>     | The total contribution the loop should resemble              |
| <i>i</i>     | position i of enclosing pair                                 |
| <i>j</i>     | position j of enclosing pair                                 |
| <i>type</i>  | base pair type of enclosing pair (must be reverse type)      |
| <i>S</i>     | integer encoded sequence                                     |
| <i>ggg</i>   | triangular matrix containing g-quadruplex contributions      |
| <i>index</i> | the index for accessing the triangular matrix                |
| <i>p</i>     | here the 5' position of the gquad is stored                  |
| <i>q</i>     | here the 3' position of the gquad is stored                  |
| <i>P</i>     | the datastructure containing the precalculated contributions |

**Returns**

1 on success, 0 if no gquad found

**16.49.2.4 backtrack\_GQuad\_IntLoop\_L()**

```
PRIVATE int backtrack_GQuad_IntLoop_L (
    int c,
```

```

    int i,
    int j,
    int type,
    short * S,
    int ** ggg,
    int maxdist,
    int * p,
    int * q,
    vrna_param_t * P )
#include <ViennaRNA/gquad.h>
backtrack an interior loop like enclosed g-quadruplex with closing pair (i,j) with underlying Lfold matrix

```

**Parameters**

|             |                                                             |
|-------------|-------------------------------------------------------------|
| <i>c</i>    | The total contribution the loop should resemble             |
| <i>i</i>    | position i of enclosing pair                                |
| <i>j</i>    | position j of enclosing pair                                |
| <i>type</i> | base pair type of enclosing pair (must be reverse type)     |
| <i>S</i>    | integer encoded sequence                                    |
| <i>ggg</i>  | triangular matrix containing g-quadruplex contributions     |
| <i>p</i>    | here the 5' position of the gquad is stored                 |
| <i>q</i>    | here the 3' position of the gquad is stored                 |
| <i>P</i>    | the datastructure containing the precalculated contibutions |

**Returns**

1 on success, 0 if no gquad found

## 16.50 Utilities

### 16.50.1 Detailed Description

Collaboration diagram for Utilities:

**Modules**

- [Utilities to deal with Nucleotide Alphabets](#)  
*Functions to cope with various aspects related to the nucleotide sequence alphabet.*
- [\(Nucleic Acid Sequence\) String Utilities](#)  
*Functions to parse, convert, manipulate, create, and compare (nucleic acid sequence) strings.*
- [Secondary Structure Utilities](#)  
*Functions to create, parse, convert, manipulate, and compare secondary structure representations.*
- [Multiple Sequence Alignment Utilities](#)  
*Functions to extract features from and to manipulate multiple sequence alignments.*
- [Files and I/O](#)  
*Functions to parse, write, and convert various file formats and to deal with file system related issues.*
- [Plotting](#)  
*Functions for Creating Secondary Structure Plots, Dot-Plots, and More.*
- [Search Algorithms](#)  
*Implementations of various search algorithms to detect strings of objects within other strings of objects.*
- [Combinatorics Algorithms](#)  
*Implementations to solve various combinatorial aspects for strings of objects.*
- [\(Abstract\) Data Structures](#)

All datastructures and typedefs shared among the ViennaRNA Package can be found here.

- [Messages](#)

Functions to print various kind of messages.

- [Unit Conversion](#)

Functions to convert between various physical units.

## Files

- file [alphabet.h](#)

Functions to process, convert, and generally handle different nucleotide and/or base pair alphabets.

- file [combinatorics.h](#)

Various implementations that deal with combinatorial aspects of objects.

- file [commands.h](#)

Parse and apply different commands that alter the behavior of secondary structure prediction and evaluation.

- file [sequence.h](#)

Functions and data structures related to sequence representations ,.

- file [file\\_formats\\_msa.h](#)

Functions dealing with file formats for Multiple Sequence Alignments (MSA)

- file [utils.h](#)

Several utilities for file handling.

- file [utils.h](#)

Various utilities to assist in plotting secondary structures and consensus structures.

- file [alignments.h](#)

Various utility- and helper-functions for sequence alignments and comparative structure prediction.

- file [basic.h](#)

General utility- and helper-functions used throughout the ViennaRNA Package.

- file [strings.h](#)

General utility- and helper-functions for RNA sequence and structure strings used throughout the ViennaRNA Package.

- file [units.h](#)

Physical Units and Functions to convert them into each other.

- file [BoyerMoore.h](#)

Variants of the Boyer-Moore string search algorithm.

- file [char\\_stream.h](#)

Implementation of a dynamic, buffered character stream.

- file [stream\\_output.h](#)

An implementation of a buffered, ordered stream output data structure.

## Macros

- `#define VRNA_INPUT_ERROR 1U`

Output flag of [get\\_input\\_line\(\)](#): "An ERROR has occurred, maybe EOF".

- `#define VRNA_INPUT_QUIT 2U`

Output flag of [get\\_input\\_line\(\)](#): "the user requested quitting the program".

- `#define VRNA_INPUT_MISC 4U`

Output flag of [get\\_input\\_line\(\)](#): "something was read".

- `#define VRNA_INPUT_FASTA_HEADER 8U`

Input/Output flag of [get\\_input\\_line\(\)](#):

if used as input option this tells [get\\_input\\_line\(\)](#) that the data to be read should comply with the FASTA format.

- `#define VRNA_INPUT_CONSTRAINT 32U`

Input flag for [get\\_input\\_line\(\)](#):

Tell [get\\_input\\_line\(\)](#) that we assume to read a structure constraint.

- **#define VRNA\_INPUT\_NO\_TRUNCATION 256U**  
*Input switch for [get\\_input\\_line\(\)](#): "do not truncate the line by eliminating white spaces at end of line".*
- **#define VRNA\_INPUT\_NO\_REST 512U**  
*Input switch for [vrna\\_file\\_fasta\\_read\\_record\(\)](#): "do fill rest array".*
- **#define VRNA\_INPUT\_NO\_SPAN 1024U**  
*Input switch for [vrna\\_file\\_fasta\\_read\\_record\(\)](#): "never allow data to span more than one line".*
- **#define VRNA\_INPUT\_NOSKIP\_BLANK\_LINES 2048U**  
*Input switch for [vrna\\_file\\_fasta\\_read\\_record\(\)](#): "do not skip empty lines".*
- **#define VRNA\_INPUT\_BLANK\_LINE 4096U**  
*Output flag for [vrna\\_file\\_fasta\\_read\\_record\(\)](#): "read an empty line".*
- **#define VRNA\_INPUT\_NOSKIP\_COMMENTS 128U**  
*Input switch for [get\\_input\\_line\(\)](#): "do not skip comment lines".*
- **#define VRNA\_INPUT\_COMMENT 8192U**  
*Output flag for [vrna\\_file\\_fasta\\_read\\_record\(\)](#): "read a comment".*
- **#define MIN2(A, B) ((A) < (B) ? (A) : (B))**  
*Get the minimum of two comparable values.*
- **#define MAX2(A, B) ((A) > (B) ? (A) : (B))**  
*Get the maximum of two comparable values.*
- **#define MIN3(A, B, C) (MIN2((MIN2((A), (B))), (C)))**  
*Get the minimum of three comparable values.*
- **#define MAX3(A, B, C) (MAX2((MAX2((A), (B))), (C)))**  
*Get the maximum of three comparable values.*

## Functions

- void \* [vrna\\_alloc](#) (unsigned size)  
*Allocate space safely.*
- void \* [vrna\\_realloc](#) (void \*p, unsigned size)  
*Reallocate space safely.*
- void [vrna\\_init\\_rand](#) (void)  
*Initialize seed for random number generator.*
- void [vrna\\_init\\_rand\\_seed](#) (unsigned int seed)  
*Initialize the random number generator with a pre-defined seed.*
- double [vrna\\_urn](#) (void)  
*get a random number from [0..1]*
- int [vrna\\_int\\_urn](#) (int from, int to)  
*Generates a pseudo random integer in a specified range.*
- char \* [vrna\\_time\\_stamp](#) (void)  
*Get a timestamp.*
- unsigned int [get\\_input\\_line](#) (char \*\*string, unsigned int options)
- int \* [vrna\\_idx\\_row\\_wise](#) (unsigned int length)  
*Get an index mapper array (iidx) for accessing the energy matrices, e.g. in partition function related functions.*
- int \* [vrna\\_idx\\_col\\_wise](#) (unsigned int length)  
*Get an index mapper array (indx) for accessing the energy matrices, e.g. in MFE related functions.*

## Variables

- unsigned short [xsubi](#) [3]  
*Current 48 bit random number.*

### 16.50.2 Macro Definition Documentation

### 16.50.2.1 VRNA\_INPUT\_FASTA\_HEADER

```
#define VRNA_INPUT_FASTA_HEADER 8U
#include <ViennaRNA/utils/basic.h>
```

Input/Output flag of [get\\_input\\_line\(\)](#):

if used as input option this tells [get\\_input\\_line\(\)](#) that the data to be read should comply with the FASTA format.  
the function will return this flag if a fasta header was read

## 16.50.3 Function Documentation

### 16.50.3.1 vrna\_alloc()

```
void * vrna_alloc (
    unsigned size )
#include <ViennaRNA/utils/basic.h>
```

Allocate space safely.

#### Parameters

|             |                                                 |
|-------------|-------------------------------------------------|
| <i>size</i> | The size of the memory to be allocated in bytes |
|-------------|-------------------------------------------------|

#### Returns

A pointer to the allocated memory

### 16.50.3.2 vrna\_realloc()

```
void * vrna_realloc (
    void * p,
    unsigned size )
#include <ViennaRNA/utils/basic.h>
```

Reallocate space safely.

#### Parameters

|             |                                                  |
|-------------|--------------------------------------------------|
| <i>p</i>    | A pointer to the memory region to be reallocated |
| <i>size</i> | The size of the memory to be allocated in bytes  |

#### Returns

A pointer to the newly allocated memory

### 16.50.3.3 vrna\_init\_rand()

```
void vrna_init_rand (
    void )
#include <ViennaRNA/utils/basic.h>
```

Initialize seed for random number generator.

#### See also

[vrna\\_init\\_rand\\_seed\(\)](#), [vrna\\_urn\(\)](#)

**16.50.3.4 vrna\_init\_rand\_seed()**

```
void vrna_init_rand_seed (
    unsigned int seed )
#include <ViennaRNA/utils/basic.h>
Initialize the random number generator with a pre-defined seed.
```

See also

[vrna\\_init\\_rand\(\)](#), [vrna\\_urn\(\)](#)

**Parameters**

|             |                                          |
|-------------|------------------------------------------|
| <i>seed</i> | The seed for the random number generator |
|-------------|------------------------------------------|

**SWIG Wrapper Notes** This function is available as an overloaded function [init\\_rand\(\)](#) where the argument *seed* is optional.

**16.50.3.5 vrna\_urn()**

```
double vrna_urn (
    void )
#include <ViennaRNA/utils/basic.h>
get a random number from [0..1]
```

See also

[vrna\\_int\\_urn\(\)](#), [vrna\\_init\\_rand\(\)](#), [vrna\\_init\\_rand\\_seed\(\)](#)

**Note**

Usually implemented by calling *erand48()*.

**Returns**

A random number in range [0..1]

**16.50.3.6 vrna\_int\_urn()**

```
int vrna_int_urn (
    int from,
    int to )
#include <ViennaRNA/utils/basic.h>
Generates a pseudo random integer in a specified range.
```

See also

[vrna\\_urn\(\)](#), [vrna\\_init\\_rand\(\)](#)

**Parameters**

|             |                           |
|-------------|---------------------------|
| <i>from</i> | The first number in range |
| <i>to</i>   | The last number in range  |

**Returns**

A pseudo random number in range [from, to]

**16.50.3.7 vrna\_time\_stamp()**

```
char * vrna_time_stamp (
    void )
#include <ViennaRNA/utils/basic.h>
Get a timestamp.
Returns a string containing the current date in the format
```

```
Fri Mar 19 21:10:57 1993
```

**Returns**

A string containing the timestamp

**16.50.3.8 get\_input\_line()**

```
unsigned int get_input_line (
    char ** string,
    unsigned int options )
#include <ViennaRNA/utils/basic.h>
Retrieve a line from 'stdin' safely while skipping comment characters and other features This function returns the
type of input it has read if recognized. An option argument allows one to switch between different reading modes.
Currently available options are:
VRNA_INPUT_COMMENT, VRNA_INPUT_NOSKIP_COMMENTS, VRNA_INPUT_NO_TRUNCATION
pass a collection of options as one value like this:
```

```
get_input_line(string, option_1 | option_2 | option_n)
```

If the function recognizes the type of input, it will report it in the return value. It also reports if a user defined 'quit' command (-sign on 'stdin') was given. Possible return values are:

[VRNA\\_INPUT\\_FASTA\\_HEADER](#), [VRNA\\_INPUT\\_ERROR](#), [VRNA\\_INPUT\\_MISC](#), [VRNA\\_INPUT\\_QUIT](#)

**Parameters**

|                |                                                              |
|----------------|--------------------------------------------------------------|
| <i>string</i>  | A pointer to the character array that contains the line read |
| <i>options</i> | A collection of options for switching the functions behavior |

**Returns**

A flag with information about what has been read

**16.50.3.9 vrna\_idx\_row\_wise()**

```
int * vrna_idx_row_wise (
    unsigned int length )
#include <ViennaRNA/utils/basic.h>
Get an index mapper array (iidx) for accessing the energy matrices, e.g. in partition function related functions.
Access of a position "(i,j)" is then accomplished by using
(i,j) ~ iidx[i]-j
```

This function is necessary as most of the two-dimensional energy matrices are actually one-dimensional arrays throughout the ViennaRNA Package

Consult the implemented code to find out about the mapping formula ;)



See also

[vrna\\_idx\\_col\\_wise\(\)](#)

Parameters

|               |                                |
|---------------|--------------------------------|
| <i>length</i> | The length of the RNA sequence |
|---------------|--------------------------------|

Returns

The mapper array

### 16.50.3.10 vrna\_idx\_col\_wise()

```
int * vrna_idx_col_wise (
    unsigned int length )
```

```
#include <ViennaRNA/utils/basic.h>
```

Get an index mapper array (indx) for accessing the energy matrices, e.g. in MFE related functions. Access of a position "(i,j)" is then accomplished by using

```
(i,j) ~ indx[j]+i
```

This function is necessary as most of the two-dimensional energy matrices are actually one-dimensional arrays throughout the ViennaRNAPackage

Consult the implemented code to find out about the mapping formula ;)

See also

[vrna\\_idx\\_row\\_wise\(\)](#)

Parameters

|               |                                |
|---------------|--------------------------------|
| <i>length</i> | The length of the RNA sequence |
|---------------|--------------------------------|

Returns

The mapper array

## 16.50.4 Variable Documentation

### 16.50.4.1 xsubi

```
unsigned short xsubi[3] [extern]
```

```
#include <ViennaRNA/utils/basic.h>
```

Current 48 bit random number.

This variable is used by [vrna\\_urn\(\)](#). These should be set to some random number seeds before the first call to [vrna\\_urn\(\)](#).

See also

[vrna\\_urn\(\)](#)

## 16.51 Exterior Loops

Functions to evaluate the free energy contributions for exterior loops.

### 16.51.1 Detailed Description

Functions to evaluate the free energy contributions for exterior loops.  
Collaboration diagram for Exterior Loops:

#### Files

- file [external.h](#)  
*Energy evaluation of exterior loops for MFE and partition function calculations.*

### Boltzmann weight (partition function) interface

- typedef struct vrna\_mx\_pf\_aux\_el\_s \* [vrna\\_mx\\_pf\\_aux\\_el\\_t](#)  
*Auxiliary helper arrays for fast exterior loop computations.*
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ext\\_stem](#) (unsigned int type, int n5d, int n3d, [vrna\\_exp\\_param\\_t](#) \*p)  
*Evaluate a stem branching off the exterior loop (Boltzmann factor version)*
- [vrna\\_mx\\_pf\\_aux\\_el\\_t vrna\\_exp\\_E\\_ext\\_fast\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_rotate](#) ([vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_free](#) ([vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ext\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_update](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int j, [vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)

### Basic free energy interface

- int [vrna\\_E\\_ext\\_stem](#) (unsigned int type, int n5d, int n3d, [vrna\\_param\\_t](#) \*p)  
*Evaluate a stem branching off the exterior loop.*
- int [vrna\\_eval\\_ext\\_stem](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of a base pair in the exterior loop.*
- int [vrna\\_E\\_ext\\_loop\\_5](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- int [vrna\\_E\\_ext\\_loop\\_3](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i)

## 16.51.2 Typedef Documentation

### 16.51.2.1 vrna\_mx\_pf\_aux\_el\_t

```
typedef struct vrna_mx_pf_aux_el_s* vrna\_mx\_pf\_aux\_el\_t
#include <ViennaRNA/loops/external.h>
```

Auxiliary helper arrays for fast exterior loop computations.

See also

[vrna\\_exp\\_E\\_ext\\_fast\\_init\(\)](#), [vrna\\_exp\\_E\\_ext\\_fast\\_rotate\(\)](#), [vrna\\_exp\\_E\\_ext\\_fast\\_free\(\)](#), [vrna\\_exp\\_E\\_ext\\_fast\(\)](#)

## 16.51.3 Function Documentation

### 16.51.3.1 vrna\_E\_ext\_stem()

```
int vrna_E_ext_stem (
    unsigned int type,
    int n5d,
    int n3d,
    vrna\_param\_t * p )
#include <ViennaRNA/loops/external.h>
```

Evaluate a stem branching off the exterior loop.

Given a base pair  $(i, j)$  encoded by *type*, compute the energy contribution including dangling-end/terminal-mismatch contributions. Instead of returning the energy contribution per-se, this function returns the corresponding Boltzmann factor. If either of the adjacent nucleotides  $(i - 1)$  and  $(j + 1)$  must not contribute stacking energy, the corresponding encoding must be  $-1$ .

See also

`vrna_E_exp_stem()`

#### Parameters

|             |                                                                                      |
|-------------|--------------------------------------------------------------------------------------|
| <i>type</i> | The base pair encoding                                                               |
| <i>n5d</i>  | The encoded nucleotide directly adjacent at the 5' side of the base pair (may be -1) |
| <i>n3d</i>  | The encoded nucleotide directly adjacent at the 3' side of the base pair (may be -1) |
| <i>p</i>    | The pre-computed energy parameters                                                   |

#### Returns

The energy contribution of the introduced exterior-loop stem

### 16.51.3.2 `vrna_eval_ext_stem()`

```
int vrna_eval_ext_stem (
    vrna_fold_compound_t * fc,
    int i,
    int j )
```

#include <ViennaRNA/loops/external.h>

Evaluate the free energy of a base pair in the exterior loop.

Evaluate the free energy of a base pair connecting two nucleotides in the exterior loop and take hard constraints into account.

Typically, this is simply dangling end contributions of the adjacent nucleotides, potentially a terminal A-U mismatch penalty, and maybe some generic soft constraint contribution for that decomposition.

#### Note

For dangles == 1 || 3 this function also evaluates the three additional pairs  $(i + 1, j)$ ,  $(i, j - 1)$ , and  $(i + 1, j - 1)$  and returns the minimum for all four possibilities in total.

#### Parameters

|           |                                                             |
|-----------|-------------------------------------------------------------|
| <i>fc</i> | Fold compound to work on (defines the model and parameters) |
| <i>i</i>  | 5' position of the base pair                                |
| <i>j</i>  | 3' position of the base pair                                |

#### Returns

Free energy contribution that arises when this pair is formed in the exterior loop

### 16.51.3.3 `vrna_exp_E_ext_stem()`

```
FLT_OR_DBL vrna_exp_E_ext_stem (
    unsigned int type,
    int n5d,
```

```

    int n3d,
    vrna_exp_param_t * p )
#include <ViennaRNA/loops/external.h>

```

Evaluate a stem branching off the exterior loop (Boltzmann factor version)

Given a base pair  $(i, j)$  encoded by *type*, compute the energy contribution including dangling-end/terminal-mismatch contributions. Instead of returning the energy contribution per-se, this function returns the corresponding Boltzmann factor. If either of the adjacent nucleotides  $(i - 1)$  and  $(j + 1)$  must not contribute stacking energy, the corresponding encoding must be  $-1$ .

See also

[vrna\\_E\\_ext\\_stem\(\)](#)

#### Parameters

|             |                                                                                      |
|-------------|--------------------------------------------------------------------------------------|
| <i>type</i> | The base pair encoding                                                               |
| <i>n5d</i>  | The encoded nucleotide directly adjacent at the 5' side of the base pair (may be -1) |
| <i>n3d</i>  | The encoded nucleotide directly adjacent at the 3' side of the base pair (may be -1) |
| <i>p</i>    | The pre-computed energy parameters (Boltzmann factor version)                        |

#### Returns

The Boltzmann weighted energy contribution of the introduced exterior-loop stem

## 16.52 Hairpin Loops

Functions to evaluate the free energy contributions for hairpin loops.

### 16.52.1 Detailed Description

Functions to evaluate the free energy contributions for hairpin loops.

Collaboration diagram for Hairpin Loops:

#### Files

- file [hairpin.h](#)

*Energy evaluation of hairpin loops for MFE and partition function calculations.*

#### Basic free energy interface

- int [vrna\\_E\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of a hairpin loop and consider hard constraints if they apply.*
- int [vrna\\_E\\_ext\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of an exterior hairpin loop and consider possible hard constraints.*
- int [vrna\\_eval\\_ext\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate free energy of an exterior hairpin loop.*
- int [vrna\\_eval\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate free energy of a hairpin loop.*
- PRIVATE int [E\\_Hairpin](#) (int size, int type, int si1, int sj1, const char \*string, [vrna\\_param\\_t](#) \*P)  
*Compute the Energy of a hairpin-loop.*

## Boltzmann weight (partition function) interface

- PRIVATE `FLT_OR_DBL exp_E_Hairpin` (int u, int type, short si1, short sj1, const char \*string, `vrna_exp_param_t` \*P)  
Compute Boltzmann weight  $e^{-\Delta G/kT}$  of a hairpin loop.
- `FLT_OR_DBL vrna_exp_E_hp_loop` (`vrna_fold_compound_t` \*fc, int i, int j)  
High-Level function for hairpin loop energy evaluation (partition function variant)

## 16.52.2 Function Documentation

### 16.52.2.1 vrna\_E\_hp\_loop()

```
int vrna_E_hp_loop (
    vrna_fold_compound_t * fc,
    int i,
    int j )
```

#include <ViennaRNA/loops/hairpin.h>

Evaluate the free energy of a hairpin loop and consider hard constraints if they apply.

This function evaluates the free energy of a hairpin loop

In case the base pair is not allowed due to a constraint conflict, this function returns `INF`.

#### Note

This function is polymorphic! The provided `vrna_fold_compound_t` may be of type `VRNA_FC_TYPE_SINGLE` or `VRNA_FC_TYPE_COMPARATIVE`

#### Parameters

|           |                                                                                       |
|-----------|---------------------------------------------------------------------------------------|
| <i>fc</i> | The <code>vrna_fold_compound_t</code> that stores all relevant model settings         |
| <i>i</i>  | The 5' nucleotide of the base pair (3' to evaluate the pair as exterior hairpin loop) |
| <i>j</i>  | The 3' nucleotide of the base pair (5' to evaluate the pair as exterior hairpin loop) |

#### Returns

The free energy of the hairpin loop in 10cal/mol

### 16.52.2.2 vrna\_E\_ext\_hp\_loop()

```
int vrna_E_ext_hp_loop (
    vrna_fold_compound_t * fc,
    int i,
    int j )
```

#include <ViennaRNA/loops/hairpin.h>

Evaluate the free energy of an exterior hairpin loop and consider possible hard constraints.

#### Note

This function is polymorphic! The provided `vrna_fold_compound_t` may be of type `VRNA_FC_TYPE_SINGLE` or `VRNA_FC_TYPE_COMPARATIVE`

### 16.52.2.3 vrna\_eval\_hp\_loop()

```
int vrna_eval_hp_loop (
    vrna_fold_compound_t * fc,
```

```

        int i,
        int j )
#include <ViennaRNA/loops/hairpin.h>
Evaluate free energy of a hairpin loop.

```

**Note**

This function is polymorphic! The provided `vrna_fold_compound_t` may be of type `VRNA_FC_TYPE_SINGLE` or `VRNA_FC_TYPE_COMPARATIVE`

**Parameters**

|           |                                                                            |
|-----------|----------------------------------------------------------------------------|
| <i>fc</i> | The <code>vrna_fold_compound_t</code> for the particular energy evaluation |
| <i>i</i>  | 5'-position of the base pair                                               |
| <i>j</i>  | 3'-position of the base pair                                               |

**Returns**

Free energy of the hairpin loop closed by  $(i, j)$  in deka-kal/mol

**SWIG Wrapper Notes** This function is attached as method `eval_hp_loop()` to objects of type `fold_compound`

**16.52.2.4 E\_Hairpin()**

```

PRIVATE int E_Hairpin (
    int size,
    int type,
    int sil,
    int sjl,
    const char * string,
    vrna_param_t * P )
#include <ViennaRNA/loops/hairpin.h>
Compute the Energy of a hairpin-loop.

```

To evaluate the free energy of a hairpin-loop, several parameters have to be known. A general hairpin-loop has this structure:

```

    a3 a4
a2      a5
a1      a6
  X - Y
  |   |
  5'  3'

```

where X-Y marks the closing pair [e.g. a (**G,C**) pair]. The length of this loop is 6 as there are six unpaired nucleotides (a1-a6) enclosed by (X,Y). The 5' mismatching nucleotide is a1 while the 3' mismatch is a6. The nucleotide sequence of this loop is "a1.a2.a3.a4.a5.a6"

**Note**

The parameter sequence should contain the sequence of the loop in capital letters of the nucleic acid alphabet if the loop size is below 7. This is useful for unusually stable tri-, tetra- and hexa-loops which are treated differently (based on experimental data) if they are tabulated.

**See also**

[scale\\_parameters\(\)](#)  
[vrna\\_param\\_t](#)

**Warning**

Not (really) thread safe! A threadsafe implementation will replace this function in a future release!  
 Energy evaluation may change due to updates in global variable "tetra\_loop"

**Parameters**

|               |                                                                                                      |
|---------------|------------------------------------------------------------------------------------------------------|
| <i>size</i>   | The size of the loop (number of unpaired nucleotides)                                                |
| <i>type</i>   | The pair type of the base pair closing the hairpin                                                   |
| <i>si1</i>    | The 5'-mismatching nucleotide                                                                        |
| <i>sj1</i>    | The 3'-mismatching nucleotide                                                                        |
| <i>string</i> | The sequence of the loop (May be <code>NULL</code> , otherwise mst be at least <i>size</i> + 2 long) |
| <i>P</i>      | The datastructure containing scaled energy parameters                                                |

**Returns**

The Free energy of the Hairpin-loop in dcal/mol

**16.52.2.5 exp\_E\_Hairpin()**

```
PRIVATE FLT_OR_DBL exp_E_Hairpin (
    int u,
    int type,
    short si1,
    short sj1,
    const char * string,
    vrna_exp_param_t * P )
#include <ViennaRNA/loops/hairpin.h>
Compute Boltzmann weight  $e^{-\Delta G/kT}$  of a hairpin loop.
multiply by scale[u+2]
```

**See also**

[get\\_scaled\\_pf\\_parameters\(\)](#)  
[vrna\\_exp\\_param\\_t](#)  
[E\\_Hairpin\(\)](#)

**Warning**

Not (really) thread safe! A threadsafe implementation will replace this function in a future release!  
 Energy evaluation may change due to updates in global variable "tetra\_loop"

**Parameters**

|               |                                                                                                      |
|---------------|------------------------------------------------------------------------------------------------------|
| <i>u</i>      | The size of the loop (number of unpaired nucleotides)                                                |
| <i>type</i>   | The pair type of the base pair closing the hairpin                                                   |
| <i>si1</i>    | The 5'-mismatching nucleotide                                                                        |
| <i>sj1</i>    | The 3'-mismatching nucleotide                                                                        |
| <i>string</i> | The sequence of the loop (May be <code>NULL</code> , otherwise mst be at least <i>size</i> + 2 long) |
| <i>P</i>      | The datastructure containing scaled Boltzmann weights of the energy parameters                       |

**Returns**

The Boltzmann weight of the Hairpin-loop

**16.52.2.6 vrna\_exp\_E\_hp\_loop()**

```
FLT_OR_DBL vrna_exp_E_hp_loop (
    vrna_fold_compound_t * fc,
    int i,
    int j )
#include <ViennaRNA/loops/hairpin.h>
```

High-Level function for hairpin loop energy evaluation (partition function variant)

**See also**

[vrna\\_E\\_hp\\_loop\(\)](#) for it's free energy counterpart

**Note**

This function is polymorphic! The provided [vrna\\_fold\\_compound\\_t](#) may be of type [VRNA\\_FC\\_TYPE\\_SINGLE](#) or [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#)

**16.53 Internal Loops**

Functions to evaluate the free energy contributions for internal loops.

**16.53.1 Detailed Description**

Functions to evaluate the free energy contributions for internal loops.  
Collaboration diagram for Internal Loops:

**Files**

- file [internal.h](#)  
*Energy evaluation of interior loops for MFE and partition function calculations.*

**Basic free energy interface**

- int [vrna\\_E\\_int\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)
- int [vrna\\_eval\\_int\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int k, int l)  
*Evaluate the free energy contribution of an interior loop with delimiting base pairs  $(i, j)$  and  $(k, l)$ .*
- int [vrna\\_E\\_ext\\_int\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int \*ip, int \*iq)
- int [vrna\\_E\\_stack](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)

**Boltzmann weight (partition function) interface**

- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_int\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_interior\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int k, int l)

**16.53.2 Function Documentation**



### 16.53.2.1 vrna\_eval\_int\_loop()

```
int vrna_eval_int_loop (
    vrna_fold_compound_t * fc,
    int i,
    int j,
    int k,
    int l )
#include <ViennaRNA/loops/internal.h>
```

Evaluate the free energy contribution of an interior loop with delimiting base pairs  $(i, j)$  and  $(k, l)$ .

#### Note

This function is polymorphic, i.e. it accepts `vrna_fold_compound_t` of type `VRNA_FC_TYPE_SINGLE` as well as `VRNA_FC_TYPE_COMPARATIVE`

**SWIG Wrapper Notes** This function is attached as method `eval_int_loop()` to objects of type `fold_compound`

## 16.54 Multibranch Loops

Functions to evaluate the free energy contributions for multibranch loops.

### 16.54.1 Detailed Description

Functions to evaluate the free energy contributions for multibranch loops.

Collaboration diagram for Multibranch Loops:

#### Files

- file [multibranch.h](#)

*Energy evaluation of multibranch loops for MFE and partition function calculations.*

### Boltzmann weight (partition function) interface

- typedef struct `vrna_mx_pf_aux_ml_s` \* [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#)  
*Auxiliary helper arrays for fast exterior loop computations.*
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_mb\\_loop\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- [vrna\\_mx\\_pf\\_aux\\_ml\\_t vrna\\_exp\\_E\\_ml\\_fast\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- void [vrna\\_exp\\_E\\_ml\\_fast\\_rotate](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ml\\_fast\\_free](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- const [FLT\\_OR\\_DBL](#) \* [vrna\\_exp\\_E\\_ml\\_fast\\_qqm](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- const [FLT\\_OR\\_DBL](#) \* [vrna\\_exp\\_E\\_ml\\_fast\\_qqm1](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ml\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)

### Basic free energy interface

- int [vrna\\_E\\_mb\\_loop\\_stack](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate energy of a multi branch helices stacking onto closing pair  $(i, j)$*
- int [vrna\\_E\\_mb\\_loop\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int \*dmli1, int \*dmli2)
- int [E\\_ml\\_rightmost\\_stem](#) (int i, int j, [vrna\\_fold\\_compound\\_t](#) \*fc)
- int [vrna\\_E\\_ml\\_stems\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int \*fmi, int \*dmli)

### 16.54.2 Typedef Documentation

### 16.54.2.1 vrna\_mx\_pf\_aux\_ml\_t

```
typedef struct vrna_mx_pf_aux_ml_s* vrna_mx_pf_aux_ml_t
#include <ViennaRNA/loops/multibranch.h>
```

Auxiliary helper arrays for fast exterior loop computations.

See also

`vrna_exp_E_ml_fast_init()`, `vrna_exp_E_ml_fast_rotate()`, `vrna_exp_E_ml_fast_free()`, `vrna_exp_E_ml_fast()`

## 16.54.3 Function Documentation

### 16.54.3.1 vrna\_E\_mb\_loop\_stack()

```
int vrna_E_mb_loop_stack (
    vrna_fold_compound_t * fc,
    int i,
    int j )
```

```
#include <ViennaRNA/loops/multibranch.h>
```

Evaluate energy of a multi branch helices stacking onto closing pair (i,j)

Computes total free energy for coaxial stacking of (i,j) with (i+1.k) or (k+1.j-1)

## 16.55 Partition Function for Two Hybridized Sequences

Partition Function Cofolding.

### 16.55.1 Detailed Description

Partition Function Cofolding.

To simplify the implementation the partition function computation is done internally in a null model that does not include the duplex initiation energy, i.e. the entropic penalty for producing a dimer from two monomers). The resulting free energies and pair probabilities are initially relative to that null model. In a second step the free energies can be corrected to include the dimerization penalty, and the pair probabilities can be divided into the conditional pair probabilities given that a re dimer is formed or not formed. See [2] for further details.

As for folding one RNA molecule, this computes the partition function of all possible structures and the base pair probabilities. Uses the same global `pf_scale` variable to avoid overflows.

After computing the partition functions of all possible dimers one can compute the probabilities of base pairs, the concentrations out of start concentrations and sofar and soaway.

Dimer formation is inherently concentration dependent. Given the free energies of the monomers A and B and dimers AB, AA, and BB one can compute the equilibrium concentrations, given input concentrations of A and B, see e.g. Dimitrov & Zuker (2004) Collaboration diagram for Partition Function for Two Hybridized Sequences:

### Files

- file `concentrations.h`  
*Concentration computations for RNA-RNA interactions.*
- file `part_func_up.h`  
*Implementations for accessibility and RNA-RNA interaction as a stepwise process.*

### Typedefs

- typedef struct `vrna_dimer_pf_s` `vrna_dimer_pf_t`  
*Typename for the data structure that stores the dimer partition functions, `vrna_dimer_pf_s`, as returned by `vrna_pf_dimer()`*
- typedef struct `vrna_dimer_pf_s` `cofoldF`  
*Backward compatibility typedef for `vrna_dimer_pf_s`.*

## Variables

- int **mirnatog**  
*Toggles no intrabp in 2nd mol.*
- double **F\_monomer** [2]  
*Free energies of the two monomers.*
- typedef struct **vrna\_dimer\_conc\_s** **vrna\_dimer\_conc\_t**  
*Typename for the data structure that stores the dimer concentrations, [vrna\\_dimer\\_conc\\_s](#), as required by [vrna\\_pf\\_dimer\\_concentration\(\)](#)*
- typedef struct **vrna\_dimer\_conc\_s** **ConcEnt**  
*Backward compatibility typedef for [vrna\\_dimer\\_conc\\_s](#).*
- [vrna\\_dimer\\_conc\\_t](#) \* [vrna\\_pf\\_dimer\\_concentrations](#) (double FcAB, double FcAA, double FcBB, double FEA, double FEB, const double \*startconc, const [vrna\\_exp\\_param\\_t](#) \*exp\_params)  
*Given two start monomer concentrations a and b, compute the concentrations in thermodynamic equilibrium of all dimers and the monomers.*

## Simplified global partition function computation using sequence(s) or multiple sequence alignment(s)

- [vrna\\_dimer\\_pf\\_t](#) [vrna\\_pf\\_co\\_fold](#) (const char \*seq, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.*

### 16.55.2 Function Documentation

#### 16.55.2.1 [vrna\\_pf\\_co\\_fold\(\)](#)

```
vrna\_dimer\_pf\_t vrna\_pf\_co\_fold (
    const char * seq,
    char * structure,
    vrna\_ep\_t ** pl )
#include <ViennaRNA/part\_func.h>
```

Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.

This simplified interface to [vrna\\_pf\\_dimer\(\)](#) computes the partition function and, if required, base pair probabilities for an RNA-RNA interaction using default options. Memory required for dynamic programming (DP) matrices will be allocated and free'd on-the-fly. Hence, after return of this function, the recursively filled matrices are not available any more for any post-processing.

#### Note

In case you want to use the filled DP matrices for any subsequent post-processing step, or you require other conditions than specified by the default model details, use [vrna\\_pf\\_dimer\(\)](#), and the data structure [vrna\\_fold\\_compound\\_t](#) instead.

#### See also

[vrna\\_pf\\_dimer\(\)](#)

#### Parameters

|                  |                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------|
| <i>seq</i>       | Two concatenated RNA sequences with a delimiting '&' in between                                      |
| <i>structure</i> | A pointer to the character array where position-wise pairing propensity will be stored. (Maybe NULL) |
| <i>pl</i>        | A pointer to a list of <a href="#">vrna_ep_t</a> to store pairing probabilities (Maybe NULL)         |

**Returns**

`vrna_dimer_pf_t` structure containing a set of energies needed for concentration computations.

**16.55.2.2 vrna\_pf\_dimer\_concentrations()**

```
vrna_dimer_conc_t * vrna_pf_dimer_concentrations (
    double FcAB,
    double FcAA,
    double FcBB,
    double FEA,
    double FEB,
    const double * startconc,
    const vrna_exp_param_t * exp_params )
```

```
#include <ViennaRNA/concentrations.h>
```

Given two start monomer concentrations a and b, compute the concentrations in thermodynamic equilibrium of all dimers and the monomers.

This function takes an array 'startconc' of input concentrations with alternating entries for the initial concentrations of molecules A and B (terminated by two zeroes), then computes the resulting equilibrium concentrations from the free energies for the dimers. Dimer free energies should be the dimer-only free energies, i.e. the FcAB entries from the `vrna_dimer_pf_t` struct.

**Parameters**

|                   |                                                                        |
|-------------------|------------------------------------------------------------------------|
| <i>FcAB</i>       | Free energy of AB dimer (FcAB entry)                                   |
| <i>FcAA</i>       | Free energy of AA dimer (FcAB entry)                                   |
| <i>FcBB</i>       | Free energy of BB dimer (FcAB entry)                                   |
| <i>FEA</i>        | Free energy of monomer A                                               |
| <i>FEB</i>        | Free energy of monomer B                                               |
| <i>startconc</i>  | List of start concentrations [a0],[b0],[a1],[b1],...,[an],[bn],[0],[0] |
| <i>exp_params</i> | The precomputed Boltzmann factors                                      |

**Returns**

`vrna_dimer_conc_t` array containing the equilibrium energies and start concentrations

## 16.56 Partition Function for two Hybridized Sequences as a Stepwise Process

RNA-RNA interaction as a stepwise process.

**16.56.1 Detailed Description**

RNA-RNA interaction as a stepwise process.

In this approach to cofolding the interaction between two RNA molecules is seen as a stepwise process. In a first step, the target molecule has to adopt a structure in which a binding site is accessible. In a second step, the ligand molecule will hybridize with a region accessible to an interaction. Consequently the algorithm is designed as a two step process: The first step is the calculation of the probability that a region within the target is unpaired, or equivalently, the calculation of the free energy needed to expose a region. In the second step we compute the free energy of an interaction for every possible binding site. Collaboration diagram for Partition Function for two Hybridized Sequences as a Stepwise Process:

**Functions**

- `pu_contrib * pf_unstru` (char \*sequence, int max\_w)

*Calculate the partition function over all unpaired regions of a maximal length.*

- `interact * pf_interact` (`const char *s1`, `const char *s2`, `pu_contrib *p_c`, `pu_contrib *p_c2`, `int max_w`, `char *cstruc`, `int incr3`, `int incr5`)

*Calculates the probability of a local interaction between two sequences.*

- `void free_interact` (`interact *pin`)  
*Frees the output of function `pf_interact()`.*
- `void free_pu_contrib_struct` (`pu_contrib *pu`)  
*Frees the output of function `pf_unstru()`.*

## 16.56.2 Function Documentation

### 16.56.2.1 pf\_unstru()

```
pu_contrib * pf_unstru (
    char * sequence,
    int max_w )
#include <ViennaRNA/part_func_up.h>
```

Calculate the partition function over all unpaired regions of a maximal length.

You have to call function `pf_fold()` providing the same sequence before calling `pf_unstru()`. If you want to calculate unpaired regions for a constrained structure, set variable 'structure' in function '`pf_fold()`' to the constrain string. It returns a `pu_contrib` struct containing four arrays of dimension  $[i = 1 \text{ to } \text{length}(\text{sequence})][j = 0 \text{ to } u-1]$  containing all possible contributions to the probabilities of unpaired regions of maximum length  $u$ . Each array in `pu_contrib` contains one of the contributions to the total probability of being unpaired: The probability of being unpaired within an exterior loop is in array `pu_contrib->E`, the probability of being unpaired within a hairpin loop is in array `pu_contrib->H`, the probability of being unpaired within an interior loop is in array `pu_contrib->I` and probability of being unpaired within a multi-loop is in array `pu_contrib->M`. The total probability of being unpaired is the sum of the four arrays of `pu_contrib`.

This function frees everything allocated automatically. To free the output structure call `free_pu_contrib()`.

#### Parameters

|                       |  |
|-----------------------|--|
| <code>sequence</code> |  |
| <code>max_w</code>    |  |

#### Returns

### 16.56.2.2 pf\_interact()

```
interact * pf_interact (
    const char * s1,
    const char * s2,
    pu_contrib * p_c,
    pu_contrib * p_c2,
    int max_w,
    char * cstruc,
    int incr3,
    int incr5 )
#include <ViennaRNA/part_func_up.h>
```

Calculates the probability of a local interaction between two sequences.

The function considers the probability that the region of interaction is unpaired within 's1' and 's2'. The longer sequence has to be given as 's1'. The shorter sequence has to be given as 's2'. Function `pf_unstru()` has to be called for 's1' and 's2', where the probabilities of being unpaired have to be given in 'p\_c' and 'p\_c2', respectively.

If you do not want to include the probabilities of being unpaired for 's2' set 'p\_c2' to NULL. If variable 'cstruc' is not NULL, constrained folding is done: The available constraints for intermolecular interaction are: '.' (no constrain), 'x' (the base has no intermolecular interaction) and '|' (the corresponding base has to be paired intermolecularly).

The parameter 'w' determines the maximal length of the interaction. The parameters 'incr5' and 'incr3' allows inclusion of unpaired residues left ('incr5') and right ('incr3') of the region of interaction in 's1'. If the 'incr' options are used, function [pf\\_unstru\(\)](#) has to be called with  $w=w+incr5+incr3$  for the longer sequence 's1'.

It returns a structure of type [interact](#) which contains the probability of the best local interaction including residue i in  $P_i$  and the minimum free energy in  $G_i$ , where i is the position in sequence 's1'. The member  $G_{ijkl}$  of structure [interact](#) is the best interaction between region  $[k,i]$   $k < i$  in longer sequence 's1' and region  $[j,l]$   $j < l$  in 's2'.  $G_{ijkl\_wo}$  is  $G_{ijkl}$  without the probability of being unpaired.

Use [free\\_interact\(\)](#) to free the returned structure, all other stuff is freed inside [pf\\_interact\(\)](#).

#### Parameters

|                             |  |
|-----------------------------|--|
| s1                          |  |
| s2                          |  |
| p_c                         |  |
| p_c2                        |  |
| max $\leftrightarrow$<br>_w |  |
| cstruc                      |  |
| incr3                       |  |
| incr5                       |  |

#### Returns

## 16.57 Reading/Writing Energy Parameter Sets from/to File

Read and Write energy parameter sets from and to files or strings.

### 16.57.1 Detailed Description

Read and Write energy parameter sets from and to files or strings.

Collaboration diagram for Reading/Writing Energy Parameter Sets from/to File:

#### Modules

- [Converting Energy Parameter Files](#)  
*Convert energy parameter files into the latest format.*

#### Macros

- #define [VRNA\\_PARAMETER\\_FORMAT\\_DEFAULT](#) 0  
*Default Energy Parameter File format.*

#### Functions

- int [vrna\\_params\\_load](#) (const char fname[], unsigned int options)  
*Load energy parameters from a file.*
- int [vrna\\_params\\_save](#) (const char fname[], unsigned int options)  
*Save energy parameters to a file.*
- int [vrna\\_params\\_load\\_from\\_string](#) (const char \*string, const char \*name, unsigned int options)  
*Load energy parameters from string.*

- int [vrna\\_params\\_load\\_defaults](#) (void)  
*Load default RNA energy parameter set.*
- int [vrna\\_params\\_load\\_RNA\\_Turner2004](#) (void)  
*Load Turner 2004 RNA energy parameter set.*
- int [vrna\\_params\\_load\\_RNA\\_Turner1999](#) (void)  
*Load Turner 1999 RNA energy parameter set.*
- int [vrna\\_params\\_load\\_RNA\\_Andronescu2007](#) (void)  
*Load Andronescu 2007 RNA energy parameter set.*
- int [vrna\\_params\\_load\\_RNA\\_Langdon2018](#) (void)  
*Load Langdon 2018 RNA energy parameter set.*
- int [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins](#) (void)  
*Load Misc Special Hairpin RNA energy parameter set.*
- int [vrna\\_params\\_load\\_DNA\\_Mathews2004](#) (void)  
*Load Mathews 2004 DNA energy parameter set.*
- int [vrna\\_params\\_load\\_DNA\\_Mathews1999](#) (void)  
*Load Mathews 1999 DNA energy parameter set.*
- const char \* [last\\_parameter\\_file](#) (void)  
*Get the file name of the parameter file that was most recently loaded.*
- void [read\\_parameter\\_file](#) (const char fname[ ])  
*Read energy parameters from a file.*
- void [write\\_parameter\\_file](#) (const char fname[ ])  
*Write energy parameters to a file.*

## 16.57.2 Macro Definition Documentation

### 16.57.2.1 VRNA\_PARAMETER\_FORMAT\_DEFAULT

```
#define VRNA_PARAMETER_FORMAT_DEFAULT 0
#include <ViennaRNA/params/io.h>
```

Default Energy Parameter File format.

See also

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#)

## 16.57.3 Function Documentation

### 16.57.3.1 vrna\_params\_load()

```
int vrna_params_load (
    const char fname[],
    unsigned int options )
#include <ViennaRNA/params/io.h>
```

Load energy parameters from a file.

See also

[vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews1999\(\)](#)

## Parameters

|                |                                                                               |
|----------------|-------------------------------------------------------------------------------|
| <i>fname</i>   | The path to the file containing the energy parameters                         |
| <i>options</i> | File format bit-mask (usually <a href="#">VRNA_PARAMETER_FORMAT_DEFAULT</a> ) |

## Returns

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as overloaded function `params_load(fname="", options=VRNA_PARAMETER_FORMAT_DEFAULT)`. Here, the empty filename string indicates to load default RNA parameters, i.e. this is equivalent to calling `vrna_params_load_defaults()`.

16.57.3.2 `vrna_params_save()`

```
int vrna_params_save (
    const char fname[],
    unsigned int options )
#include <ViennaRNA/params/io.h>
Save energy parameters to a file.
```

## See also

[vrna\\_params\\_load\(\)](#)

## Parameters

|                |                                                                                       |
|----------------|---------------------------------------------------------------------------------------|
| <i>fname</i>   | A filename (path) for the file where the current energy parameters will be written to |
| <i>options</i> | File format bit-mask (usually <a href="#">VRNA_PARAMETER_FORMAT_DEFAULT</a> )         |

## Returns

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as overloaded function `params_save(fname, options=VRNA_PARAMETER_FORMAT_DEFAULT)`.

16.57.3.3 `vrna_params_load_from_string()`

```
int vrna_params_load_from_string (
    const char * string,
    const char * name,
    unsigned int options )
#include <ViennaRNA/params/io.h>
Load energy parameters from string.
```

The string must follow the default energy parameter file convention! The optional `name` argument allows one to specify a name for the parameter set which is stored internally.

## See also

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Matthews2004\(\)](#)



## Parameters

|                |                                                                               |
|----------------|-------------------------------------------------------------------------------|
| <i>string</i>  | A 0-terminated string containing energy parameters                            |
| <i>name</i>    | A name for the parameter set in <i>string</i> (Maybe NULL)                    |
| <i>options</i> | File format bit-mask (usually <a href="#">VRNA_PARAMETER_FORMAT_DEFAULT</a> ) |

## Returns

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as overloaded function `params_load_from_string(string, name="", options=VRNA_PARAMETER_FORMAT_DEFAULT)`.

16.57.3.4 `vrna_params_load_defaults()`

```
int vrna_params_load_defaults (
    void )
#include <ViennaRNA/params/io.h>
```

Load default RNA energy parameter set.

This is a convenience function to load the Turner 2004 RNA free energy parameters. It's the same as calling `vrna_params_load_RNA_Turner2004()`

## See also

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathev](#)

## Returns

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as overloaded function `params_load()`.

16.57.3.5 `vrna_params_load_RNA_Turner2004()`

```
int vrna_params_load_RNA_Turner2004 (
    void )
#include <ViennaRNA/params/io.h>
```

Load Turner 2004 RNA energy parameter set.

## See also

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathev](#)

## Returns

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_RNA_Turner2004()`.

**16.57.3.6 vrna\_params\_load\_RNA\_Turner1999()**

```
int vrna_params_load_RNA_Turner1999 (
    void )
#include <ViennaRNA/params/io.h>
Load Turner 1999 RNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathev](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_RNA_Turner1999()`.

**16.57.3.7 vrna\_params\_load\_RNA\_Andronescu2007()**

```
int vrna_params_load_RNA_Andronescu2007 (
    void )
#include <ViennaRNA/params/io.h>
Load Andronescu 2007 RNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathev](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_RNA_Andronescu2007()`.

**16.57.3.8 vrna\_params\_load\_RNA\_Langdon2018()**

```
int vrna_params_load_RNA_Langdon2018 (
    void )
#include <ViennaRNA/params/io.h>
Load Langdon 2018 RNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathev](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_RNA_Langdon2018()`.

**16.57.3.9 vrna\_params\_load\_RNA\_misc\_special\_hairpins()**

```
int vrna_params_load_RNA_misc_special_hairpins (
    void )
#include <ViennaRNA/params/io.h>
Load Misc Special Hairpin RNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews1999\(\)](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_RNA_misc_special_hairpins()`.

**16.57.3.10 vrna\_params\_load\_DNA\_Mathews2004()**

```
int vrna_params_load_DNA_Mathews2004 (
    void )
#include <ViennaRNA/params/io.h>
Load Mathews 2004 DNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews1999\(\)](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_DNA_Mathews2004()`.

**16.57.3.11 vrna\_params\_load\_DNA\_Mathews1999()**

```
int vrna_params_load_DNA_Mathews1999 (
    void )
#include <ViennaRNA/params/io.h>
Load Mathews 1999 DNA energy parameter set.
```

**See also**

[vrna\\_params\\_load\(\)](#), [vrna\\_params\\_load\\_from\\_string\(\)](#), [vrna\\_params\\_save\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner2004\(\)](#), [vrna\\_params\\_load\\_RNA\\_Turner1999\(\)](#), [vrna\\_params\\_load\\_RNA\\_Andronescu2007\(\)](#), [vrna\\_params\\_load\\_RNA\\_Langdon2018\(\)](#), [vrna\\_params\\_load\\_RNA\\_misc\\_special\\_hairpins\(\)](#), [vrna\\_params\\_load\\_DNA\\_Mathews2004\(\)](#), [vrna\\_params\\_load\\_defaults\(\)](#)

**Returns**

Non-zero on success, 0 on failure

**SWIG Wrapper Notes** This function is available as function `params_load_DNA_Mathews1999()`.

**16.57.3.12 last\_parameter\_file()**

```
const char * last_parameter_file (
    void )
#include <ViennaRNA/params/io.h>
```

Get the file name of the parameter file that was most recently loaded.

**Returns**

The file name of the last parameter file, or NULL if parameters are still at defaults

**16.57.3.13 read\_parameter\_file()**

```
void read_parameter_file (
    const char fname[] )
#include <ViennaRNA/params/io.h>
```

Read energy parameters from a file.

**Deprecated** Use [vrna\\_params\\_load\(\)](#) instead!

**Parameters**

|              |                                                       |
|--------------|-------------------------------------------------------|
| <i>fname</i> | The path to the file containing the energy parameters |
|--------------|-------------------------------------------------------|

**16.57.3.14 write\_parameter\_file()**

```
void write_parameter_file (
    const char fname[] )
#include <ViennaRNA/params/io.h>
```

Write energy parameters to a file.

**Deprecated** Use [vrna\\_params\\_save\(\)](#) instead!

**Parameters**

|              |                                                                                       |
|--------------|---------------------------------------------------------------------------------------|
| <i>fname</i> | A filename (path) for the file where the current energy parameters will be written to |
|--------------|---------------------------------------------------------------------------------------|

**16.58 Converting Energy Parameter Files**

Convert energy parameter files into the latest format.

**16.58.1 Detailed Description**

Convert energy parameter files into the latest format.

To preserve some backward compatibility the RNAlib also provides functions to convert energy parameter files from the format used in version 1.4-1.8 into the new format used since version 2.0 Collaboration diagram for Converting Energy Parameter Files:

**Files**

- file [1.8.4\\_epars.h](#)

*Free energy parameters for parameter file conversion.*

- file [1.8.4\\_intloops.h](#)

*Free energy parameters for interior loop contributions needed by the parameter file conversion functions.*

## Macros

- `#define VRNA_CONVERT_OUTPUT_ALL 1U`
- `#define VRNA_CONVERT_OUTPUT_HP 2U`
- `#define VRNA_CONVERT_OUTPUT_STACK 4U`
- `#define VRNA_CONVERT_OUTPUT_MM_HP 8U`
- `#define VRNA_CONVERT_OUTPUT_MM_INT 16U`
- `#define VRNA_CONVERT_OUTPUT_MM_INT_1N 32U`
- `#define VRNA_CONVERT_OUTPUT_MM_INT_23 64U`
- `#define VRNA_CONVERT_OUTPUT_MM_MULTI 128U`
- `#define VRNA_CONVERT_OUTPUT_MM_EXT 256U`
- `#define VRNA_CONVERT_OUTPUT_DANGLE5 512U`
- `#define VRNA_CONVERT_OUTPUT_DANGLE3 1024U`
- `#define VRNA_CONVERT_OUTPUT_INT_11 2048U`
- `#define VRNA_CONVERT_OUTPUT_INT_21 4096U`
- `#define VRNA_CONVERT_OUTPUT_INT_22 8192U`
- `#define VRNA_CONVERT_OUTPUT_BULGE 16384U`
- `#define VRNA_CONVERT_OUTPUT_INT 32768U`
- `#define VRNA_CONVERT_OUTPUT_ML 65536U`
- `#define VRNA_CONVERT_OUTPUT_MISC 131072U`
- `#define VRNA_CONVERT_OUTPUT_SPECIAL_HP 262144U`
- `#define VRNA_CONVERT_OUTPUT_VANILLA 524288U`
- `#define VRNA_CONVERT_OUTPUT_NINIO 1048576U`
- `#define VRNA_CONVERT_OUTPUT_DUMP 2097152U`

## Functions

- void [convert\\_parameter\\_file](#) (const char \*iname, const char \*oname, unsigned int options)

## 16.58.2 Macro Definition Documentation

### 16.58.2.1 VRNA\_CONVERT\_OUTPUT\_ALL

```
#define VRNA_CONVERT_OUTPUT_ALL 1U
#include <ViennaRNA/params/convert.h>
```

Flag to indicate printing of a complete parameter set

### 16.58.2.2 VRNA\_CONVERT\_OUTPUT\_HP

```
#define VRNA_CONVERT_OUTPUT_HP 2U
#include <ViennaRNA/params/convert.h>
```

Flag to indicate printing of hairpin contributions

### 16.58.2.3 VRNA\_CONVERT\_OUTPUT\_STACK

```
#define VRNA_CONVERT_OUTPUT_STACK 4U
#include <ViennaRNA/params/convert.h>
```

Flag to indicate printing of base pair stack contributions

#### 16.58.2.4 VRNA\_CONVERT\_OUTPUT\_MM\_HP

```
#define VRNA_CONVERT_OUTPUT_MM_HP 8U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of hairpin mismatch contribution
```

#### 16.58.2.5 VRNA\_CONVERT\_OUTPUT\_MM\_INT

```
#define VRNA_CONVERT_OUTPUT_MM_INT 16U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of interior loop mismatch contribution
```

#### 16.58.2.6 VRNA\_CONVERT\_OUTPUT\_MM\_INT\_1N

```
#define VRNA_CONVERT_OUTPUT_MM_INT_1N 32U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of 1:n interior loop mismatch contribution
```

#### 16.58.2.7 VRNA\_CONVERT\_OUTPUT\_MM\_INT\_23

```
#define VRNA_CONVERT_OUTPUT_MM_INT_23 64U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of 2:3 interior loop mismatch contribution
```

#### 16.58.2.8 VRNA\_CONVERT\_OUTPUT\_MM\_MULTI

```
#define VRNA_CONVERT_OUTPUT_MM_MULTI 128U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of multi loop mismatch contribution
```

#### 16.58.2.9 VRNA\_CONVERT\_OUTPUT\_MM\_EXT

```
#define VRNA_CONVERT_OUTPUT_MM_EXT 256U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of exterior loop mismatch contribution
```

#### 16.58.2.10 VRNA\_CONVERT\_OUTPUT\_DANGLE5

```
#define VRNA_CONVERT_OUTPUT_DANGLE5 512U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of 5' dangle contribution
```

#### 16.58.2.11 VRNA\_CONVERT\_OUTPUT\_DANGLE3

```
#define VRNA_CONVERT_OUTPUT_DANGLE3 1024U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of 3' dangle contribution
```

#### 16.58.2.12 VRNA\_CONVERT\_OUTPUT\_INT\_11

```
#define VRNA_CONVERT_OUTPUT_INT_11 2048U
#include <ViennaRNA/params/convert.h>
```

Flag to indicate printing of 1:1 interior loop contribution

#### 16.58.2.13 VRNA\_CONVERT\_OUTPUT\_INT\_21

```
#define VRNA_CONVERT_OUTPUT_INT_21 4096U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of 2:1 interior loop contribution
```

#### 16.58.2.14 VRNA\_CONVERT\_OUTPUT\_INT\_22

```
#define VRNA_CONVERT_OUTPUT_INT_22 8192U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of 2:2 interior loop contribution
```

#### 16.58.2.15 VRNA\_CONVERT\_OUTPUT\_BULGE

```
#define VRNA_CONVERT_OUTPUT_BULGE 16384U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of bulge loop contribution
```

#### 16.58.2.16 VRNA\_CONVERT\_OUTPUT\_INT

```
#define VRNA_CONVERT_OUTPUT_INT 32768U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of interior loop contribution
```

#### 16.58.2.17 VRNA\_CONVERT\_OUTPUT\_ML

```
#define VRNA_CONVERT_OUTPUT_ML 65536U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of multi loop contribution
```

#### 16.58.2.18 VRNA\_CONVERT\_OUTPUT\_MISC

```
#define VRNA_CONVERT_OUTPUT_MISC 131072U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of misc contributions (such as terminalAU)
```

#### 16.58.2.19 VRNA\_CONVERT\_OUTPUT\_SPECIAL\_HP

```
#define VRNA_CONVERT_OUTPUT_SPECIAL_HP 262144U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of special hairpin contributions (tri-, tetra-, hexa-loops)
```

#### 16.58.2.20 VRNA\_CONVERT\_OUTPUT\_VANILLA

```
#define VRNA_CONVERT_OUTPUT_VANILLA 524288U  
#include <ViennaRNA/params/convert.h>  
Flag to indicate printing of given parameters only
```

**Note**

This option overrides all other output options, except `VRNA_CONVERT_OUTPUT_DUMP` !

**16.58.2.21 VRNA\_CONVERT\_OUTPUT\_NINIO**

```
#define VRNA_CONVERT_OUTPUT_NINIO 1048576U
#include <ViennaRNA/params/convert.h>
Flag to indicate printing of interior loop asymmetry contribution
```

**16.58.2.22 VRNA\_CONVERT\_OUTPUT\_DUMP**

```
#define VRNA_CONVERT_OUTPUT_DUMP 2097152U
#include <ViennaRNA/params/convert.h>
Flag to indicate dumping the energy contributions from the library instead of an input file
```

**16.58.3 Function Documentation****16.58.3.1 convert\_parameter\_file()**

```
void convert_parameter_file (
    const char * iname,
    const char * oname,
    unsigned int options )
#include <ViennaRNA/params/convert.h>
Convert/dump a Vienna 1.8.4 formatted energy parameter file
The options argument allows one to control the different output modes.
Currently available options are:
```

`VRNA_CONVERT_OUTPUT_ALL`, `VRNA_CONVERT_OUTPUT_HP`, `VRNA_CONVERT_OUTPUT_STACK`  
`VRNA_CONVERT_OUTPUT_MM_HP`, `VRNA_CONVERT_OUTPUT_MM_INT`, `VRNA_CONVERT_OUTPUT_MM_INT_1N`  
`VRNA_CONVERT_OUTPUT_MM_INT_23`, `VRNA_CONVERT_OUTPUT_MM_MULTI`, `VRNA_CONVERT_OUTPUT_MM_EXT`  
`VRNA_CONVERT_OUTPUT_DANGLE5`, `VRNA_CONVERT_OUTPUT_DANGLE3`, `VRNA_CONVERT_OUTPUT_INT_11`  
`VRNA_CONVERT_OUTPUT_INT_21`, `VRNA_CONVERT_OUTPUT_INT_22`, `VRNA_CONVERT_OUTPUT_BULGE`  
`VRNA_CONVERT_OUTPUT_INT`, `VRNA_CONVERT_OUTPUT_ML`, `VRNA_CONVERT_OUTPUT_MISC`  
`VRNA_CONVERT_OUTPUT_SPECIAL_HP`, `VRNA_CONVERT_OUTPUT_VANILLA`, `VRNA_CONVERT_OUTPUT_NINIO`  
`VRNA_CONVERT_OUTPUT_DUMP`

The defined options are fine for bitwise compare- and assignment-operations, e. g.: pass a collection of options as a single value like this:

```
convert_parameter_file(ifile, ofile, option_1 | option_2 | option_n)
```

**Parameters**

|                |                                                            |
|----------------|------------------------------------------------------------|
| <i>iname</i>   | The input file name (If NULL input is read from stdin)     |
| <i>oname</i>   | The output file name (If NULL output is written to stdout) |
| <i>options</i> | The options (as described above)                           |

**16.59 Utilities to deal with Nucleotide Alphabets**

Functions to cope with various aspects related to the nucleotide sequence alphabet.



### 16.59.1 Detailed Description

Functions to cope with various aspects related to the nucleotide sequence alphabet.  
Collaboration diagram for Utilities to deal with Nucleotide Alphabets:

#### Files

- file [alphabet.h](#)  
*Functions to process, convert, and generally handle different nucleotide and/or base pair alphabets.*
- file [sequence.h](#)  
*Functions and data structures related to sequence representations ,.*

#### Data Structures

- struct [vrna\\_sequence\\_s](#)  
*Data structure representing a nucleotide sequence. [More...](#)*
- struct [vrna\\_alignment\\_s](#)

#### Typedefs

- typedef struct [vrna\\_sequence\\_s](#) [vrna\\_seq\\_t](#)  
*Typename for nucleotide sequence representation data structure [vrna\\_sequence\\_s](#).*

#### Enumerations

- enum [vrna\\_seq\\_type\\_e](#) { [VRNA\\_SEQ\\_UNKNOWN](#) , [VRNA\\_SEQ\\_RNA](#) , [VRNA\\_SEQ\\_DNA](#) }  
*A enumerator used in [vrna\\_sequence\\_s](#) to distinguish different nucleotide sequences.*

#### Functions

- char \* [vrna\\_ptypes](#) (const short \*S, [vrna\\_md\\_t](#) \*md)  
*Get an array of the numerical encoding for each possible base pair (i,j)*
- short \* [vrna\\_seq\\_encode](#) (const char \*sequence, [vrna\\_md\\_t](#) \*md)  
*Get a numerical representation of the nucleotide sequence.*
- short \* [vrna\\_seq\\_encode\\_simple](#) (const char \*sequence, [vrna\\_md\\_t](#) \*md)  
*Get a numerical representation of the nucleotide sequence (simple version)*
- int [vrna\\_nucleotide\\_encode](#) (char c, [vrna\\_md\\_t](#) \*md)  
*Encode a nucleotide character to numerical value.*
- char [vrna\\_nucleotide\\_decode](#) (int enc, [vrna\\_md\\_t](#) \*md)  
*Decode a numerical representation of a nucleotide back into nucleotide alphabet.*

### 16.59.2 Data Structure Documentation

#### 16.59.2.1 struct vrna\_sequence\_s

Data structure representing a nucleotide sequence.

##### Data Fields

- [vrna\\_seq\\_type\\_e](#) type  
*The type of sequence.*
- char \* **string**  
*The string representation of the sequence.*
- short \* **encoding**  
*The integer representation of the sequence.*
- unsigned int **length**  
*The length of the sequence.*

### 16.59.2.2 struct vrna\_alignment\_s

Collaboration diagram for vrna\_alignment\_s:

## 16.59.3 Enumeration Type Documentation

### 16.59.3.1 vrna\_seq\_type\_e

```
enum vrna_seq_type_e
#include <ViennaRNA/sequence.h>
```

A enumerator used in [vrna\\_sequence\\_s](#) to distinguish different nucleotide sequences.

Enumerator

|                  |                                                |
|------------------|------------------------------------------------|
| VRNA_SEQ_UNKNOWN | Nucleotide sequence represents an Unkown type. |
| VRNA_SEQ_RNA     | Nucleotide sequence represents an RNA type.    |
| VRNA_SEQ_DNA     | Nucleotide sequence represents a DNA type.     |

## 16.59.4 Function Documentation

### 16.59.4.1 vrna\_ptypes()

```
char * vrna_ptypes (
    const short * S,
    vrna_md_t * md )
#include <ViennaRNA/alphabet.h>
```

Get an array of the numerical encoding for each possible base pair (i,j)

Note

This array is always indexed in column-wise order, in contrast to previously different indexing between mfe and pf variants!

See also

[vrna\\_idx\\_col\\_wise\(\)](#), [vrna\\_fold\\_compound\\_t](#)

### 16.59.4.2 vrna\_seq\_encode()

```
short * vrna_seq_encode (
    const char * sequence,
    vrna_md_t * md )
#include <ViennaRNA/alphabet.h>
```

Get a numerical representation of the nucleotide sequence.

Parameters

|                 |                                                                                            |
|-----------------|--------------------------------------------------------------------------------------------|
| <i>sequence</i> | The input sequence in upper-case letters                                                   |
| <i>md</i>       | A pointer to a <a href="#">vrna_md_t</a> data structure that specifies the conversion type |

**Returns**

A list of integer encodings for each sequence letter (1-based). Position 0 denotes the length of the list

**SWIG Wrapper Notes** In the target scripting language, this function is wrapped as overloaded function `seq_↔ encode()` where the last parameter, the `model_details` data structure, is optional. If it is omitted, default model settings are applied, i.e. default nucleotide letter conversion. The wrapped function returns a list/tuple of integer representations of the input sequence.

**16.59.4.3 vrna\_nucleotide\_encode()**

```
int vrna_nucleotide_encode (
    char c,
    vrna_md_t * md )
```

```
#include <ViennaRNA/alphabet.h>
```

Encode a nucleotide character to numerical value.

This function encodes a nucleotide character to its numerical representation as required by many functions in RNAlib.

**See also**

[vrna\\_nucleotide\\_decode\(\)](#), [vrna\\_seq\\_encode\(\)](#)

**Parameters**

|           |                                                       |
|-----------|-------------------------------------------------------|
| <i>c</i>  | The nucleotide character to encode                    |
| <i>md</i> | The model details that determine the kind of encoding |

**Returns**

The encoded nucleotide

**16.59.4.4 vrna\_nucleotide\_decode()**

```
char vrna_nucleotide_decode (
    int enc,
    vrna_md_t * md )
```

```
#include <ViennaRNA/alphabet.h>
```

Decode a numerical representation of a nucleotide back into nucleotide alphabet.

This function decodes a numerical representation of a nucleotide character back into nucleotide alphabet

**See also**

[vrna\\_nucleotide\\_encode\(\)](#), [vrna\\_seq\\_encode\(\)](#)

**Parameters**

|            |                                                       |
|------------|-------------------------------------------------------|
| <i>enc</i> | The encoded nucleotide                                |
| <i>md</i>  | The model details that determine the kind of decoding |

## Returns

The decoded nucleotide character

## 16.60 (Nucleic Acid Sequence) String Utilites

Functions to parse, convert, manipulate, create, and compare (nucleic acid sequence) strings.

### 16.60.1 Detailed Description

Functions to parse, convert, manipulate, create, and compare (nucleic acid sequence) strings.

Collaboration diagram for (Nucleic Acid Sequence) String Utilites:

### Files

- file [strings.h](#)

*General utility- and helper-functions for RNA sequence and structure strings used throughout the ViennaRNA Package.*

### Macros

- `#define XSTR(s) STR(s)`  
*Stringify a macro after expansion.*
- `#define STR(s) #s`  
*Stringify a macro argument.*
- `#define FILENAME_MAX_LENGTH 80`  
*Maximum length of filenames that are generated by our programs.*
- `#define FILENAME_ID_LENGTH 42`  
*Maximum length of id taken from fasta header for filename generation.*
- `#define VRNA_TRIM_LEADING 1U`  
*Trim only characters leading the string.*
- `#define VRNA_TRIM_TRAILING 2U`  
*Trim only characters trailing the string.*
- `#define VRNA_TRIM_IN_BETWEEN 4U`  
*Trim only characters within the string.*
- `#define VRNA_TRIM_SUBST_BY_FIRST 8U`  
*Replace remaining characters after trimming with the first delimiter in list.*
- `#define VRNA_TRIM_DEFAULT ( VRNA_TRIM_LEADING | VRNA_TRIM_TRAILING )`  
*Default settings for trimming, i.e. trim leading and trailing.*
- `#define VRNA_TRIM_ALL ( VRNA_TRIM_DEFAULT | VRNA_TRIM_IN_BETWEEN )`  
*Trim characters anywhere in the string.*

### Functions

- `char * vrna_strdup_printf (const char *format,...)`  
*Safely create a formatted string.*
- `char * vrna_strdup_vprintf (const char *format, va_list argp)`  
*Safely create a formatted string.*
- `int vrna_strcat_printf (char **dest, const char *format,...)`  
*Safely append a formatted string to another string.*
- `int vrna_strcat_vprintf (char **dest, const char *format, va_list args)`  
*Safely append a formatted string to another string.*
- `unsigned int vrna_strtrim (char *string, const char *delimiters, unsigned int keep, unsigned int options)`  
*Trim a string by removing (multiple) occurrences of a particular character.*

- char \*\* [vrna\\_strsplit](#) (const char \*string, const char \*delimiter)  
*Split a string into tokens using a delimiting character.*
- char \* [vrna\\_random\\_string](#) (int l, const char symbols[])  
*Create a random string using characters from a specified symbol set.*
- int [vrna\\_hamming\\_distance](#) (const char \*s1, const char \*s2)  
*Calculate hamming distance between two sequences.*
- int [vrna\\_hamming\\_distance\\_bound](#) (const char \*s1, const char \*s2, int n)  
*Calculate hamming distance between two sequences up to a specified length.*
- void [vrna\\_seq\\_toRNA](#) (char \*sequence)  
*Convert an input sequence (possibly containing DNA alphabet characters) to RNA alphabet.*
- void [vrna\\_seq\\_toupper](#) (char \*sequence)  
*Convert an input sequence to uppercase.*
- void [vrna\\_seq\\_reverse](#) (char \*sequence)  
*Reverse a string in-place.*
- char \* [vrna\\_DNA\\_complement](#) (const char \*sequence)  
*Retrieve a DNA sequence which resembles the complement of the input sequence.*
- char \* [vrna\\_seq\\_ungapped](#) (const char \*sequence)  
*Remove gap characters from a nucleotide sequence.*
- char \* [vrna\\_cut\\_point\\_insert](#) (const char \*string, int cp)  
*Add a separating '&' character into a string according to cut-point position.*
- char \* [vrna\\_cut\\_point\\_remove](#) (const char \*string, int \*cp)  
*Remove a separating '&' character from a string.*

## 16.60.2 Macro Definition Documentation

### 16.60.2.1 FILENAME\_MAX\_LENGTH

```
#define FILENAME_MAX_LENGTH 80
```

```
#include <ViennaRNA/utils/strings.h>
```

Maximum length of filenames that are generated by our programs.

This definition should be used throughout the complete ViennaRNA package wherever a static array holding filenames of output files is declared.

### 16.60.2.2 FILENAME\_ID\_LENGTH

```
#define FILENAME_ID_LENGTH 42
```

```
#include <ViennaRNA/utils/strings.h>
```

Maximum length of id taken from fasta header for filename generation.

this has to be smaller than FILENAME\_MAX\_LENGTH since in most cases, some suffix will be appended to the ID

### 16.60.2.3 VRNA\_TRIM\_LEADING

```
#define VRNA_TRIM_LEADING 1U
```

```
#include <ViennaRNA/utils/strings.h>
```

Trim only characters leading the string.

See also

[vrna\\_strtrim\(\)](#)

#### 16.60.2.4 VRNA\_TRIM\_TRAILING

```
#define VRNA_TRIM_TRAILING 2U
#include <ViennaRNA/utils/strings.h>
Trim only characters trailing the string.
```

See also

[vrna\\_strtrim\(\)](#)

#### 16.60.2.5 VRNA\_TRIM\_IN\_BETWEEN

```
#define VRNA_TRIM_IN_BETWEEN 4U
#include <ViennaRNA/utils/strings.h>
Trim only characters within the string.
```

See also

[vrna\\_strtrim\(\)](#)

#### 16.60.2.6 VRNA\_TRIM\_SUBST\_BY\_FIRST

```
#define VRNA_TRIM_SUBST_BY_FIRST 8U
#include <ViennaRNA/utils/strings.h>
Replace remaining characters after trimming with the first delimiter in list.
```

See also

[vrna\\_strtrim\(\)](#)

#### 16.60.2.7 VRNA\_TRIM\_DEFAULT

```
#define VRNA_TRIM_DEFAULT ( VRNA_TRIM_LEADING | VRNA_TRIM_TRAILING )
#include <ViennaRNA/utils/strings.h>
Default settings for trimming, i.e. trim leading and trailing.
```

See also

[vrna\\_strtrim\(\)](#)

#### 16.60.2.8 VRNA\_TRIM\_ALL

```
#define VRNA_TRIM_ALL ( VRNA_TRIM_DEFAULT | VRNA_TRIM_IN_BETWEEN )
#include <ViennaRNA/utils/strings.h>
Trim characters anywhere in the string.
```

See also

[vrna\\_strtrim\(\)](#)

### 16.60.3 Function Documentation

### 16.60.3.1 `vrna_strdup_printf()`

```
char * vrna_strdup_printf (
    const char * format,
    ... )
#include <ViennaRNA/utils/strings.h>
```

Safely create a formatted string.

This function is a safe implementation for creating a formatted character array, similar to *sprintf*. Internally, it uses the *asprintf* function if available to dynamically allocate a large enough character array to store the supplied content. If *asprintf* is not available, mimic it's behavior using *vsprintf*.

#### Note

The returned pointer of this function should always be passed to *free()* to release the allocated memory

#### See also

[vrna\\_strdup\\_vprintf\(\)](#), [vrna\\_strcat\\_printf\(\)](#)

#### Parameters

|               |                                                      |
|---------------|------------------------------------------------------|
| <i>format</i> | The format string (See also <i>asprintf</i> )        |
| ...           | The list of variables used to fill the format string |

#### Returns

The formatted, null-terminated string, or NULL if something has gone wrong

### 16.60.3.2 `vrna_strdup_vprintf()`

```
char * vrna_strdup_vprintf (
    const char * format,
    va_list argp )
#include <ViennaRNA/utils/strings.h>
```

Safely create a formatted string.

This function is the *va\_list* version of [vrna\\_strdup\\_printf\(\)](#)

#### Note

The returned pointer of this function should always be passed to *free()* to release the allocated memory

#### See also

[vrna\\_strdup\\_printf\(\)](#), [vrna\\_strcat\\_printf\(\)](#), [vrna\\_strcat\\_vprintf\(\)](#)

#### Parameters

|               |                                                 |
|---------------|-------------------------------------------------|
| <i>format</i> | The format string (See also <i>asprintf</i> )   |
| <i>argp</i>   | The list of arguments to fill the format string |

**Returns**

The formatted, null-terminated string, or NULL if something has gone wrong

**16.60.3.3 vrna\_strcat\_printf()**

```
int vrna_strcat_printf (
    char ** dest,
    const char * format,
    ... )
#include <ViennaRNA/utils/strings.h>
```

Safely append a formatted string to another string.

This function is a safe implementation for appending a formatted character array, similar to a combination of *strcat* and *sprintf*. The function automatically allocates enough memory to store both, the previous content stored at `dest` and the appended format string. If the `dest` pointer is NULL, the function allocate memory only for the format string. The function returns the number of characters in the resulting string or -1 in case of an error.

**See also**

[vrna\\_strcat\\_vprintf\(\)](#), [vrna\\_strdup\\_printf\(\)](#), [vrna\\_strdup\\_vprintf\(\)](#)

**Parameters**

|               |                                                                             |
|---------------|-----------------------------------------------------------------------------|
| <i>dest</i>   | The address of a char *pointer where the formatted string is to be appended |
| <i>format</i> | The format string (See also <code>sprintf</code> )                          |
| ...           | The list of variables used to fill the format string                        |

**Returns**

The number of characters in the final string, or -1 on error

**16.60.3.4 vrna\_strcat\_vprintf()**

```
int vrna_strcat_vprintf (
    char ** dest,
    const char * format,
    va_list args )
#include <ViennaRNA/utils/strings.h>
```

Safely append a formatted string to another string.

This function is the *va\_list* version of [vrna\\_strcat\\_printf\(\)](#)

**See also**

[vrna\\_strcat\\_printf\(\)](#), [vrna\\_strdup\\_printf\(\)](#), [vrna\\_strdup\\_vprintf\(\)](#)

**Parameters**

|               |                                                                             |
|---------------|-----------------------------------------------------------------------------|
| <i>dest</i>   | The address of a char *pointer where the formatted string is to be appended |
| <i>format</i> | The format string (See also <code>sprintf</code> )                          |
| <i>args</i>   | The list of argument to fill the format string                              |



**Returns**

The number of characters in the final string, or -1 on error

**16.60.3.5 vrna\_strtrim()**

```
unsigned int vrna_strtrim (
    char * string,
    const char * delimiters,
    unsigned int keep,
    unsigned int options )
#include <ViennaRNA/utils/strings.h>
```

Trim a string by removing (multiple) occurrences of a particular character.

This function removes (multiple) consecutive occurrences of a set of characters (*delimiters*) within an input string. It may be used to remove leading and/or trailing whitespaces or to restrict the maximum number of consecutive occurrences of the delimiting characters *delimiters*. Setting *keep*=0 removes all occurrences, while other values reduce multiple consecutive occurrences to at most *keep* delimiters. This might be useful if one would like to reduce multiple whitespaces to a single one, or to remove empty fields within a comma-separated value string.

The parameter *delimiters* may be a pointer to a 0-terminated char string containing a set of any ASCII character. If *NULL* is passed as delimiter set or an empty char string, all whitespace characters are trimmed. The *options* parameter is a bit vector that specifies which part of the string should undergo trimming. The implementation distinguishes the leading ([VRNA\\_TRIM\\_LEADING](#)), trailing ([VRNA\\_TRIM\\_TRAILING](#)), and in-between ([VRNA\\_TRIM\\_IN\\_BETWEEN](#)) part with respect to the delimiter set. Combinations of these parts can be specified by using logical-or operator.

The following example code removes all leading and trailing whitespace characters from the input string:

```
char    string[20] = " \t blablabla ";
unsigned int r    = vrna_strtrim(&(string[0]),
                                NULL,
                                0,
                                VRNA_TRIM_DEFAULT);
```

**Note**

The delimiter always consists of a single character from the set of characters provided. In case of alternative delimiters and non-null *keep* parameter, the first *keep* delimiters are preserved within the string. Use [VRNA\\_TRIM\\_SUBST\\_BY\\_FIRST](#) to substitute all remaining delimiting characters with the first from the *delimiters* list.

**See also**

[VRNA\\_TRIM\\_LEADING](#), [VRNA\\_TRIM\\_TRAILING](#), [VRNA\\_TRIM\\_IN\\_BETWEEN](#), [VRNA\\_TRIM\\_SUBST\\_BY\\_FIRST](#), [VRNA\\_TRIM\\_DEFAULT](#), [VRNA\\_TRIM\\_ALL](#)

**Parameters**

|                   |                                                                                     |
|-------------------|-------------------------------------------------------------------------------------|
| <i>string</i>     | The '\0'-terminated input string to trim                                            |
| <i>delimiters</i> | The delimiter characters as 0-terminated char array (or <i>NULL</i> )               |
| <i>keep</i>       | The maximum number of consecutive occurrences of the delimiter in the output string |
| <i>options</i>    | The option bit vector specifying the mode of operation                              |

**Returns**

The number of delimiters removed from the string

**SWIG Wrapper Notes** Since many scripting languages treat strings as immutable objects, this function does not modify the input string directly. Instead, it returns the modified string as second return value, together with the number of removed delimiters.

The scripting language interface provides an overloaded version of this function, with default parameters *delimiters*=*NULL*, *keep*=0, and *options*=[VRNA\\_TRIM\\_DEFAULT](#).

### 16.60.3.6 `vrna_strsplit()`

```
char ** vrna_strsplit (
    const char * string,
    const char * delimiter )
```

#include <ViennaRNA/utils/strings.h>

Split a string into tokens using a delimiting character.

This function splits a string into an array of strings using a single character that delimits the elements within the string. The default delimiter is the ampersand ' & ' and will be used when `NULL` is passed as a second argument. The returned list is `NULL` terminated, i.e. the last element is `NULL`. If the delimiter is not found, the returned list contains exactly one element: the input string.

For instance, the following code:

```
char **tok = vrna_strsplit("GGGG&CCCC&AAAAA", NULL);
for (char **ptr = tok; *ptr; ptr++) {
    printf("%s\n", *ptr);
    free(*ptr);
}
free(tok);
```

produces this output:

```
* GGGG
* CCCC
* AAAAA
*
```

and properly free's the memory occupied by the returned element array.

#### Note

This function internally uses `strtok_r()` and is therefore considered to be thread-safe. Also note, that it is the users responsibility to free the memory of the array and that of the individual element strings!

In case the input string consists of consecutive delimiters, starts or ends with one or multiple delimiters, empty strings are produced in the output list, indicating the empty fields of data resulting from the split. Use [vrna\\_strtrim\(\)](#) prior to a call to this function to remove any leading, trailing, or in-between empty fields.

#### See also

[vrna\\_strtrim\(\)](#)

#### Parameters

|                  |                                                                         |
|------------------|-------------------------------------------------------------------------|
| <i>string</i>    | The input string that should be split into elements                     |
| <i>delimiter</i> | The delimiting character. If <code>NULL</code> , the delimiter is " & " |

#### Returns

A `NULL` terminated list of the elements in the string

### 16.60.3.7 `vrna_random_string()`

```
char * vrna_random_string (
    int l,
    const char symbols[] )
```

#include <ViennaRNA/utils/strings.h>

Create a random string using characters from a specified symbol set.

**Parameters**

|                |                            |
|----------------|----------------------------|
| <i>l</i>       | The length of the sequence |
| <i>symbols</i> | The symbol set             |

**Returns**

A random string of length 'l' containing characters from the symbolset

**16.60.3.8 vrna\_hamming\_distance()**

```
int vrna_hamming_distance (
    const char * s1,
    const char * s2 )
#include <ViennaRNA/utils/strings.h>
Calculate hamming distance between two sequences.
```

**Parameters**

|           |                     |
|-----------|---------------------|
| <i>s1</i> | The first sequence  |
| <i>s2</i> | The second sequence |

**Returns**

The hamming distance between s1 and s2

**16.60.3.9 vrna\_hamming\_distance\_bound()**

```
int vrna_hamming_distance_bound (
    const char * s1,
    const char * s2,
    int n )
#include <ViennaRNA/utils/strings.h>
Calculate hamming distance between two sequences up to a specified length.
This function is similar to vrna\_hamming\_distance\(\) but instead of comparing both sequences up to their actual length only the first 'n' characters are taken into account
```

**Parameters**

|           |                                                                       |
|-----------|-----------------------------------------------------------------------|
| <i>s1</i> | The first sequence                                                    |
| <i>s2</i> | The second sequence                                                   |
| <i>n</i>  | The length of the subsequences to consider (starting from the 5' end) |

**Returns**

The hamming distance between s1 and s2

**16.60.3.10 vrna\_seq\_toRNA()**

```
void vrna_seq_toRNA (
    char * sequence )
#include <ViennaRNA/utils/strings.h>
```

Convert an input sequence (possibly containing DNA alphabet characters) to RNA alphabet. This function substitutes *T* and *t* with *U* and *u*, respectively

#### Parameters

|                 |                              |
|-----------------|------------------------------|
| <i>sequence</i> | The sequence to be converted |
|-----------------|------------------------------|

#### 16.60.3.11 vrna\_seq\_toupper()

```
void vrna_seq_toupper (
    char * sequence )
#include <ViennaRNA/utils/strings.h>
```

Convert an input sequence to uppercase.

#### Parameters

|                 |                              |
|-----------------|------------------------------|
| <i>sequence</i> | The sequence to be converted |
|-----------------|------------------------------|

#### 16.60.3.12 vrna\_seq\_reverse()

```
void vrna_seq_reverse (
    char * sequence )
#include <ViennaRNA/utils/strings.h>
```

Reverse a string in-place.

This function reverses a character string in the form of an array of characters in-place, i.e. it changes the input parameter.

#### Postcondition

After execution, the input *sequence* consists of the reverse string prior to the execution.

#### See also

[vrna\\_DNA\\_complement\(\)](#)

#### Parameters

|                 |                       |
|-----------------|-----------------------|
| <i>sequence</i> | The string to reverse |
|-----------------|-----------------------|

#### 16.60.3.13 vrna\_DNA\_complement()

```
char * vrna_DNA_complement (
    const char * sequence )
#include <ViennaRNA/utils/strings.h>
```

Retrieve a DNA sequence which resembles the complement of the input sequence.

This function returns a new DNA string which is the complement of the input, i.e. the nucleotide letters A,C,G, and T are substituted by their complements T,G,C, and A, respectively.

Any characters not belonging to the alphabet of the 4 canonical bases of DNA are not altered.

#### Note

This function also handles lower-case input sequences and treats U of the RNA alphabet equally to T

See also

[vrna\\_seq\\_reverse\(\)](#)

#### Parameters

|                 |                        |
|-----------------|------------------------|
| <i>sequence</i> | the input DNA sequence |
|-----------------|------------------------|

#### Returns

The complement of the input DNA sequence

### 16.60.3.14 [vrna\\_seq\\_ungapped\(\)](#)

```
char * vrna_seq_ungapped (
    const char * sequence )
#include <ViennaRNA/utils/strings.h>
Remove gap characters from a nucleotide sequence.
```

#### Parameters

|                 |                                                   |
|-----------------|---------------------------------------------------|
| <i>sequence</i> | The original, null-terminated nucleotide sequence |
|-----------------|---------------------------------------------------|

#### Returns

A copy of the input sequence with all gap characters removed

### 16.60.3.15 [vrna\\_cut\\_point\\_insert\(\)](#)

```
char * vrna_cut_point_insert (
    const char * string,
    int cp )
#include <ViennaRNA/utils/strings.h>
Add a separating '&' character into a string according to cut-point position.
If the cut-point position is less or equal to zero, this function just returns a copy of the provided string. Otherwise,
the cut-point character is set at the corresponding position
```

#### Parameters

|               |                        |
|---------------|------------------------|
| <i>string</i> | The original string    |
| <i>cp</i>     | The cut-point position |

#### Returns

A copy of the provided string including the cut-point character

### 16.60.3.16 [vrna\\_cut\\_point\\_remove\(\)](#)

```
char * vrna_cut_point_remove (
    const char * string,
    int * cp )
#include <ViennaRNA/utils/strings.h>
```

Remove a separating '&' character from a string.

This function removes the cut-point indicating '&' character from a string and memorizes its position in a provided integer variable. If not '&' is found in the input, the integer variable is set to -1. The function returns a copy of the input string with the '&' being sliced out.

#### Parameters

|               |                        |
|---------------|------------------------|
| <i>string</i> | The original string    |
| <i>cp</i>     | The cut-point position |

#### Returns

A copy of the input string with the '&' being sliced out

## 16.61 Secondary Structure Utilities

Functions to create, parse, convert, manipulate, and compare secondary structure representations.

### 16.61.1 Detailed Description

Functions to create, parse, convert, manipulate, and compare secondary structure representations.

Collaboration diagram for Secondary Structure Utilities:

#### Modules

- [Dot-Bracket Notation of Secondary Structures](#)

*The Dot-Bracket notation as introduced already in the early times of the ViennaRNA Package denotes base pairs by matching pairs of parenthesis ( ) and unpaired nucleotides by dots . .*

- [Washington University Secondary Structure \(WUSS\) notation](#)

*The WUSS notation, as frequently used for consensus secondary structures in [Stockholm 1.0 format](#).*

- [Pair Table Representation of Secondary Structures](#)
- [Pair List Representation of Secondary Structures](#)
- [Abstract Shapes Representation of Secondary Structures](#)

*Abstract Shapes, introduced by Giegerich et al. in (2004) [10], collapse the secondary structure while retaining the nestedness of helices and hairpin loops.*

- [Helix List Representation of Secondary Structures](#)
- [Tree Representation of Secondary Structures](#)

*Secondary structures can be readily represented as trees, where internal nodes represent base pairs, and leaves represent unpaired nucleotides. The dot-bracket structure string already is a tree represented by a string of parenthesis (base pairs) and dots for the leaf nodes (unpaired nucleotides).*

- [Distance measures between Secondary Structures](#)
- [Deprecated Interface for Secondary Structure Utilities](#)

#### Files

- file [structures.h](#)

*Various utility- and helper-functions for secondary structure parsing, converting, etc.*

#### Functions

- `int * vrna\_loopidx\_from\_ptable (const short *pt)`  
*Get a loop index representation of a structure.*
- `unsigned int * vrna\_refBPcnt\_matrix (const short *reference_pt, unsigned int turn)`  
*Make a reference base pair count matrix.*
- `unsigned int * vrna\_refBPdist\_matrix (const short *pt1, const short *pt2, unsigned int turn)`

*Make a reference base pair distance matrix.*

- `char * vrna_db_from_probs` (`const FLT_OR_DBL *pr`, `unsigned int length`)

*Create a dot-bracket like structure string from base pair probability matrix.*

- `char vrna_bpp_symbol` (`const float *x`)

*Get a pseudo dot bracket notation for a given probability information.*

- `char * vrna_db_from_bp_stack` (`vrna_bp_stack_t *bp`, `unsigned int length`)

*Create a dot-bracket/parenthesis structure from backtracking stack.*

## 16.61.2 Function Documentation

### 16.61.2.1 vrna\_refBPcnt\_matrix()

```
unsigned int * vrna_refBPcnt_matrix (
    const short * reference_pt,
    unsigned int turn )
#include <ViennaRNA/utils/structures.h>
```

Make a reference base pair count matrix.

Get an upper triangular matrix containing the number of basepairs of a reference structure for each interval [i,j] with i<j. Access it via `iindx!!!`

### 16.61.2.2 vrna\_refBPdist\_matrix()

```
unsigned int * vrna_refBPdist_matrix (
    const short * pt1,
    const short * pt2,
    unsigned int turn )
#include <ViennaRNA/utils/structures.h>
```

Make a reference base pair distance matrix.

Get an upper triangular matrix containing the base pair distance of two reference structures for each interval [i,j] with i<j. Access it via `iindx!!!`

### 16.61.2.3 vrna\_db\_from\_probs()

```
char * vrna_db_from_probs (
    const FLT_OR_DBL * pr,
    unsigned int length )
#include <ViennaRNA/utils/structures.h>
```

Create a dot-bracket like structure string from base pair probability matrix.

**SWIG Wrapper Notes** This function is available as parameter-less method `db_from_probs()` bound to objects of type `fold_compound`. Parameters `pr` and `length` are implicitly taken from the `fold_compound` object the method is bound to. Upon missing base pair probabilities, this method returns an empty string.

### 16.61.2.4 vrna\_db\_from\_bp\_stack()

```
char * vrna_db_from_bp_stack (
    vrna_bp_stack_t * bp,
    unsigned int length )
#include <ViennaRNA/utils/structures.h>
```

Create a dot-bracket/parenthesis structure from backtracking stack.

This function is capable to create dot-bracket structures from suboptimal structure prediction sensu M. Zuker

## Parameters

|               |                                                  |
|---------------|--------------------------------------------------|
| <i>bp</i>     | Base pair stack containing the traced base pairs |
| <i>length</i> | The length of the structure                      |

## Returns

The secondary structure in dot-bracket notation as provided in the input

## 16.62 Dot-Bracket Notation of Secondary Structures

The Dot-Bracket notation as introduced already in the early times of the ViennaRNA Package denotes base pairs by matching pairs of parenthesis ( ) and unpaired nucleotides by dots ..

### 16.62.1 Detailed Description

The Dot-Bracket notation as introduced already in the early times of the ViennaRNA Package denotes base pairs by matching pairs of parenthesis ( ) and unpaired nucleotides by dots ..

As a simple example, consider a helix of size 4 enclosing a hairpin of size 4. In dot-bracket notation, this is annotated as

```
((((.....))))
```

#### Extended Dot-Bracket Notation

A more generalized version of the original Dot-Bracket notation may use additional pairs of brackets, such as <>, {}, and [], and matching pairs of uppercase/lowercase letters. This allows for anoting pseudo-knots, since different pairs of brackets are not required to be nested.

The follwing annotations of a simple structure with two crossing helices of size 4 are equivalent:

```
<<<<[[[...>>>>]]]
```

```
((((AAAA.....))))aaaa
```

AAAA{{{{{{...aaaa}}}}}

## Macros

- `#define VRNA_BRACKETS_ALPHA 4U`  
*Bitflag to indicate secondary structure notations using uppercase/lowercase letters from the latin alphabet.*
- `#define VRNA_BRACKETS_RND 8U`  
*Bitflag to indicate secondary structure notations using round brackets (parenthesis), ( )*
- `#define VRNA_BRACKETS_CLY 16U`  
*Bitflag to indicate secondary structure notations using curly brackets, { }*
- `#define VRNA_BRACKETS_ANG 32U`  
*Bitflag to indicate secondary structure notations using angular brackets, <>*
- `#define VRNA_BRACKETS_SQR 64U`  
*Bitflag to indicate secondary structure notations using square brackets, [ ]*
- `#define VRNA_BRACKETS_DEFAULT`  
*Default bitmask to indicate secondary structure notation using any pair of brackets.*
- `#define VRNA_BRACKETS_ANY`  
*Bitmask to indicate secondary structure notation using any pair of brackets or uppercase/lowercase alphabet letters.*

## Functions

- `char * vrna_db_pack (const char *struc)`  
*Pack secondary secondary structure, 5:1 compression using base 3 encoding.*
- `char * vrna_db_unpack (const char *packed)`  
*Unpack secondary structure previously packed with `vrna_db_pack()`*
- `void vrna_db_flatten (char *structure, unsigned int options)`



*Substitute pairs of brackets in a string with parenthesis.*

- void [vrna\\_db\\_flatten\\_to](#) (char \*string, const char target[3], unsigned int options)

*Substitute pairs of brackets in a string with another type of pair characters.*

- char \* [vrna\\_db\\_from\\_ptable](#) (const short \*pt)

*Convert a pair table into dot-parenthesis notation.*

- char \* [vrna\\_db\\_from\\_plist](#) ([vrna\\_ep\\_t](#) \*pairs, unsigned int n)

*Convert a list of base pairs into dot-bracket notation.*

- char \* [vrna\\_db\\_to\\_element\\_string](#) (const char \*structure)

*Convert a secondary structure in dot-bracket notation to a nucleotide annotation of loop contexts.*

- char \* [vrna\\_db\\_pk\\_remove](#) (const char \*structure, unsigned int options)

*Remove pseudo-knots from an input structure.*

## 16.62.2 Macro Definition Documentation

### 16.62.2.1 VRNA\_BRACKETS\_ALPHA

```
#define VRNA_BRACKETS_ALPHA 4U
```

```
#include <ViennaRNA/utils/structures.h>
```

Bitflag to indicate secondary structure notations using uppercase/lowercase letters from the latin alphabet.

See also

[vrna\\_ptable\\_from\\_string\(\)](#)

### 16.62.2.2 VRNA\_BRACKETS\_RND

```
#define VRNA_BRACKETS_RND 8U
```

```
#include <ViennaRNA/utils/structures.h>
```

Bitflag to indicate secondary structure notations using round brackets (parenthesis), ( )

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#)

### 16.62.2.3 VRNA\_BRACKETS\_CLY

```
#define VRNA_BRACKETS_CLY 16U
```

```
#include <ViennaRNA/utils/structures.h>
```

Bitflag to indicate secondary structure notations using curly brackets, { }

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#)

### 16.62.2.4 VRNA\_BRACKETS\_ANG

```
#define VRNA_BRACKETS_ANG 32U
```

```
#include <ViennaRNA/utils/structures.h>
```

Bitflag to indicate secondary structure notations using angular brackets, <>

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#)

### 16.62.2.5 VRNA\_BRACKETS\_SQR

```
#define VRNA_BRACKETS_SQR 64U
#include <ViennaRNA/utils/structures.h>
Bitflag to indicate secondary structure notations using square brackets, []
```

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#)

### 16.62.2.6 VRNA\_BRACKETS\_DEFAULT

```
#define VRNA_BRACKETS_DEFAULT
#include <ViennaRNA/utils/structures.h>
```

**Value:**

```
(VRNA_BRACKETS_RND | \
 VRNA_BRACKETS_CLY | \
 VRNA_BRACKETS_ANG | \
 VRNA_BRACKETS_SQR)
```

Default bitmask to indicate secondary structure notation using any pair of brackets.

This set of matching brackets/parenthesis is always nested, i.e. pseudo-knot free, in WUSS format. However, in general different kinds of brackets are mostly used for annotating pseudo-knots. Thus special care has to be taken to remove pseudo-knots if this bitmask is used in functions that return secondary structures without pseudo-knots!

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#), [vrna\\_db\\_pk\\_remove\(\)](#) [vrna\\_pt\\_pk\\_remove\(\)](#)

### 16.62.2.7 VRNA\_BRACKETS\_ANY

```
#define VRNA_BRACKETS_ANY
#include <ViennaRNA/utils/structures.h>
```

**Value:**

```
(VRNA_BRACKETS_RND | \
 VRNA_BRACKETS_CLY | \
 VRNA_BRACKETS_ANG | \
 VRNA_BRACKETS_SQR | \
 VRNA_BRACKETS_ALPHA)
```

Bitmask to indicate secondary structure notation using any pair of brackets or uppercase/lowercase alphabet letters.

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_pk\\_remove\(\)](#), [vrna\\_db\\_flatten\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#)

## 16.62.3 Function Documentation

### 16.62.3.1 vrna\_db\_pack()

```
char * vrna_db_pack (
    const char * struc )
#include <ViennaRNA/utils/structures.h>
```

Pack secondary secondary structure, 5:1 compression using base 3 encoding.

Returns a binary string encoding of the secondary structure using a 5:1 compression scheme. The string is NULL terminated and can therefore be used with standard string functions such as strcmp(). Useful for programs that need to keep many structures in memory.

See also

[vrna\\_db\\_unpack\(\)](#)

## Parameters

|               |                                                 |
|---------------|-------------------------------------------------|
| <i>struct</i> | The secondary structure in dot-bracket notation |
|---------------|-------------------------------------------------|

## Returns

The binary encoded structure

**16.62.3.2 vrna\_db\_unpack()**

```
char * vrna_db_unpack (
    const char * packed )
#include <ViennaRNA/utils/structures.h>
```

Unpack secondary structure previously packed with [vrna\\_db\\_pack\(\)](#)  
 Translate a compressed binary string produced by [vrna\\_db\\_pack\(\)](#) back into the familiar dot-bracket notation.

## See also

[vrna\\_db\\_pack\(\)](#)

## Parameters

|               |                                               |
|---------------|-----------------------------------------------|
| <i>packed</i> | The binary encoded packed secondary structure |
|---------------|-----------------------------------------------|

## Returns

The unpacked secondary structure in dot-bracket notation

**16.62.3.3 vrna\_db\_flatten()**

```
void vrna_db_flatten (
    char * structure,
    unsigned int options )
#include <ViennaRNA/utils/structures.h>
```

Substitute pairs of brackets in a string with parenthesis.  
 This function can be used to replace brackets of unusual types, such as angular brackets <> , to dot-bracket format.  
 The `options` parameter is used to specify which types of brackets will be replaced by round parenthesis ().

## See also

[vrna\\_db\\_flatten\\_to\(\)](#), [VRNA\\_BRACKETS\\_RND](#), [VRNA\\_BRACKETS\\_ANG](#), [VRNA\\_BRACKETS\\_CLY](#),  
[VRNA\\_BRACKETS\\_SQR](#), [VRNA\\_BRACKETS\\_DEFAULT](#)

## Parameters

|                  |                                                                      |
|------------------|----------------------------------------------------------------------|
| <i>structure</i> | The structure string where brackets are flattened in-place           |
| <i>options</i>   | A bitmask to specify which types of brackets should be flattened out |

**SWIG Wrapper Notes** This function flattens an input structure string in-place! The second parameter is optional and defaults to [VRNA\\_BRACKETS\\_DEFAULT](#).

An overloaded version of this function exists, where an additional second parameter can be passed to specify the target brackets, i.e. the type of matching pair characters all brackets will be flattened to. Therefore, in the scripting language interface this function is a replace-

ment for [vrna\\_db\\_flatten\\_to\(\)](#).

#### 16.62.3.4 vrna\_db\_flatten\_to()

```
void vrna_db_flatten_to (
    char * string,
    const char target[3],
    unsigned int options )
#include <ViennaRNA/utils/structures.h>
```

Substitute pairs of brackets in a string with another type of pair characters.

This function can be used to replace brackets in a structure annotation string, such as square brackets `[]`, to another type of pair characters, e.g. angular brackets `<>`.

The `target` array must contain a character for the 'pair open' annotation at position 0, and one for 'pair close' at position 1. `Options` parameter is used to specify which types of brackets will be replaced by the new pairs.

See also

[vrna\\_db\\_flatten\(\)](#), [VRNA\\_BRACKETS\\_RND](#), [VRNA\\_BRACKETS\\_ANG](#), [VRNA\\_BRACKETS\\_CLY](#), [VRNA\\_BRACKETS\\_SQR](#), [VRNA\\_BRACKETS\\_DEFAULT](#)

#### Parameters

|                |                                                                      |
|----------------|----------------------------------------------------------------------|
| <i>string</i>  | The structure string where brackets are flattened in-place           |
| <i>target</i>  | The new pair characters the string will be flattened to              |
| <i>options</i> | A bitmask to specify which types of brackets should be flattened out |

**SWIG Wrapper Notes** This function is available as an overloaded version of [vrna\\_db\\_flatten\(\)](#)

#### 16.62.3.5 vrna\_db\_from\_ptable()

```
char * vrna_db_from_ptable (
    const short * pt )
#include <ViennaRNA/utils/structures.h>
```

Convert a pair table into dot-parenthesis notation.

This function also converts pair table formatted structures that contain pseudoknots. Non-nested base pairs result in additional pairs of parenthesis and brackets within the resulting dot-parenthesis string. The following pairs are available: `()`, `[]`, `{}`, `<>`, as well as pairs of matching upper-/lower-case characters from the alphabet A-Z.

#### Note

In cases where the level of non-nested base pairs exceeds the maximum number of 30 different base pair indicators (4 parenthesis/brackets, 26 matching characters), a warning is printed and the remaining base pairs are left out from the conversion.

#### Parameters

|           |                             |
|-----------|-----------------------------|
| <i>pt</i> | The pair table to be copied |
|-----------|-----------------------------|

#### Returns

A char pointer to the dot-bracket string

**16.62.3.6 vrna\_db\_from\_plist()**

```
char * vrna_db_from_plist (
    vrna_ep_t * pairs,
    unsigned int n )
#include <ViennaRNA/utils/structures.h>
Convert a list of base pairs into dot-bracket notation.
```

See also

[vrna\\_plist\(\)](#)

**Parameters**

|              |                                                                                           |
|--------------|-------------------------------------------------------------------------------------------|
| <i>pairs</i> | A <a href="#">vrna_ep_t</a> containing the pairs to be included in the dot-bracket string |
| <i>n</i>     | The length of the structure (number of nucleotides)                                       |

**Returns**

The dot-bracket string containing the provided base pairs

**16.62.3.7 vrna\_db\_to\_element\_string()**

```
char * vrna_db_to_element_string (
    const char * structure )
#include <ViennaRNA/utils/structures.h>
Convert a secondary structure in dot-bracket notation to a nucleotide annotation of loop contexts.
```

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

**Returns**

A string annotating each nucleotide according to it's structural context

**16.62.3.8 vrna\_db\_pk\_remove()**

```
char * vrna_db_pk_remove (
    const char * structure,
    unsigned int options )
#include <ViennaRNA/utils/structures.h>
```

Remove pseudo-knots from an input structure.

This function removes pseudo-knots from an input structure by determining the minimum number of base pairs that need to be removed to make the structure pseudo-knot free.

To accomplish that, we use a dynamic programming algorithm similar to the Nussinov maximum matching approach.

The input structure must be in a dot-bracket string like form where crossing base pairs are denoted by the use of additional types of matching brackets, e.g. <>, {}, [], {}. Furthermore, crossing pairs may be annotated by matching uppercase/lowercase letters from the alphabet A–Z. For the latter, the uppercase letter must be the 5' and the lowercase letter the 3' nucleotide of the base pair. The actual type of brackets to be recognized by this function must be specified through the *options* parameter.

**Note**

Brackets in the input structure string that are not covered by the `options` bitmask will be silently ignored!

**See also**

[vrna\\_pt\\_pk\\_remove\(\)](#), [vrna\\_db\\_flatten\(\)](#), [VRNA\\_BRACKETS\\_RND](#), [VRNA\\_BRACKETS\\_ANG](#), [VRNA\\_BRACKETS\\_CLY](#), [VRNA\\_BRACKETS\\_SQR](#), [VRNA\\_BRACKETS\\_ALPHA](#), [VRNA\\_BRACKETS\\_DEFAULT](#), [VRNA\\_BRACKETS\\_ANY](#)

**Parameters**

|                  |                                                                     |
|------------------|---------------------------------------------------------------------|
| <i>structure</i> | Input structure in dot-bracket format that may include pseudo-knots |
| <i>options</i>   | A bitmask to specify which types of brackets should be processed    |

**Returns**

The input structure devoid of pseudo-knots in dot-bracket notation

**SWIG Wrapper Notes** This function is available as an overloaded function `db_pk_remove()` where the optional second parameter `options` defaults to [VRNA\\_BRACKETS\\_ANY](#).

## 16.63 Washington University Secondary Structure (WUSS) notation

The WUSS notation, as frequently used for consensus secondary structures in [Stockholm 1.0 format](#).

### 16.63.1 Detailed Description

The WUSS notation, as frequently used for consensus secondary structures in [Stockholm 1.0 format](#).

This notation allows for a fine-grained annotation of base pairs and unpaired nucleotides, including pseudo-knots. Below, you'll find a list of secondary structure elements and their corresponding WUSS annotation (See also the infernal user guide at <http://eddylab.org/infernal/Userguide.pdf>)

- **Base pairs**

Nested base pairs are annotated by matching pairs of the symbols `<>`, `()`, `{}`, and `[]`. Each of the matching pairs of parenthesis have their special meaning, however, when used as input in our programs, e.g. structure constraint, these details are usually ignored. Furthermore, base pairs that constitute as pseudo-knot are denoted by letters from the latin alphabet and are, if not denoted otherwise, ignored entirely in our programs.

- **Hairpin loops**

Unpaired nucleotides that constitute the hairpin loop are indicated by underscores, `_`.

Example: `<<<<<_____>>>>>`

- **Bulges and interior loops**

Residues that constitute a bulge or interior loop are denoted by dashes, `-`.

Example: `(( (--<_____>- )) )`

- **Multibranch loops**

Unpaired nucleotides in multibranch loops are indicated by commas, `,`.

Example: `(( („<_____>, <_____> )) )`

- **External residues**

Single stranded nucleotides in the exterior loop, i.e. not enclosed by any other pair are denoted by colons, `:`.

Example: `<<<_____>>>:::`

- **Insertions**

In cases where an alignment represents the consensus with a known structure, insertions relative to the known structure are denoted by periods, `.`. Regions where local structural alignment was invoked, leaving regions of both target and query sequence unaligned, are indicated by tildes, `~`.

**Note**

These symbols only appear in alignments of a known (query) structure annotation to a target sequence of unknown structure.

- **Pseudo-knots**

The WUSS notation allows for annotation of pseudo-knots using pairs of upper-case/lower-case letters.

**Note**

Our programs and library functions usually ignore pseudo-knots entirely treating them as unpaired nucleotides, if not stated otherwise.

Example: <<<\_AAA\_\_\_\_>>>aaa

Collaboration diagram for Washington University Secondary Structure (WUSS) notation:

**Functions**

- char \* [vrna\\_db\\_from\\_WUSS](#) (const char \*wuss)  
*Convert a WUSS annotation string to dot-bracket format.*

**16.63.2 Function Documentation****16.63.2.1 vrna\_db\_from\_WUSS()**

```
char * vrna_db_from_WUSS (
    const char * wuss )
#include <ViennaRNA/utils/structures.h>
Convert a WUSS annotation string to dot-bracket format.
```

**Note**

This function flattens all brackets, and treats pseudo-knots annotated by matching pairs of upper/lowercase letters as unpaired nucleotides

**Parameters**

|             |                                   |
|-------------|-----------------------------------|
| <i>wuss</i> | The input string in WUSS notation |
|-------------|-----------------------------------|

**Returns**

A dot-bracket notation of the input secondary structure

**16.64 Pair Table Representation of Secondary Structures****16.64.1 Detailed Description**

Collaboration diagram for Pair Table Representation of Secondary Structures:

**Functions**

- short \* [vrna\\_ptable](#) (const char \*structure)  
*Create a pair table from a dot-bracket notation of a secondary structure.*
- short \* [vrna\\_ptable\\_from\\_string](#) (const char \*structure, unsigned int options)  
*Create a pair table for a secondary structure string.*
- short \* [vrna\\_pt\\_pk\\_get](#) (const char \*structure)

- Create a pair table of a secondary structure (pseudo-knot version)*
- short \* [vrna\\_ptable\\_copy](#) (const short \*pt)  
*Get an exact copy of a pair table.*
- short \* [vrna\\_pt\\_ali\\_get](#) (const char \*structure)  
*Create a pair table of a secondary structure (snoop align version)*
- short \* [vrna\\_pt\\_snoop\\_get](#) (const char \*structure)  
*Create a pair table of a secondary structure (snoop version)*
- short \* [vrna\\_pt\\_pk\\_remove](#) (const short \*ptable, unsigned int options)  
*Remove pseudo-knots from a pair table.*

## 16.64.2 Function Documentation

### 16.64.2.1 [vrna\\_ptable\(\)](#)

```
short * vrna_ptable (
    const char * structure )
#include <ViennaRNA/utils/structures.h>
```

Create a pair table from a dot-bracket notation of a secondary structure.

Returns a newly allocated table, such that table[i]=j if (i,j) pair or 0 if i is unpaired, table[0] contains the length of the structure.

See also

[vrna\\_ptable\\_from\\_string\(\)](#), [vrna\\_db\\_from\\_ptable\(\)](#)

#### Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

#### Returns

A pointer to the created pair\_table

**SWIG Wrapper Notes** This functions is wrapped as overloaded function `ptable()` that takes an optional argument `options` to specify which type of matching brackets should be considered during conversion. The default set is round brackets, i.e. [VRNA\\_BRACKETS\\_RND](#).

### 16.64.2.2 [vrna\\_ptable\\_from\\_string\(\)](#)

```
short * vrna_ptable_from_string (
    const char * structure,
    unsigned int options )
#include <ViennaRNA/utils/structures.h>
```

Create a pair table for a secondary structure string.

This function takes an input string of a secondary structure annotation in [Dot-Bracket Notation](#) (a.k.a. [Dot-Parenthesis Notation](#)) or dot-bracket-ext-notation, and converts it into a pair table representation.

#### Note

This function also extracts crossing base pairs, i.e. pseudo-knots if more than a single matching bracket type is allowed through the bitmask `options`.



See also

[vrna\\_ptable\(\)](#), [vrna\\_db\\_from\\_ptable\(\)](#), [vrna\\_db\\_flatten\\_to\(\)](#), [vrna\\_pt\\_pk\\_remove\(\)](#) [VRNA\\_BRACKETS\\_RND](#),  
[VRNA\\_BRACKETS\\_ANG](#), [VRNA\\_BRACKETS\\_CLY](#), [VRNA\\_BRACKETS\\_SQR](#), [VRNA\\_BRACKETS\\_ALPHA](#),  
[VRNA\\_BRACKETS\\_DEFAULT](#), [VRNA\\_BRACKETS\\_ANY](#)

## Parameters

|                  |                                                                                    |
|------------------|------------------------------------------------------------------------------------|
| <i>structure</i> | Secondary structure in dot-bracket-ext-notation                                    |
| <i>options</i>   | A bitmask to specify which brackets are recognized during conversion to pair table |

## Returns

A pointer to a new pair table of the provided secondary structure

**SWIG Wrapper Notes** This functions is wrapped as overloaded function `ptable()` that takes an optional argument `options` to specify which type of matching brackets should be considered during conversion. The default set is round brackets, i.e. `VRNA_BRACKETS_RND`.

**16.64.2.3 vrna\_pt\_pk\_get()**

```
short * vrna_pt_pk_get (
    const char * structure )
```

```
#include <ViennaRNA/utils/structures.h>
```

Create a pair table of a secondary structure (pseudo-knot version)

Returns a newly allocated table, such that `table[i]=j` if (i,j) pair or 0 if i is unpaired, `table[0]` contains the length of the structure.

In contrast to `vrna_ptable()` this function also recognizes the base pairs denoted by '[' and ']' brackets. Thus, this function behaves like

```
vrna_ptable_from_string(structure, #VRNA_BRACKETS_RND | VRNA_BRACKETS_SQR)
```

## See also

[vrna\\_ptable\\_from\\_string\(\)](#)

## Parameters

|                  |                                                            |
|------------------|------------------------------------------------------------|
| <i>structure</i> | The secondary structure in (extended) dot-bracket notation |
|------------------|------------------------------------------------------------|

## Returns

A pointer to the created `pair_table`

**16.64.2.4 vrna\_ptable\_copy()**

```
short * vrna_ptable_copy (
    const short * pt )
```

```
#include <ViennaRNA/utils/structures.h>
```

Get an exact copy of a pair table.

## Parameters

|           |                             |
|-----------|-----------------------------|
| <i>pt</i> | The pair table to be copied |
|-----------|-----------------------------|

**Returns**

A pointer to the copy of 'pt'

**16.64.2.5 vrna\_pt\_snoop\_get()**

```
short * vrna_pt_snoop_get (
    const char * structure )
```

```
#include <ViennaRNA/utils/structures.h>
```

Create a pair table of a secondary structure (snoop version)

returns a newly allocated table, such that: table[i]=j if (i,j) pair or 0 if i is unpaired, table[0] contains the length of the structure. The special pseudoknotted H/ACA-mRNA structure is taken into account.

**16.64.2.6 vrna\_pt\_pk\_remove()**

```
short * vrna_pt_pk_remove (
    const short * ptable,
    unsigned int options )
```

```
#include <ViennaRNA/utils/structures.h>
```

Remove pseudo-knots from a pair table.

This function removes pseudo-knots from an input structure by determining the minimum number of base pairs that need to be removed to make the structure pseudo-knot free.

To accomplish that, we use a dynamic programming algorithm similar to the Nussinov maximum matching approach.

**See also**

[vrna\\_db\\_pk\\_remove\(\)](#)

**Parameters**

|                |                                               |
|----------------|-----------------------------------------------|
| <i>ptable</i>  | Input structure that may include pseudo-knots |
| <i>options</i> |                                               |

**Returns**

The input structure devoid of pseudo-knots

**16.65 Pair List Representation of Secondary Structures****16.65.1 Detailed Description**

Collaboration diagram for Pair List Representation of Secondary Structures:

**Data Structures**

- struct [vrna\\_elem\\_prob\\_s](#)

*Data structure representing a single entry of an element probability list (e.g. list of pair probabilities) [More...](#)*

**Macros**

- #define **VRNA\_PLIST\_TYPE\_BASEPAIR** 0  
*A Base Pair element.*
- #define **VRNA\_PLIST\_TYPE\_GQUAD** 1  
*A G-Quadruplex element.*
- #define **VRNA\_PLIST\_TYPE\_H\_MOTIF** 2

- *A Hairpin loop motif element.*
- `#define VRNA_PLIST_TYPE_I_MOTIF 3`
- *An Internal loop motif element.*
- `#define VRNA_PLIST_TYPE_UD_MOTIF 4`
- *An Unstructured Domain motif element.*
- `#define VRNA_PLIST_TYPE_STACK 5`
- *A Base Pair stack element.*
- `#define VRNA_PLIST_TYPE_UNPAIRED 6`
- *An unpaired base.*
- `#define VRNA_PLIST_TYPE_TRIPLE 7`
- *One pair of a base triplet.*

## Typedefs

- `typedef struct vrna_elem_prob_s vrna_ep_t`  
Convenience typedef for data structure [vrna\\_elem\\_prob\\_s](#).

## Functions

- `vrna_ep_t * vrna_plist` (const char \*struc, float pr)  
Create a [vrna\\_ep\\_t](#) from a dot-bracket string.

## 16.65.2 Data Structure Documentation

### 16.65.2.1 struct vrna\_elem\_prob\_s

Data structure representing a single entry of an element probability list (e.g. list of pair probabilities)

See also

[vrna\\_plist\(\)](#), [vrna\\_plist\\_from\\_probs\(\)](#), [vrna\\_db\\_from\\_plist\(\)](#), [VRNA\\_PLIST\\_TYPE\\_BASEPAIR](#), [VRNA\\_PLIST\\_TYPE\\_GQUAD](#), [VRNA\\_PLIST\\_TYPE\\_H\\_MOTIF](#), [VRNA\\_PLIST\\_TYPE\\_I\\_MOTIF](#), [VRNA\\_PLIST\\_TYPE\\_UD\\_MOTIF](#), [VRNA\\_PLIST\\_TYPE\\_STACK](#)

## Data Fields

- int **i**  
*Start position (usually 5' nucleotide that starts the element, e.g. base pair)*
- int **j**  
*End position (usually 3' nucleotide that ends the element, e.g. base pair)*
- float **p**  
*Probability of the element.*
- int **type**  
*Type of the element.*

## 16.65.3 Function Documentation

### 16.65.3.1 vrna\_plist()

```
vrna_ep_t * vrna_plist (
    const char * struc,
    float pr )
#include <ViennaRNA/utils/structures.h>
Create a vrna\_ep\_t from a dot-bracket string.
```

The dot-bracket string is parsed and for each base pair an entry in the plist is created. The probability of each pair in the list is set by a function parameter.

The end of the plist is marked by sequence positions *i* as well as *j* equal to 0. This condition should be used to stop looping over its entries

#### Parameters

|              |                                                      |
|--------------|------------------------------------------------------|
| <i>struc</i> | The secondary structure in dot-bracket notation      |
| <i>pr</i>    | The probability for each base pair used in the plist |

#### Returns

The plist array

## 16.66 Abstract Shapes Representation of Secondary Structures

Abstract Shapes, introduced by Giegerich et al. in (2004) [10], collapse the secondary structure while retaining the nestedness of helices and hairpin loops.

### 16.66.1 Detailed Description

Abstract Shapes, introduced by Giegerich et al. in (2004) [10], collapse the secondary structure while retaining the nestedness of helices and hairpin loops.

The abstract shapes representation abstracts the structure from individual base pairs and their corresponding location in the sequence, while retaining the inherent nestedness of helices and hairpin loops.

Below is a description of what is included in the abstract shapes abstraction for each respective level together with an example structure:

```
CGUCUUAACUCAUCACCGUGUGGAGCUGCGACCCUCCCUAGAUUCGAAGACGAG
(((((((...(((...((...))))))...(((...((...))...)))))))).
```

| Shape Level | Description                                                                            | Result                             |
|-------------|----------------------------------------------------------------------------------------|------------------------------------|
| 1           | Most accurate - all loops and all unpaired                                             | [ _ [ _ ] ] _ [ _ [ ] _ ←<br>] ] _ |
| 2           | Nesting pattern for all loop types and unpaired regions in external loop and multiloop | [ [ _ ] ] [ _ [ ] _ ] ]            |
| 3           | Nesting pattern for all loop types but no unpaired regions                             | [ [ [ ] ] [ [ ] ] ]                |
| 4           | Helix nesting pattern in external loop and multiloop                                   | [ [ [ ] [ [ ] ] ]                  |
| 5           | Most abstract - helix nesting pattern and no unpaired regions                          | [ [ [ ] [ ] ]                      |

#### Note

Our implementations also provide the special Shape Level 0, which does not collapse any structural features but simply convert base pairs and unpaired nucleotides into their corresponding set of symbols for abstract shapes.

Collaboration diagram for Abstract Shapes Representation of Secondary Structures:

### Functions

- char \* [vrna\\_abstract\\_shapes](#) (const char \*structure, unsigned int level)  
*Convert a secondary structure in dot-bracket notation to its abstract shapes representation.*
- char \* [vrna\\_abstract\\_shapes\\_pt](#) (const short \*pt, unsigned int level)  
*Convert a secondary structure to its abstract shapes representation.*

## 16.66.2 Function Documentation

### 16.66.2.1 `vrna_abstract_shapes()`

```
char * vrna_abstract_shapes (
    const char * structure,
    unsigned int level )
#include <ViennaRNA/utils/structures.h>
```

Convert a secondary structure in dot-bracket notation to its abstract shapes representation.

This function converts a secondary structure into its abstract shapes representation as presented by Giegerich et al. 2004 [10].

See also

[vrna\\_abstract\\_shapes\\_pt\(\)](#)

#### Parameters

|                  |                                                        |
|------------------|--------------------------------------------------------|
| <i>structure</i> | A secondary structure in dot-bracket notation          |
| <i>level</i>     | The abstraction level (integer in the range of 0 to 5) |

#### Returns

The secondary structure in abstract shapes notation

**SWIG Wrapper Notes** This function is available as an overloaded function `abstract_shapes()` where the optional second parameter `level` defaults to 5.

### 16.66.2.2 `vrna_abstract_shapes_pt()`

```
char * vrna_abstract_shapes_pt (
    const short * pt,
    unsigned int level )
#include <ViennaRNA/utils/structures.h>
```

Convert a secondary structure to its abstract shapes representation.

This function converts a secondary structure into its abstract shapes representation as presented by Giegerich et al. 2004 [10]. This function is equivalent to `vrna_db_to_shapes()`, but requires a pair table input instead of a dot-bracket structure.

#### Note

The length of the structure must be present at `pt[0]`!

See also

[vrna\\_abstract\\_shapes\(\)](#)

#### Parameters

|              |                                                        |
|--------------|--------------------------------------------------------|
| <i>pt</i>    | A secondary structure in pair table format             |
| <i>level</i> | The abstraction level (integer in the range of 0 to 5) |

**Returns**

The secondary structure in abstract shapes notation

**SWIG Wrapper Notes** This function is available as an overloaded function `abstract_shapes()` where the optional second parameter `level` defaults to 5.

## 16.67 Helix List Representation of Secondary Structures

### 16.67.1 Detailed Description

Collaboration diagram for Helix List Representation of Secondary Structures:

**Data Structures**

- struct [vrna\\_hx\\_s](#)

*Data structure representing an entry of a helix list. [More...](#)*

**Typedefs**

- typedef struct [vrna\\_hx\\_s](#) [vrna\\_hx\\_t](#)

*Convenience typedef for data structure [vrna\\_hx\\_s](#).*

**Functions**

- [vrna\\_hx\\_t \\* vrna\\_hx\\_from\\_ptable](#) (short \*pt)

*Convert a pair table representation of a secondary structure into a helix list.*

- [vrna\\_hx\\_t \\* vrna\\_hx\\_merge](#) (const [vrna\\_hx\\_t](#) \*list, int maxdist)

*Create a merged helix list from another helix list.*

### 16.67.2 Data Structure Documentation

#### 16.67.2.1 struct vrna\_hx\_s

Data structure representing an entry of a helix list.

### 16.67.3 Function Documentation

#### 16.67.3.1 vrna\_hx\_from\_ptable()

```
vrna_hx_t * vrna_hx_from_ptable (
    short * pt )
```

```
#include <ViennaRNA/utils/structures.h>
```

Convert a pair table representation of a secondary structure into a helix list.

**Parameters**

|           |                                                      |
|-----------|------------------------------------------------------|
| <i>pt</i> | The secondary structure in pair table representation |
|-----------|------------------------------------------------------|

## Returns

The secondary structure represented as a helix list

## 16.68 Tree Representation of Secondary Structures

Secondary structures can be readily represented as trees, where internal nodes represent base pairs, and leaves represent unpaired nucleotides. The dot-bracket structure string already is a tree represented by a string of parenthesis (base pairs) and dots for the leaf nodes (unpaired nucleotides).

### 16.68.1 Detailed Description

Secondary structures can be readily represented as trees, where internal nodes represent base pairs, and leaves represent unpaired nucleotides. The dot-bracket structure string already is a tree represented by a string of parenthesis (base pairs) and dots for the leaf nodes (unpaired nucleotides).

Alternatively, one may find representations with two types of node labels,  $P$  for paired and  $U$  for unpaired; a dot is then replaced by  $(U)$ , and each closed bracket is assigned an additional identifier  $P$ . We call this the expanded notation. In [8] a condensed representation of the secondary structure is proposed, the so-called homeomorphically irreducible tree (HIT) representation. Here a stack is represented as a single pair of matching brackets labeled  $P$  and weighted by the number of base pairs. Correspondingly, a contiguous strain of unpaired bases is shown as one pair of matching brackets labeled  $U$  and weighted by its length. Generally any string consisting of matching brackets and identifiers is equivalent to a plane tree with as many different types of nodes as there are identifiers.

Bruce Shapiro proposed a coarse grained representation [21], which, does not retain the full information of the secondary structure. He represents the different structure elements by single matching brackets and labels them as

- $H$  (hairpin loop),
- $I$  (interior loop),
- $B$  (bulge),
- $M$  (multi-loop), and
- $S$  (stack).

We extend his alphabet by an extra letter for external elements  $E$ . Again these identifiers may be followed by a weight corresponding to the number of unpaired bases or base pairs in the structure element. All tree representations (except for the dot-bracket form) can be encapsulated into a virtual root (labeled  $R$ ).

The following example illustrates the different linear tree representations used by the package:

Consider the secondary structure represented by the dot-bracket string (full tree) `. ( ( . . ( ( ( . . . ) ) ) . . ( ( . . ) ) ) ) .` which is the most convenient condensed notation used by our programs and library functions.

Then, the following tree representations are equivalent:

- Expanded tree:  
`( (U) ( ( (U) (U) ( ( (U) (U) (U) P) P) P) (U) (U) ( ( (U) (U) P) P) P) (U) R)`
- HIT representation (Fontana et al. 1993 [8]):  
`( (U1) ( (U2) ( (U3) P3) (U2) ( (U2) P2) P2) (U1) R)`
- Coarse Grained Tree Representation (Shapiro 1988 [21]):
  - Short (with root node  $R$ , without stem nodes  $S$ ):  
`( (H) ( (H) M) R)`
  - Full (with root node  $R$ ):  
`( ( ( ( (H) S) ( (H) S) M) S) R)`
  - Extended (with root node  $R$ , with external nodes  $E$ ):  
`( ( ( ( ( (H) S) ( (H) S) M) S) E) R)`
  - Weighted (with root node  $R$ , with external nodes  $E$ ):  
`( ( ( ( ( (H3) S3) ( (H2) S2) M4) S2) E2) R)`



The Expanded tree is rather clumsy and mostly included for the sake of completeness. The different versions of Coarse Grained [Tree](#) Representations are variations of Shapiro's linear tree notation. For the output of aligned structures from string editing, different representations are needed, where we put the label on both sides. The above examples for tree representations would then look like:

```
* a) (UU) (P (P (P (P (UU) (UU) (P (P (P (UU) (UU) (UU) P) P) (UU) (UU) (P (P (UU) (U...
* b) (UU) (P2 (P2 (U2U2) (P2 (U3U3) P3) (U2U2) (P2 (U2U2) P2) P2) (UU) P2) (UU)
* c) (B (M (HH) (HH) M) B)
*   (S (B (S (M (S (HH) S) (S (HH) S) M) S) B) S)
*   (E (S (B (S (M (S (HH) S) (S (HH) S) M) S) B) S) E)
* d) (R (E2 (S2 (B1 (S2 (M4 (S3 (H3) S3) ( (H2) S2) M4) S2) B1) S2) E2) R)
*
```

Aligned structures additionally contain the gap character `_`. Collaboration diagram for Tree Representation of Secondary Structures:

## Macros

- `#define VRNA_STRUCTURE_TREE_HIT 1U`  
*Homeomorphically Irreducible [Tree](#) (HIT) representation of a secondary structure.*
- `#define VRNA_STRUCTURE_TREE_SHAPIRO_SHORT 2U`  
*(short) Coarse Grained representation of a secondary structure*
- `#define VRNA_STRUCTURE_TREE_SHAPIRO 3U`  
*(full) Coarse Grained representation of a secondary structure*
- `#define VRNA_STRUCTURE_TREE_SHAPIRO_EXT 4U`  
*(extended) Coarse Grained representation of a secondary structure*
- `#define VRNA_STRUCTURE_TREE_SHAPIRO_WEIGHT 5U`  
*(weighted) Coarse Grained representation of a secondary structure*
- `#define VRNA_STRUCTURE_TREE_EXPANDED 6U`  
*Expanded [Tree](#) representation of a secondary structure.*

## Functions

- `char * vrna_db_to_tree_string (const char *structure, unsigned int type)`  
*Convert a Dot-Bracket structure string into tree string representation.*
- `char * vrna_tree_string_unweight (const char *structure)`  
*Remove weights from a linear string tree representation of a secondary structure.*
- `char * vrna_tree_string_to_db (const char *tree)`  
*Convert a linear tree string representation of a secondary structure back to Dot-Bracket notation.*

## 16.68.2 Macro Definition Documentation

### 16.68.2.1 VRNA\_STRUCTURE\_TREE\_HIT

```
#define VRNA_STRUCTURE_TREE_HIT 1U
#include <ViennaRNA/utils/structures.h>
Homeomorphically Irreducible Tree (HIT) representation of a secondary structure.
```

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

### 16.68.2.2 VRNA\_STRUCTURE\_TREE\_SHAPIRO\_SHORT

```
#define VRNA_STRUCTURE_TREE_SHAPIRO_SHORT 2U
#include <ViennaRNA/utils/structures.h>
```

(short) Coarse Grained representation of a secondary structure

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

### 16.68.2.3 VRNA\_STRUCTURE\_TREE\_SHAPIRO

```
#define VRNA_STRUCTURE_TREE_SHAPIRO 3U
#include <ViennaRNA/utils/structures.h>
```

(full) Coarse Grained representation of a secondary structure

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

### 16.68.2.4 VRNA\_STRUCTURE\_TREE\_SHAPIRO\_EXT

```
#define VRNA_STRUCTURE_TREE_SHAPIRO_EXT 4U
#include <ViennaRNA/utils/structures.h>
```

(extended) Coarse Grained representation of a secondary structure

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

### 16.68.2.5 VRNA\_STRUCTURE\_TREE\_SHAPIRO\_WEIGHT

```
#define VRNA_STRUCTURE_TREE_SHAPIRO_WEIGHT 5U
#include <ViennaRNA/utils/structures.h>
```

(weighted) Coarse Grained representation of a secondary structure

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

### 16.68.2.6 VRNA\_STRUCTURE\_TREE\_EXPANDED

```
#define VRNA_STRUCTURE_TREE_EXPANDED 6U
#include <ViennaRNA/utils/structures.h>
```

Expanded [Tree](#) representation of a secondary structure.

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

## 16.68.3 Function Documentation

**16.68.3.1 vrna\_db\_to\_tree\_string()**

```
char * vrna_db_to_tree_string (
    const char * structure,
    unsigned int type )
#include <ViennaRNA/utils/structures.h>
```

Convert a Dot-Bracket structure string into tree string representation.

This function allows one to convert a secondary structure in dot-bracket notation into one of the various tree representations for secondary structures. The resulting tree is then represented as a string of parenthesis and node symbols, similar to the Newick format.

Currently we support conversion into the following formats, denoted by the value of parameter `type`:

- [VRNA\\_STRUCTURE\\_TREE\\_HIT](#) - Homeomorphically Irreducible [Tree](#) (HIT) representation of a secondary structure. (See also Fontana et al. 1993 [8])
- [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_SHORT](#) - (short) Coarse Grained representation of a secondary structure (same as Shapiro 1988 [21], but with root node  $R$  and without  $S$  nodes for the stems)
- [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO](#) - (full) Coarse Grained representation of a secondary structure (See also Shapiro 1988 [21])
- [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_EXT](#) - (extended) Coarse Grained representation of a secondary structure (same as Shapiro 1988 [21], but external nodes denoted as  $E$ )
- [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_WEIGHT](#) - (weighted) Coarse Grained representation of a secondary structure (same as [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_EXT](#) but with additional weights for number of unpaired nucleotides in loop, and number of pairs in stems)
- [VRNA\\_STRUCTURE\\_TREE\\_EXPANDED](#) - Expanded [Tree](#) representation of a secondary structure.

See also

[Tree Representations of Secondary Structures](#)

**Parameters**

|                  |                                                              |
|------------------|--------------------------------------------------------------|
| <i>structure</i> | The null-terminated dot-bracket structure string             |
| <i>type</i>      | A switch to determine the type of tree string representation |

**Returns**

A tree representation of the input `structure`

**16.68.3.2 vrna\_tree\_string\_unweight()**

```
char * vrna_tree_string_unweight (
    const char * structure )
#include <ViennaRNA/utils/structures.h>
```

Remove weights from a linear string tree representation of a secondary structure.

This function strips the weights of a linear string tree representation such as [HIT](#), or Coarse Grained [Tree](#) sensu Shapiro [21]

See also

[vrna\\_db\\_to\\_tree\\_string\(\)](#)

**Parameters**

|                  |                                                                           |
|------------------|---------------------------------------------------------------------------|
| <i>structure</i> | A linear string tree representation of a secondary structure with weights |
|------------------|---------------------------------------------------------------------------|

**Returns**

A linear string tree representation of a secondary structure without weights

**16.68.3.3 vrna\_tree\_string\_to\_db()**

```
char * vrna_tree_string_to_db (
    const char * tree )
```

```
#include <ViennaRNA/utils/structures.h>
```

Convert a linear tree string representation of a secondary structure back to Dot-Bracket notation.

**Warning**

This function only accepts *Expanded* and *HIT* tree representations!

**See also**

[vrna\\_db\\_to\\_tree\\_string\(\)](#), [VRNA\\_STRUCTURE\\_TREE\\_EXPANDED](#), [VRNA\\_STRUCTURE\\_TREE\\_HIT](#),  
Tree Representations of Secondary Structures

**Parameters**

|             |                                                              |
|-------------|--------------------------------------------------------------|
| <i>tree</i> | A linear tree string representation of a secondary structure |
|-------------|--------------------------------------------------------------|

**Returns**

A dot-bracket notation of the secondary structure provided in `tree`

**16.69 Distance measures between Secondary Structures****16.69.1 Detailed Description**

Collaboration diagram for Distance measures between Secondary Structures:

**Functions**

- int [vrna\\_bp\\_distance\\_pt](#) (const short \*pt1, const short \*pt2)  
Compute the "base pair" distance between two pair tables pt1 and pt2 of secondary structures.
- int [vrna\\_bp\\_distance](#) (const char \*str1, const char \*str2)  
Compute the "base pair" distance between two secondary structures s1 and s2.

**16.69.2 Function Documentation****16.69.2.1 vrna\_bp\_distance\_pt()**

```
int vrna_bp_distance_pt (
    const short * pt1,
    const short * pt2 )
```

```
#include <ViennaRNA/utils/structures.h>
```

Compute the "base pair" distance between two pair tables pt1 and pt2 of secondary structures.

The pair tables should have the same length. dist = number of base pairs in one structure but not in the other same as edit distance with open-pair close-pair as move-set

See also

[vrna\\_bp\\_distance\(\)](#)

Parameters

|            |                                          |
|------------|------------------------------------------|
| <i>pt1</i> | First structure in dot-bracket notation  |
| <i>pt2</i> | Second structure in dot-bracket notation |

Returns

The base pair distance between *pt1* and *pt2*

**SWIG Wrapper Notes** This function is available as an overloaded method [bp\\_distance\(\)](#).

### 16.69.2.2 vrna\_bp\_distance()

```
int vrna_bp_distance (
    const char * str1,
    const char * str2 )
#include <ViennaRNA/utils/structures.h>
```

Compute the "base pair" distance between two secondary structures *s1* and *s2*.

This is a wrapper around [vrna\\_bp\\_distance\\_pt\(\)](#). The sequences should have the same length. *dist* = number of base pairs in one structure but not in the other same as edit distance with open-pair close-pair as move-set

See also

[vrna\\_bp\\_distance\\_pt\(\)](#)

Parameters

|             |                                          |
|-------------|------------------------------------------|
| <i>str1</i> | First structure in dot-bracket notation  |
| <i>str2</i> | Second structure in dot-bracket notation |

Returns

The base pair distance between *str1* and *str2*

**SWIG Wrapper Notes** This function is available as an overloaded method [bp\\_distance\(\)](#). Note that the SWIG wrapper takes two structure in dot-bracket notation and converts them into pair tables using [vrna\\_ptable\\_from\\_string\(\)](#). The resulting pair tables are then internally passed to [vrna\\_bp\\_distance\\_pt\(\)](#). To control which kind of matching brackets will be used during conversion, the optional argument *options* can be used. See also the description of [vrna\\_ptable\\_from\\_string\(\)](#) for available options. (default: **VRNA\_BRACKETS\_RND**).

## 16.70 Multiple Sequence Alignment Utilities

Functions to extract features from and to manipulate multiple sequence alignments.

### 16.70.1 Detailed Description

Functions to extract features from and to manipulate multiple sequence alignments.  
Collaboration diagram for Multiple Sequence Alignment Utilities:

#### Modules

- [Deprecated Interface for Multiple Sequence Alignment Utilities](#)

## Files

- file [alignments.h](#)  
*Various utility- and helper-functions for sequence alignments and comparative structure prediction.*

## Data Structures

- struct [vrna\\_pinfo\\_s](#)  
*A base pair info structure. [More...](#)*

## Macros

- `#define VRNA_ALN_DEFAULT 0U`  
*Use default alignment settings.*
- `#define VRNA_ALN_RNA 1U`  
*Convert to RNA alphabet.*
- `#define VRNA_ALN_DNA 2U`  
*Convert to DNA alphabet.*
- `#define VRNA_ALN_UPPERCASE 4U`  
*Convert to uppercase nucleotide letters.*
- `#define VRNA_ALN_LOWERCASE 8U`  
*Convert to lowercase nucleotide letters.*
- `#define VRNA_MEASURE_SHANNON_ENTROPY 1U`  
*Flag indicating Shannon Entropy measure.*

## Typedefs

- typedef struct [vrna\\_pinfo\\_s](#) [vrna\\_pinfo\\_t](#)  
*Typename for the base pair info representing data structure [vrna\\_pinfo\\_s](#).*

## Functions

- int [vrna\\_aln\\_mpi](#) (const char \*\*alignment)  
*Get the mean pairwise identity in steps from ?to?(ident)*
- [vrna\\_pinfo\\_t](#) \* [vrna\\_aln\\_pinfo](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*structure, double threshold)  
*Retrieve an array of [vrna\\_pinfo\\_t](#) structures from precomputed pair probabilities.*
- char \*\* [vrna\\_aln\\_slice](#) (const char \*\*alignment, unsigned int i, unsigned int j)  
*Slice out a subalignment from a larger alignment.*
- void [vrna\\_aln\\_free](#) (char \*\*alignment)  
*Free memory occupied by a set of aligned sequences.*
- char \*\* [vrna\\_aln\\_uppercase](#) (const char \*\*alignment)  
*Create a copy of an alignment with only uppercase letters in the sequences.*
- char \*\* [vrna\\_aln\\_toRNA](#) (const char \*\*alignment)  
*Create a copy of an alignment where DNA alphabet is replaced by RNA alphabet.*
- char \*\* [vrna\\_aln\\_copy](#) (const char \*\*alignment, unsigned int options)  
*Make a copy of a multiple sequence alignment.*
- float \* [vrna\\_aln\\_conservation\\_struct](#) (const char \*\*alignment, const char \*structure, const [vrna\\_md\\_t](#) \*md)  
*Compute base pair conservation of a consensus structure.*
- float \* [vrna\\_aln\\_conservation\\_col](#) (const char \*\*alignment, const [vrna\\_md\\_t](#) \*md\_p, unsigned int options)  
*Compute nucleotide conservation in an alignment.*
- char \* [vrna\\_aln\\_consensus\\_sequence](#) (const char \*\*alignment, const [vrna\\_md\\_t](#) \*md\_p)  
*Compute the consensus sequence for a given multiple sequence alignment.*
- char \* [vrna\\_aln\\_consensus\\_mis](#) (const char \*\*alignment, const [vrna\\_md\\_t](#) \*md\_p)  
*Compute the Most Informative Sequence (MIS) for a given multiple sequence alignment.*

## 16.70.2 Data Structure Documentation

### 16.70.2.1 struct vrna\_pinfo\_s

A base pair info structure.

For each base pair (i,j) with i,j in [0, n-1] the structure lists:

- its probability 'p'
- an entropy-like measure for its well-definedness 'ent'
- the frequency of each type of pair in 'bp[]'
  - 'bp[0]' contains the number of non-compatible sequences
  - 'bp[1]' the number of CG pairs, etc.

#### Data Fields

- unsigned **i**  
*nucleotide position i*
- unsigned **j**  
*nucleotide position j*
- float **p**  
*Probability.*
- float **ent**  
*Pseudo entropy for  $p(i, j) = S_i + S_j - p_{ij} * \ln(p_{ij})$ .*
- short **bp** [8]  
*Frequencies of pair\_types.*
- char **comp**  
*1 iff pair is in mfe structure*

## 16.70.3 Macro Definition Documentation

### 16.70.3.1 VRNA\_MEASURE\_SHANNON\_ENTROPY

```
#define VRNA_MEASURE_SHANNON_ENTROPY 1U
#include <ViennaRNA/utils/alignments.h>
```

Flag indicating Shannon Entropy measure.

Shannon Entropy is defined as  $H = - \sum_c p_c \cdot \log_2 p_c$

## 16.70.4 Function Documentation

### 16.70.4.1 vrna\_aln\_mpi()

```
int vrna_aln_mpi (
    const char ** alignment )
#include <ViennaRNA/utils/alignments.h>
```

Get the mean pairwise identity in steps from ?to?(ident)

#### Parameters

|                  |                   |
|------------------|-------------------|
| <i>alignment</i> | Aligned sequences |
|------------------|-------------------|

**Returns**

The mean pairwise identity

**16.70.4.2 vrna\_aln\_pinfo()**

```
vrna_pinfo_t * vrna_aln_pinfo (
    vrna_fold_compound_t * vc,
    const char * structure,
    double threshold )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Retrieve an array of `vrna_pinfo_t` structures from precomputed pair probabilities.

This array of structures contains information about positionwise pair probabilities, base pair entropy and more

**See also**

[vrna\\_pinfo\\_t](#), and [vrna\\_pf\(\)](#)

**Parameters**

|                  |                                                                                                                                        |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| <i>vc</i>        | The <a href="#">vrna_fold_compound_t</a> of type <a href="#">VRNA_FC_TYPE_COMPARATIVE</a> with precomputed partition function matrices |
| <i>structure</i> | An optional structure in dot-bracket notation (Maybe NULL)                                                                             |
| <i>threshold</i> | Do not include results with pair probabilities below threshold                                                                         |

**Returns**

The [vrna\\_pinfo\\_t](#) array

**16.70.4.3 vrna\_aln\_slice()**

```
char ** vrna_aln_slice (
    const char ** alignment,
    unsigned int i,
    unsigned int j )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Slice out a subalignment from a larger alignment.

**Note**

The user is responsible to free the memory occupied by the returned subalignment

**See also**

[vrna\\_aln\\_free\(\)](#)

**Parameters**

|                  |                                                |
|------------------|------------------------------------------------|
| <i>alignment</i> | The input alignment                            |
| <i>i</i>         | The first column of the subalignment (1-based) |
| <i>j</i>         | The last column of the subalignment (1-based)  |



**Returns**

The subalignment between column  $i$  and  $j$

**16.70.4.4 vrna\_aln\_free()**

```
void vrna_aln_free (
    char ** alignment )
#include <ViennaRNA/utils/alignments.h>
Free memory occupied by a set of aligned sequences.
```

**Parameters**

|                  |                     |
|------------------|---------------------|
| <i>alignment</i> | The input alignment |
|------------------|---------------------|

**16.70.4.5 vrna\_aln\_uppercase()**

```
char ** vrna_aln_uppercase (
    const char ** alignment )
#include <ViennaRNA/utils/alignments.h>
Create a copy of an alignment with only uppercase letters in the sequences.
```

**See also**

[vrna\\_aln\\_copy](#)

**Parameters**

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
|------------------|--------------------------------------------------------------------------|

**Returns**

A copy of the input alignment where lowercase sequence letters are replaced by uppercase letters

**16.70.4.6 vrna\_aln\_toRNA()**

```
char ** vrna_aln_toRNA (
    const char ** alignment )
#include <ViennaRNA/utils/alignments.h>
Create a copy of an alignment where DNA alphabet is replaced by RNA alphabet.
```

**See also**

[vrna\\_aln\\_copy](#)

**Parameters**

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
|------------------|--------------------------------------------------------------------------|

**Returns**

A copy of the input alignment where DNA alphabet is replaced by RNA alphabet (T -> U)

**16.70.4.7 vrna\_aln\_copy()**

```
char ** vrna_aln_copy (
    const char ** alignment,
    unsigned int options )
#include <ViennaRNA/utils/alignments.h>
```

Make a copy of a multiple sequence alignment.

This function allows one to create a copy of a multiple sequence alignment. The `options` parameter additionally allows for sequence manipulation, such as converting DNA to RNA alphabet, and conversion to uppercase letters.

See also

[vrna\\_aln\\_copy\(\)](#), [VRNA\\_ALN\\_RNA](#), [VRNA\\_ALN\\_UPPERCASE](#), [VRNA\\_ALN\\_DEFAULT](#)

**Parameters**

|                  |                                                                           |
|------------------|---------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated)  |
| <i>options</i>   | Option flags indicating whether the aligned sequences should be converted |

**Returns**

A (manipulated) copy of the input alignment

**16.70.4.8 vrna\_aln\_conservation\_struct()**

```
float * vrna_aln_conservation_struct (
    const char ** alignment,
    const char * structure,
    const vrna_md_t * md )
#include <ViennaRNA/utils/alignments.h>
```

Compute base pair conservation of a consensus structure.

This function computes the base pair conservation (fraction of canonical base pairs) of a consensus structure given a multiple sequence alignment. The base pair types that are considered canonical may be specified using the [vrna\\_md\\_t.pair](#) array. Passing *NULL* as parameter `md` results in default pairing rules, i.e. canonical Watson-Crick and GU Wobble pairs.

**Parameters**

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
| <i>structure</i> | The consensus structure in dot-bracket notation                          |
| <i>md</i>        | Model details that specify compatible base pairs (Maybe <i>NULL</i> )    |

**Returns**

A 1-based vector of base pair conservations

**SWIG Wrapper Notes** This function is available in an overloaded form where the last parameter may be omitted, indicating `md = NULL`

**16.70.4.9 vrna\_aln\_conservation\_col()**

```
float * vrna_aln_conservation_col (
    const char ** alignment,
    const vrna_md_t * md,
    unsigned int options )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Compute nucleotide conservation in an alignment.

This function computes the conservation of nucleotides in alignment columns. The simple measure is Shannon Entropy and can be selected by passing the `VRNA_MEASURE_SHANNON_ENTROPY` flag in the `options` parameter.

#### Note

Currently, only `VRNA_MEASURE_SHANNON_ENTROPY` is supported as conservation measure.

#### See also

`VRNA_MEASURE_SHANNON_ENTROPY`

#### Parameters

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
| <i>md</i>        | Model details that specify known nucleotides (Maybe <i>NULL</i> )        |
| <i>options</i>   | A flag indicating which measure of conservation should be applied        |

#### Returns

A 1-based vector of column conservations

**SWIG Wrapper Notes** This function is available in an overloaded form where the last two parameters may be omitted, indicating `md = NULL`, and `options = VRNA_MEASURE_SHANNON_ENTROPY`, respectively.

#### 16.70.4.10 `vrna_aln_consensus_sequence()`

```
char * vrna_aln_consensus_sequence (
    const char ** alignment,
    const vrna_md_t * md_p )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Compute the consensus sequence for a given multiple sequence alignment.

#### Parameters

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
| <i>md_p</i>      | Model details that specify known nucleotides (Maybe <i>NULL</i> )        |

#### Returns

The consensus sequence of the alignment, i.e. the most frequent nucleotide for each alignment column

#### 16.70.4.11 `vrna_aln_consensus_mis()`

```
char * vrna_aln_consensus_mis (
    const char ** alignment,
    const vrna_md_t * md_p )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Compute the Most Informative Sequence (MIS) for a given multiple sequence alignment.

The most informative sequence (MIS) [9] displays for each alignment column the nucleotides with frequency greater than the background frequency, projected into IUPAC notation. Columns where gaps are over-represented are in lower case.

## Parameters

|                  |                                                                          |
|------------------|--------------------------------------------------------------------------|
| <i>alignment</i> | The input sequence alignment (last entry must be <i>NULL</i> terminated) |
| <i>md_p</i>      | Model details that specify known nucleotides (Maybe <i>NULL</i> )        |

## Returns

The most informative sequence for the alignment

## 16.71 Files and I/O

Functions to parse, write, and convert various file formats and to deal with file system related issues.

### 16.71.1 Detailed Description

Functions to parse, write, and convert various file formats and to deal with file system related issues.  
Collaboration diagram for Files and I/O:

## Modules

- [Nucleic Acid Sequences and Structures](#)  
*Functions to read/write different file formats for nucleic acid sequences and secondary structures.*
- [Multiple Sequence Alignments](#)  
*Functions to read/write multiple sequence alignments (MSA) in various file formats.*
- [Command Files](#)  
*Functions to parse and interpret the content of [Command Files](#).*

## Files

- file [commands.h](#)  
*Parse and apply different commands that alter the behavior of secondary structure prediction and evaluation.*
- file [ribo.h](#)  
*Parse RiboSum Scoring Matrices for Covariance Scoring of Alignments.*
- file [file\\_formats.h](#)  
*Read and write different file formats for RNA sequences, structures.*
- file [file\\_formats\\_msa.h](#)  
*Functions dealing with file formats for Multiple Sequence Alignments (MSA)*
- file [utils.h](#)  
*Several utilities for file handling.*

## Functions

- float \*\* **get\_ribosum** (const char \*\*Aseq, int n\_seq, int length)  
*Retrieve a RiboSum Scoring Matrix for a given Alignment.*
- float \*\* **readribosum** (char \*name)  
*Read a RiboSum or other user-defined Scoring Matrix and Store into global Memory.*
- void **vrna\_file\_copy** (FILE \*from, FILE \*to)  
*Inefficient 'cp'.*
- char \* **vrna\_read\_line** (FILE \*fp)  
*Read a line of arbitrary length from a stream.*
- int **vrna\_mkdir\_p** (const char \*path)  
*Recursively create a directory tree.*
- char \* **vrna\_basename** (const char \*path)

*Extract the filename from a file path.*

- char \* **vrna\_dirname** (const char \*path)

*Extract the directory part of a file path.*

- char \* **vrna\_filename\_sanitize** (const char \*name, const char \*replacement)

*Sanitize a file name.*

- int **vrna\_file\_exists** (const char \*filename)

*Check if a file already exists in the file system.*

## 16.71.2 Function Documentation

### 16.71.2.1 vrna\_read\_line()

```
char * vrna_read_line (
    FILE * fp )
#include <ViennaRNA/io/utils.h>
```

Read a line of arbitrary length from a stream.

Returns a pointer to the resulting string. The necessary memory is allocated and should be released using *free()* when the string is no longer needed.

#### Parameters

|           |                                                                  |
|-----------|------------------------------------------------------------------|
| <i>fp</i> | A file pointer to the stream where the function should read from |
|-----------|------------------------------------------------------------------|

#### Returns

A pointer to the resulting string

### 16.71.2.2 vrna\_filename\_sanitize()

```
char * vrna_filename_sanitize (
    const char * name,
    const char * replacement )
#include <ViennaRNA/io/utils.h>
```

Sanitize a file name.

Returns a new file name where all invalid characters are substituted by a replacement character. If no replacement character is supplied, invalid characters are simply removed from the filename. File names may also never exceed a length of 255 characters. Longer file names will undergo a 'smart' truncation process, where the filenames' suffix, i.e. everything after the last dot '.', is attempted to be kept intact. Hence, only the filename part before the suffix is reduced in such a way that the total filename complies to the length restriction of 255 characters. If no suffix is present or the suffix itself already exceeds the maximum length, the filename is simply truncated from the back of the string.

For now we consider the following characters invalid:

- backslash '\'
- slash '/'
- question mark '?'
- percent sign %
- asterisk '\*'
- colon ':'
- pipe symbol '|'

- double quote `""`
- triangular brackets `'<'` and `'>'`

Furthermore, the (resulting) file name must not be a reserved file name, such as:

- `'.'`
- `'..'`

#### Note

This function allocates a new block of memory for the sanitized string. It also may return (a) NULL if the input is pointing to NULL, or (b) an empty string if the input only consists of invalid characters which are simply removed!

#### Parameters

|                    |                                    |
|--------------------|------------------------------------|
| <i>name</i>        | The input file name                |
| <i>replacement</i> | The replacement character, or NULL |

#### Returns

The sanitized file name, or NULL

#### 16.71.2.3 `vrna_file_exists()`

```
int vrna_file_exists (
    const char * filename )
#include <ViennaRNA/io/utils.h>
Check if a file already exists in the file system.
```

#### Parameters

|                 |                                                       |
|-----------------|-------------------------------------------------------|
| <i>filename</i> | The name of (path to) the file to check for existence |
|-----------------|-------------------------------------------------------|

#### Returns

0 if it doesn't exist, 1 otherwise

## 16.72 Nucleic Acid Sequences and Structures

Functions to read/write different file formats for nucleic acid sequences and secondary structures.

### 16.72.1 Detailed Description

Functions to read/write different file formats for nucleic acid sequences and secondary structures.  
Collaboration diagram for Nucleic Acid Sequences and Structures:

#### Files

- file [file\\_formats.h](#)  
*Read and write different file formats for RNA sequences, structures.*

#### Macros

- `#define` [VRNA\\_OPTION\\_MULTILINE](#) 32U

*Tell a function that an input is assumed to span several lines.*

- `#define VRNA_CONSTRAINT_MULTILINE 32U`  
*parse multiline constraint*

## Functions

- void `vrna_file_helixlist` (const char \*seq, const char \*db, float energy, FILE \*file)  
*Print a secondary structure as helix list.*
- void `vrna_file_connect` (const char \*seq, const char \*db, float energy, const char \*identifier, FILE \*file)  
*Print a secondary structure as connect table.*
- void `vrna_file_bpseq` (const char \*seq, const char \*db, FILE \*file)  
*Print a secondary structure in bpseq format.*
- void `vrna_file_json` (const char \*seq, const char \*db, double energy, const char \*identifier, FILE \*file)  
*Print a secondary structure in jsonformat.*
- unsigned int `vrna_file_fasta_read_record` (char \*\*header, char \*\*sequence, char \*\*\*rest, FILE \*file, unsigned int options)
- char \* `vrna_extract_record_rest_structure` (const char \*\*lines, unsigned int length, unsigned int option)  
*Extract a dot-bracket structure string from (multiline)character array.*
- int `vrna_file_SHAPE_read` (const char \*file\_name, int length, double default\_value, char \*sequence, double \*values)  
*Read data from a given SHAPE reactivity input file.*
- void `vrna_extract_record_rest_constraint` (char \*\*cstruc, const char \*\*lines, unsigned int option)  
*Extract a hard constraint encoded as pseudo dot-bracket string.*
- unsigned int `read_record` (char \*\*header, char \*\*sequence, char \*\*\*rest, unsigned int options)  
*Get a data record from stdin.*

## 16.72.2 Macro Definition Documentation

### 16.72.2.1 VRNA\_OPTION\_MULTILINE

```
#define VRNA_OPTION_MULTILINE 32U
```

```
#include <ViennaRNA/io/file_formats.h>
```

Tell a function that an input is assumed to span several lines.

If used as input-option a function might also be returning this state telling that it has read data from multiple lines.

See also

`vrna_extract_record_rest_structure()`, `vrna_file_fasta_read_record()`

### 16.72.2.2 VRNA\_CONSTRAINT\_MULTILINE

```
#define VRNA_CONSTRAINT_MULTILINE 32U
```

```
#include <ViennaRNA/io/file_formats.h>
```

parse multiline constraint

**Deprecated** see `vrna_extract_record_rest_structure()`

## 16.72.3 Function Documentation

**16.72.3.1 vrna\_file\_helixlist()**

```
void vrna_file_helixlist (
    const char * seq,
    const char * db,
    float energy,
    FILE * file )
#include <ViennaRNA/io/file_formats.h>
Print a secondary structure as helix list.
```

**Parameters**

|               |                                                                                 |
|---------------|---------------------------------------------------------------------------------|
| <i>seq</i>    | The RNA sequence                                                                |
| <i>db</i>     | The structure in dot-bracket format                                             |
| <i>energy</i> | Free energy of the structure in kcal/mol                                        |
| <i>file</i>   | The file handle used to print to (print defaults to 'stdout' if(file == NULL) ) |

**16.72.3.2 vrna\_file\_connect()**

```
void vrna_file_connect (
    const char * seq,
    const char * db,
    float energy,
    const char * identifier,
    FILE * file )
#include <ViennaRNA/io/file_formats.h>
Print a secondary structure as connect table.
Connect table file format looks like this:
```

```
* 300 ENERGY = 7.0 example
* 1 G      0   2   22   1
* 2 G      1   3   21   2
*
```

where the headerline is followed by 6 columns with:

1. Base number: index n
2. Base (A, C, G, T, U, X)
3. Index n-1 (0 if first nucleotide)
4. Index n+1 (0 if last nucleotide)
5. Number of the base to which n is paired. No pairing is indicated by 0 (zero).
6. Natural numbering.

**Parameters**

|                   |                                                                                 |
|-------------------|---------------------------------------------------------------------------------|
| <i>seq</i>        | The RNA sequence                                                                |
| <i>db</i>         | The structure in dot-bracket format                                             |
| <i>energy</i>     | The free energy of the structure                                                |
| <i>identifier</i> | An optional identifier for the sequence                                         |
| <i>file</i>       | The file handle used to print to (print defaults to 'stdout' if(file == NULL) ) |



**16.72.3.3 vrna\_file\_bpseq()**

```
void vrna_file_bpseq (
    const char * seq,
    const char * db,
    FILE * file )
#include <ViennaRNA/io/file_formats.h>
Print a secondary structure in bpseq format.
```

**Parameters**

|             |                                                                                 |
|-------------|---------------------------------------------------------------------------------|
| <i>seq</i>  | The RNA sequence                                                                |
| <i>db</i>   | The structure in dot-bracket format                                             |
| <i>file</i> | The file handle used to print to (print defaults to 'stdout' if(file == NULL) ) |

**16.72.3.4 vrna\_file\_json()**

```
void vrna_file_json (
    const char * seq,
    const char * db,
    double energy,
    const char * identifier,
    FILE * file )
#include <ViennaRNA/io/file_formats.h>
Print a secondary structure in jsonformat.
```

**Parameters**

|                   |                                                                                 |
|-------------------|---------------------------------------------------------------------------------|
| <i>seq</i>        | The RNA sequence                                                                |
| <i>db</i>         | The structure in dot-bracket format                                             |
| <i>energy</i>     | The free energy                                                                 |
| <i>identifier</i> | An identifier for the sequence                                                  |
| <i>file</i>       | The file handle used to print to (print defaults to 'stdout' if(file == NULL) ) |

**16.72.3.5 vrna\_file\_fasta\_read\_record()**

```
unsigned int vrna_file_fasta_read_record (
    char ** header,
    char ** sequence,
    char *** rest,
    FILE * file,
    unsigned int options )
#include <ViennaRNA/io/file_formats.h>
```

@brief Get a (fasta) data set from a file or stdin

This function may be used to obtain complete datasets from a filehandle or stdin. A dataset is always defined to contain at least a sequence. If data starts with a fasta header, i.e. a line like  
@verbatim >some header info

then [vrna\\_file\\_fasta\\_read\\_record\(\)](#) will assume that the sequence that follows the header may span over several lines. To disable this behavior and to assign a single line to the argument 'sequence' one can pass [VRNA\\_INPUT\\_NO\\_SPAN](#) in the 'options' argument. If no fasta header is read in the beginning of a data block, a sequence must not span over multiple lines!

Unless the options [VRNA\\_INPUT\\_NOSKIP\\_COMMENTS](#) or [VRNA\\_INPUT\\_NOSKIP\\_BLANK\\_LINES](#) are passed, a sequence may be interrupted by lines starting with a comment character or empty lines.

A sequence is regarded as completely read if it was either assumed to not span over multiple lines, a secondary structure or structure constraint follows the sequence on the next line, or a new header marks the beginning of a new sequence...

All lines following the sequence (this includes comments) that do not initiate a new dataset according to the above definition are available through the line-array 'rest'. Here one can usually find the structure constraint or other information belonging to the current dataset. Filling of 'rest' may be prevented by passing [VRNA\\_INPUT\\_NO\\_REST](#) to the options argument.

#### Note

This function will exit any program with an error message if no sequence could be read!

This function is NOT threadsafe! It uses a global variable to store information about the next data block.

The main purpose of this function is to be able to easily parse blocks of data in the header of a loop where all calculations for the appropriate data is done inside the loop. The loop may be then left on certain return values, e.g.:

```
@endverbatim
char *id, *seq, **rest;
int i;
id = seq = NULL;
rest = NULL;
while(!(vrna_file_fasta_read_record(&id, &seq, &rest, NULL, 0) & (VRNA_INPUT_ERROR | VRNA_INPUT_QUIT))){
    if(id)
        printf("%s\n", id);
    printf("%s\n", seq);
    if(rest)
        for(i=0;rest[i];i++){
            printf("%s\n", rest[i]);
            free(rest[i]);
        }
    free(rest);
    free(seq);
    free(id);
}
```

In the example above, the while loop will be terminated when [vrna\\_file\\_fasta\\_read\\_record\(\)](#) returns either an error, EOF, or a user initiated quit request.

As long as data is read from stdin (we are passing NULL as the file pointer), the id is printed if it is available for the current block of data. The sequence will be printed in any case and if some more lines belong to the current block of data each line will be printed as well.

#### Note

Do not forget to free the memory occupied by header, sequence and rest!

#### Parameters

|                 |                                                                                                      |
|-----------------|------------------------------------------------------------------------------------------------------|
| <i>header</i>   | A pointer which will be set such that it points to the header of the record                          |
| <i>sequence</i> | A pointer which will be set such that it points to the sequence of the record                        |
| <i>rest</i>     | A pointer which will be set such that it points to an array of lines which also belong to the record |
| <i>file</i>     | A file handle to read from (if NULL, this function reads from stdin)                                 |
| <i>options</i>  | Some options which may be passed to alter the behavior of the function, use 0 for no options         |

#### Returns

A flag with information about what the function actually did read

#### 16.72.3.6 vrna\_extract\_record\_rest\_structure()

```
char * vrna_extract_record_rest_structure (
    const char ** lines,
```

```

        unsigned int length,
        unsigned int option )
#include <ViennaRNA/io/file_formats.h>

```

Extract a dot-bracket structure string from (multiline)character array.

This function extracts a dot-bracket structure string from the 'rest' array as returned by [vrna\\_file\\_fasta\\_read\\_record\(\)](#) and returns it. All occurrences of comments within the 'lines' array will be skipped as long as they do not break the structure string. If no structure could be read, this function returns NULL.

#### Precondition

The argument 'lines' has to be a 2-dimensional character array as obtained by [vrna\\_file\\_fasta\\_read\\_record\(\)](#)

#### See also

[vrna\\_file\\_fasta\\_read\\_record\(\)](#)

#### Parameters

|               |                                                                                               |
|---------------|-----------------------------------------------------------------------------------------------|
| <i>lines</i>  | The (multiline) character array to be parsed                                                  |
| <i>length</i> | The assumed length of the dot-bracket string (passing a value < 1 results in no length limit) |
| <i>option</i> | Some options which may be passed to alter the behavior of the function, use 0 for no options  |

#### Returns

The dot-bracket string read from lines or NULL

### 16.72.3.7 vrna\_file\_SHAPE\_read()

```

int vrna_file_SHAPE_read (
    const char * file_name,
    int length,
    double default_value,
    char * sequence,
    double * values )
#include <ViennaRNA/io/file_formats.h>

```

Read data from a given SHAPE reactivity input file.

This function parses the informations from a given file and stores the result in the preallocated string sequence and the double array values.

#### Parameters

|                      |                                                                                           |
|----------------------|-------------------------------------------------------------------------------------------|
| <i>file_name</i>     | Path to the constraints file                                                              |
| <i>length</i>        | Length of the sequence (file entries exceeding this limit will cause an error)            |
| <i>default_value</i> | Value for missing indices                                                                 |
| <i>sequence</i>      | Pointer to an array used for storing the sequence obtained from the SHAPE reactivity file |
| <i>values</i>        | Pointer to an array used for storing the values obtained from the SHAPE reactivity file   |

### 16.72.3.8 vrna\_extract\_record\_rest\_constraint()

```

void vrna_extract_record_rest_constraint (
    char ** cstruc,
    const char ** lines,
    unsigned int option )

```

```
#include <ViennaRNA/io/file_formats.h>
```

Extract a hard constraint encoded as pseudo dot-bracket string.

**Deprecated** Use `vrna_extract_record_rest_structure()` instead!

#### Precondition

The argument 'lines' has to be a 2-dimensional character array as obtained by `vrna_file_fasta_read_record()`

#### See also

`vrna_file_fasta_read_record()`, `VRNA_CONSTRAINT_DB_PIPE`, `VRNA_CONSTRAINT_DB_DOT`, `VRNA_CONSTRAINT_DB_`  
`VRNA_CONSTRAINT_DB_ANG_BRACK`, `VRNA_CONSTRAINT_DB_RND_BRACK`

#### Parameters

|               |                                                                                    |
|---------------|------------------------------------------------------------------------------------|
| <i>cstruc</i> | A pointer to a character array that is used as pseudo dot-bracket output           |
| <i>lines</i>  | A 2-dimensional character array with the extension lines from the FASTA input      |
| <i>option</i> | The option flags that define the behavior and recognition pattern of this function |

#### 16.72.3.9 read\_record()

```
unsigned int read_record (
    char ** header,
    char ** sequence,
    char *** rest,
    unsigned int options )
```

```
#include <ViennaRNA/io/file_formats.h>
```

Get a data record from stdin.

**Deprecated** This function is deprecated! Use `vrna_file_fasta_read_record()` as a replacment.

## 16.73 Multiple Sequence Alignments

Functions to read/write multiple sequence alignments (MSA) in various file formats.

### 16.73.1 Detailed Description

Functions to read/write multiple sequence alignments (MSA) in various file formats.  
 Collaboration diagram for Multiple Sequence Alignments:

#### Files

- file `file_formats_msa.h`  
*Functions dealing with file formats for Multiple Sequence Alignments (MSA)*

#### Macros

- `#define VRNA_FILE_FORMAT_MSA_CLUSTAL 1U`  
*Option flag indicating ClustalW formatted files.*
- `#define VRNA_FILE_FORMAT_MSA_STOCKHOLM 2U`  
*Option flag indicating Stockholm 1.0 formatted files.*
- `#define VRNA_FILE_FORMAT_MSA_FASTA 4U`  
*Option flag indicating FASTA (Pearson) formatted files.*

- `#define VRNA_FILE_FORMAT_MSA_MAF 8U`  
*Option flag indicating MAF formatted files.*
- `#define VRNA_FILE_FORMAT_MSA_MIS 16U`  
*Option flag indicating most informative sequence (MIS) output.*
- `#define VRNA_FILE_FORMAT_MSA_DEFAULT`  
*Option flag indicating the set of default file formats.*
- `#define VRNA_FILE_FORMAT_MSA_NOCHECK 4096U`  
*Option flag to disable validation of the alignment.*
- `#define VRNA_FILE_FORMAT_MSA_UNKNOWN 8192U`  
*Return flag of `vrna_file_msa_detect_format()` to indicate unknown or malformed alignment.*
- `#define VRNA_FILE_FORMAT_MSA_APPEND 16384U`  
*Option flag indicating to append data to a multiple sequence alignment file rather than overwriting it.*
- `#define VRNA_FILE_FORMAT_MSA_QUIET 32768U`  
*Option flag to suppress unnecessary spam messages on `stderr`*
- `#define VRNA_FILE_FORMAT_MSA_SILENT 65536U`  
*Option flag to completely silence any warnings on `stderr`*

## Functions

- `int vrna_file_msa_read` (const char \*filename, char \*\*\*names, char \*\*\*aln, char \*\*id, char \*\*structure, unsigned int options)  
*Read a multiple sequence alignment from file.*
- `int vrna_file_msa_read_record` (FILE \*fp, char \*\*\*names, char \*\*\*aln, char \*\*id, char \*\*structure, unsigned int options)  
*Read a multiple sequence alignment from file handle.*
- `unsigned int vrna_file_msa_detect_format` (const char \*filename, unsigned int options)  
*Detect the format of a multiple sequence alignment file.*
- `int vrna_file_msa_write` (const char \*filename, const char \*\*names, const char \*\*aln, const char \*id, const char \*structure, const char \*source, unsigned int options)  
*Write multiple sequence alignment file.*

## 16.73.2 Macro Definition Documentation

### 16.73.2.1 VRNA\_FILE\_FORMAT\_MSA\_CLUSTAL

```
#define VRNA_FILE_FORMAT_MSA_CLUSTAL 1U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating ClustalW formatted files.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#)

### 16.73.2.2 VRNA\_FILE\_FORMAT\_MSA\_STOCKHOLM

```
#define VRNA_FILE_FORMAT_MSA_STOCKHOLM 2U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating Stockholm 1.0 formatted files.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#)

**16.73.2.3 VRNA\_FILE\_FORMAT\_MSA\_FASTA**

```
#define VRNA_FILE_FORMAT_MSA_FASTA 4U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating FASTA (Pearson) formatted files.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#)

**16.73.2.4 VRNA\_FILE\_FORMAT\_MSA\_MAF**

```
#define VRNA_FILE_FORMAT_MSA_MAF 8U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating MAF formatted files.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#)

**16.73.2.5 VRNA\_FILE\_FORMAT\_MSA\_MIS**

```
#define VRNA_FILE_FORMAT_MSA_MIS 16U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating most informative sequence (MIS) output.

The default reference sequence output for an alignment is simply a consensus sequence. This flag allows to write the most informative sequence (MIS) instead.

See also

[vrna\\_file\\_msa\\_write\(\)](#)

**16.73.2.6 VRNA\_FILE\_FORMAT\_MSA\_DEFAULT**

```
#define VRNA_FILE_FORMAT_MSA_DEFAULT
#include <ViennaRNA/io/file_formats_msa.h>
```

**Value:**

```
( \
  VRNA_FILE_FORMAT_MSA_CLUSTAL \
  | VRNA_FILE_FORMAT_MSA_STOCKHOLM \
  | VRNA_FILE_FORMAT_MSA_FASTA \
  | VRNA_FILE_FORMAT_MSA_MAF \
)
```

Option flag indicating the set of default file formats.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#)

**16.73.2.7 VRNA\_FILE\_FORMAT\_MSA\_NOCHECK**

```
#define VRNA_FILE_FORMAT_MSA_NOCHECK 4096U
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag to disable validation of the alignment.

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#)

**16.73.2.8 VRNA\_FILE\_FORMAT\_MSA\_UNKNOWN**

```
#define VRNA_FILE_FORMAT_MSA_UNKNOWN 8192U
```

```
#include <ViennaRNA/io/file_formats_msa.h>
```

Return flag of [vrna\\_file\\_msa\\_detect\\_format\(\)](#) to indicate unknown or malformed alignment.

See also

[vrna\\_file\\_msa\\_detect\\_format\(\)](#)

**16.73.2.9 VRNA\_FILE\_FORMAT\_MSA\_APPEND**

```
#define VRNA_FILE_FORMAT_MSA_APPEND 16384U
```

```
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag indicating to append data to a multiple sequence alignment file rather than overwriting it.

See also

[vrna\\_file\\_msa\\_write\(\)](#)

**16.73.2.10 VRNA\_FILE\_FORMAT\_MSA\_QUIET**

```
#define VRNA_FILE_FORMAT_MSA_QUIET 32768U
```

```
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag to suppress unnecessary spam messages on `stderr`

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#)

**16.73.2.11 VRNA\_FILE\_FORMAT\_MSA\_SILENT**

```
#define VRNA_FILE_FORMAT_MSA_SILENT 65536U
```

```
#include <ViennaRNA/io/file_formats_msa.h>
```

Option flag to completely silence any warnings on `stderr`

See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_read\\_record\(\)](#)

**16.73.3 Function Documentation****16.73.3.1 vrna\_file\_msa\_read()**

```
int vrna_file_msa_read (
    const char * filename,
    char *** names,
    char *** aln,
    char ** id,
    char ** structure,
    unsigned int options )
#include <ViennaRNA/io/file_formats_msa.h>
```

Read a multiple sequence alignment from file.

This function reads the (first) multiple sequence alignment from an input file. The read alignment is split into the sequence id/name part and the actual sequence information and stored in memory as arrays of ids/names and sequences. If the alignment file format allows for additional information, such as an ID of the entire alignment or

consensus structure information, this data is retrieved as well and made available. The `options` parameter allows to specify the set of alignment file formats that should be used to retrieve the data. If 0 is passed as option, the list of alignment file formats defaults to `VRNA_FILE_FORMAT_MSA_DEFAULT`.

Currently, the list of parsable multiple sequence alignment file formats consists of:

- [ClustalW format](#)
- [Stockholm 1.0 format](#)
- [FASTA \(Pearson\) format](#)
- [MAF format](#)

#### Note

After successfully reading an alignment, this function performs a validation of the data that includes uniqueness of the sequence identifiers, and equal sequence lengths. This check can be deactivated by passing `VRNA_FILE_FORMAT_MSA_NOCHECK` in the `options` parameter.

It is the users responsibility to free any memory occupied by the output arguments `names`, `aln`, `id`, and `structure` after calling this function. The function automatically sets the latter two arguments to `NULL` in case no corresponding data could be retrieved from the input alignment.

#### See also

[vrna\\_file\\_msa\\_read\\_record\(\)](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_CLUSTAL](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_FASTA](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_MAF](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_DEFAULT](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_NOCHECK](#)

#### Parameters

|                  |                                                                                                   |
|------------------|---------------------------------------------------------------------------------------------------|
| <i>filename</i>  | The name of input file that contains the alignment                                                |
| <i>names</i>     | An address to the pointer where sequence identifiers should be written to                         |
| <i>aln</i>       | An address to the pointer where aligned sequences should be written to                            |
| <i>id</i>        | An address to the pointer where the alignment ID should be written to (Maybe NULL)                |
| <i>structure</i> | An address to the pointer where consensus structure information should be written to (Maybe NULL) |
| <i>options</i>   | Options to manipulate the behavior of this function                                               |

#### Returns

The number of sequences in the alignment, or -1 if no alignment record could be found

**SWIG Wrapper Notes** In the target scripting language, only the first and last argument, `filename` and `options`, are passed to the corresponding function. The other arguments, which serve as output in the C-library, are available as additional return values. Hence, a function call in python may look like this:

```
num_seq, names, aln, id, structure = RNA.file_msa_read("msa.stk", RNA.FILE_FORMAT_MSA_STOCKHOLM)
```

After successfully reading the first record, the variable `num_seq` contains the number of sequences in the alignment (the actual return value of the C-function), while the variables `names`, `aln`, `id`, and `structure` are lists of the sequence names and aligned sequences, as well as strings holding the alignment ID and the structure as stated in the `SS_cons` line, respectively. Note, the last two return values may be empty strings in case the alignment does not provide the required data.

This function exists as an overloaded version where the `options` parameter may be omitted! In that case, the `options` parameter defaults to `VRNA_FILE_FORMAT_MSA_STOCKHOLM`.

#### 16.73.3.2 vrna\_file\_msa\_read\_record()

```
int vrna_file_msa_read_record (
    FILE * fp,
```



```

char *** names,
char *** aln,
char ** id,
char ** structure,
unsigned int options )
#include <ViennaRNA/io/file_formats_msa.h>

```

Read a multiple sequence alignment from file handle.

Similar to [vrna\\_file\\_msa\\_read\(\)](#), this function reads a multiple sequence alignment from an input file handle. Since using a file handle, this function is not limited to the first alignment record, but allows for looping over all alignments within the input.

The read alignment is split into the sequence id/name part and the actual sequence information and stored in memory as arrays of ids/names and sequences. If the alignment file format allows for additional information, such as an ID of the entire alignment or consensus structure information, this data is retrieved as well and made available. The `options` parameter allows to specify the alignment file format used to retrieve the data. A single format must be specified here, see [vrna\\_file\\_msa\\_detect\\_format\(\)](#) for helping to determine the correct MSA file format.

Currently, the list of parsable multiple sequence alignment file formats consists of:

- [ClustalW format](#)
- [Stockholm 1.0 format](#)
- [FASTA \(Pearson\) format](#)
- [MAF format](#)

#### Note

After successfully reading an alignment, this function performs a validation of the data that includes uniqueness of the sequence identifiers, and equal sequence lengths. This check can be deactivated by passing [VRNA\\_FILE\\_FORMAT\\_MSA\\_NOCHECK](#) in the `options` parameter.

It is the users responsibility to free any memory occupied by the output arguments `names`, `aln`, `id`, and `structure` after calling this function. The function automatically sets the latter two arguments to `NULL` in case no corresponding data could be retrieved from the input alignment.

#### See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_msa\\_detect\\_format\(\)](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_CLUSTAL](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_FASTA](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_MAF](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_DEFAULT](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_NOCHECK](#)

#### Parameters

|                  |                                                                                                   |
|------------------|---------------------------------------------------------------------------------------------------|
| <i>fp</i>        | The file pointer the data will be retrieved from                                                  |
| <i>names</i>     | An address to the pointer where sequence identifiers should be written to                         |
| <i>aln</i>       | An address to the pointer where aligned sequences should be written to                            |
| <i>id</i>        | An address to the pointer where the alignment ID should be written to (Maybe NULL)                |
| <i>structure</i> | An address to the pointer where consensus structure information should be written to (Maybe NULL) |
| <i>options</i>   | Options to manipulate the behavior of this function                                               |

#### Returns

The number of sequences in the alignment, or -1 if no alignment record could be found

**SWIG Wrapper Notes** In the target scripting language, only the first and last argument, `fp` and `options`, are passed to the corresponding function. The other arguments, which serve as output in the C-library, are available as additional return values. Hence, a function call in python may look like this:

```
f = open('msa.stk', 'r')
```

```
num_seq, names, aln, id, structure = RNA.file_msa_read_record(f, RNA.FILE_FORMAT_MSA_STOCKHOLM)
f.close()
```

After successfully reading the first record, the variable `num_seq` contains the number of sequences in the alignment (the actual return value of the C-function), while the variables `names`, `aln`, `id`, and `structure` are lists of the sequence names and aligned sequences, as well as strings holding the alignment ID and the structure as stated in the `SS_cons` line, respectively. Note, the last two return values may be empty strings in case the alignment does not provide the required data.

This function exists as an overloaded version where the `options` parameter may be omitted! In that case, the `options` parameter defaults to [VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#).

### 16.73.3.3 `vrna_file_msa_detect_format()`

```
unsigned int vrna_file_msa_detect_format (
    const char * filename,
    unsigned int options )
#include <ViennaRNA/io/file_formats_msa.h>
```

Detect the format of a multiple sequence alignment file.

This function attempts to determine the format of a file that supposedly contains a multiple sequence alignment (MSA). This is useful in cases where a MSA file contains more than a single record and therefore [vrna\\_file\\_msa\\_read\(\)](#) can not be applied, since it only retrieves the first. Here, one can try to guess the correct file format using this function and then loop over the file, record by record using one of the low-level record retrieval functions for the corresponding MSA file format.

#### Note

This function parses the entire first record within the specified file. As a result, it returns [VRNA\\_FILE\\_FORMAT\\_MSA\\_UNKNOWN](#) not only if it can't detect the file's format, but also in cases where the file doesn't contain sequences!

#### See also

[vrna\\_file\\_msa\\_read\(\)](#), [vrna\\_file\\_stockholm\\_read\\_record\(\)](#), [vrna\\_file\\_clustal\\_read\\_record\(\)](#), [vrna\\_file\\_fasta\\_read\\_record\(\)](#)

#### Parameters

|                 |                                                     |
|-----------------|-----------------------------------------------------|
| <i>filename</i> | The name of input file that contains the alignment  |
| <i>options</i>  | Options to manipulate the behavior of this function |

#### Returns

The MSA file format, or [VRNA\\_FILE\\_FORMAT\\_MSA\\_UNKNOWN](#)

**SWIG Wrapper Notes** This function exists as an overloaded version where the `options` parameter may be omitted! In that case, the `options` parameter defaults to [VRNA\\_FILE\\_FORMAT\\_MSA\\_DEFAULT](#).

### 16.73.3.4 `vrna_file_msa_write()`

```
int vrna_file_msa_write (
    const char * filename,
    const char ** names,
    const char ** aln,
    const char * id,
    const char * structure,
    const char * source,
    unsigned int options )
#include <ViennaRNA/io/file_formats_msa.h>
```

Write multiple sequence alignment file.

**Note**

Currently, we only support [Stockholm 1.0 format](#) output

**See also**

[VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_APPEND](#), [VRNA\\_FILE\\_FORMAT\\_MSA\\_MIS](#)

**Parameters**

|                  |                                                     |
|------------------|-----------------------------------------------------|
| <i>filename</i>  | The output filename                                 |
| <i>names</i>     | The array of sequence names / identifies            |
| <i>aln</i>       | The array of aligned sequences                      |
| <i>id</i>        | An optional ID for the alignment                    |
| <i>structure</i> | An optional consensus structure                     |
| <i>source</i>    | A string describing the source of the alignment     |
| <i>options</i>   | Options to manipulate the behavior of this function |

**Returns**

Non-null upon successfully writing the alignment to file

**SWIG Wrapper Notes** In the target scripting language, this function exists as a set of overloaded versions, where the last four parameters may be omitted. If the `options` parameter is missing the options default to ([VRNA\\_FILE\\_FORMAT\\_MSA\\_STOCKHOLM](#) | [VRNA\\_FILE\\_FORMAT\\_MSA\\_APPEND](#)).

## 16.74 Command Files

Functions to parse and interpret the content of [Command Files](#).

### 16.74.1 Detailed Description

Functions to parse and interpret the content of [Command Files](#).

Collaboration diagram for Command Files:

**Files**

- file [commands.h](#)

*Parse and apply different commands that alter the behavior of secondary structure prediction and evaluation.*

**Macros**

- `#define VRNA_CMD_PARSE_HC 1U`  
*Command parse/apply flag indicating hard constraints.*
- `#define VRNA_CMD_PARSE_SC 2U`  
*Command parse/apply flag indicating soft constraints.*
- `#define VRNA_CMD_PARSE_UD 4U`  
*Command parse/apply flag indicating unstructured domains.*
- `#define VRNA_CMD_PARSE_SD 8U`  
*Command parse/apply flag indicating structured domains.*
- `#define VRNA_CMD_PARSE_DEFAULTS`  
*Command parse/apply flag indicating default set of commands.*

## Typedefs

- typedef struct vrna\_command\_s \* **vrna\_cmd\_t**  
*A data structure that contains commands.*

## Functions

- [vrna\\_cmd\\_t vrna\\_file\\_commands\\_read](#) (const char \*filename, unsigned int options)  
*Extract a list of commands from a command file.*
- int [vrna\\_file\\_commands\\_apply](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*filename, unsigned int options)  
*Apply a list of commands from a command file.*
- int [vrna\\_commands\\_apply](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_cmd\\_t](#) commands, unsigned int options)  
*Apply a list of commands to a [vrna\\_fold\\_compound\\_t](#).*
- void [vrna\\_commands\\_free](#) ([vrna\\_cmd\\_t](#) commands)  
*Free memory occupied by a list of commands.*

## 16.74.2 Macro Definition Documentation

### 16.74.2.1 VRNA\_CMD\_PARSE\_HC

```
#define VRNA_CMD_PARSE_HC 1U
#include <ViennaRNA/commands.h>
```

Command parse/apply flag indicating hard constraints.

See also

[vrna\\_cmd\\_t](#), [vrna\\_file\\_commands\\_read\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_apply\(\)](#)

### 16.74.2.2 VRNA\_CMD\_PARSE\_SC

```
#define VRNA_CMD_PARSE_SC 2U
#include <ViennaRNA/commands.h>
```

Command parse/apply flag indicating soft constraints.

See also

[vrna\\_cmd\\_t](#), [vrna\\_file\\_commands\\_read\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_apply\(\)](#)

### 16.74.2.3 VRNA\_CMD\_PARSE\_UD

```
#define VRNA_CMD_PARSE_UD 4U
#include <ViennaRNA/commands.h>
```

Command parse/apply flag indicating unstructured domains.

See also

[vrna\\_cmd\\_t](#), [vrna\\_file\\_commands\\_read\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_apply\(\)](#)

### 16.74.2.4 VRNA\_CMD\_PARSE\_SD

```
#define VRNA_CMD_PARSE_SD 8U
#include <ViennaRNA/commands.h>
Command parse/apply flag indicating structured domains.
```

See also

[vrna\\_cmd\\_t](#), [vrna\\_file\\_commands\\_read\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_apply\(\)](#)

### 16.74.2.5 VRNA\_CMD\_PARSE\_DEFAULTS

```
#define VRNA_CMD_PARSE_DEFAULTS
#include <ViennaRNA/commands.h>
```

**Value:**

```
(VRNA_CMD_PARSE_HC \
 | VRNA_CMD_PARSE_SC \
 | VRNA_CMD_PARSE_UD \
 | VRNA_CMD_PARSE_SD \
)
```

Command parse/apply flag indicating default set of commands.

See also

[vrna\\_cmd\\_t](#), [vrna\\_file\\_commands\\_read\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_apply\(\)](#)

## 16.74.3 Function Documentation

### 16.74.3.1 vrna\_file\_commands\_read()

```
vrna_cmd_t vrna_file_commands_read (
    const char * filename,
    unsigned int options )
#include <ViennaRNA/commands.h>
```

Extract a list of commands from a command file.

Read a list of commands specified in the input file and return them as list of abstract commands

See also

[vrna\\_commands\\_apply\(\)](#), [vrna\\_file\\_commands\\_apply\(\)](#), [vrna\\_commands\\_free\(\)](#)

**Parameters**

|                 |                                                          |
|-----------------|----------------------------------------------------------|
| <i>filename</i> | The filename                                             |
| <i>options</i>  | Options to limit the type of commands read from the file |

**Returns**

A list of abstract commands

### 16.74.3.2 vrna\_file\_commands\_apply()

```
int vrna_file_commands_apply (
    vrna_fold_compound_t * vc,
    const char * filename,
    unsigned int options )
#include <ViennaRNA/commands.h>
```

Apply a list of commands from a command file.

This function is a shortcut to directly parse a commands file and apply all successfully parsed commands to a `vrna_fold_compound_t` data structure. It is the same as:

```
int r;
struct vrna_command_s *cmds;
cmds = vrna_file_commands_read(filename, options);
r = vrna_commands_apply(vc, cmds, options);
vrna_commands_free(cmds);
return r;
```

#### Parameters

|                 |                                                                           |
|-----------------|---------------------------------------------------------------------------|
| <i>vc</i>       | The <code>vrna_fold_compound_t</code> the command list will be applied to |
| <i>filename</i> | The filename                                                              |
| <i>options</i>  | Options to limit the type of commands read from the file                  |

#### Returns

The number of commands successfully applied

**SWIG Wrapper Notes** This function is attached as method `file_commands_apply()` to objects of type `fold_↵  
compound`

#### 16.74.3.3 vrna\_commands\_apply()

```
int vrna_commands_apply (
    vrna_fold_compound_t * vc,
    vrna_cmd_t commands,
    unsigned int options )
#include <ViennaRNA/commands.h>
Apply a list of commands to a vrna_fold_compound_t.
```

#### Parameters

|                 |                                                                           |
|-----------------|---------------------------------------------------------------------------|
| <i>vc</i>       | The <code>vrna_fold_compound_t</code> the command list will be applied to |
| <i>commands</i> | The commands to apply                                                     |
| <i>options</i>  | Options to limit the type of commands read from the file                  |

#### Returns

The number of commands successfully applied

#### 16.74.3.4 vrna\_commands\_free()

```
void vrna_commands_free (
    vrna_cmd_t commands )
#include <ViennaRNA/commands.h>
Free memory occupied by a list of commands.
Release memory occupied by a list of commands
```

#### Parameters

|                 |                                 |
|-----------------|---------------------------------|
| <i>commands</i> | A pointer to a list of commands |
|-----------------|---------------------------------|

## 16.75 Plotting

Functions for Creating Secondary Structure Plots, Dot-Plots, and More.

### 16.75.1 Detailed Description

Functions for Creating Secondary Structure Plots, Dot-Plots, and More.

Collaboration diagram for Plotting:

#### Modules

- [Layouts and Coordinates](#)  
*Functions to compute coordinate layouts for secondary structure plots.*
- [Annotation](#)  
*Functions to generate annotations for Secondary Structure Plots, Dot-Plots, and Others.*
- [Alignment Plots](#)  
*Functions to generate Alignment plots with annotated consensus structure.*
- [Deprecated Interface for Plotting Utilities](#)

#### Files

- file [alignments.h](#)  
*Various functions for plotting Sequence / Structure Alignments.*
- file [layouts.h](#)  
*Secondary structure plot layout algorithms.*
- file [probabilities.h](#)  
*Various functions for plotting RNA secondary structures, dot-plots and other visualizations.*
- file [structures.h](#)  
*Various functions for plotting RNA secondary structures.*
- file [utils.h](#)  
*Various utilities to assist in plotting secondary structures and consensus structures.*
- file [RNApuzzler.h](#)  
*Implementation of the RNApuzzler RNA secondary structure layout algorithm [24].*
- file [RNAturtle.h](#)  
*Implementation of the RNAturtle RNA secondary structure layout algorithm [24].*

#### Data Structures

- struct [vrna\\_dotplot\\_auxdata\\_t](#)

#### Functions

- int [PS\\_dot\\_plot\\_list](#) (char \*seq, char \*filename, [vrna\\_ep\\_t](#) \*pl, [vrna\\_ep\\_t](#) \*mf, char \*comment)  
*Produce a postscript dot-plot from two pair lists.*
- int [PS\\_dot\\_plot](#) (char \*string, char \*file)  
*Produce postscript dot-plot.*
- int [vrna\\_file\\_PS\\_rnaplot](#) (const char \*seq, const char \*structure, const char \*file, [vrna\\_md\\_t](#) \*md\_p)  
*Produce a secondary structure graph in PostScript and write it to 'filename'.*
- int [vrna\\_file\\_PS\\_rnaplot\\_a](#) (const char \*seq, const char \*structure, const char \*file, const char \*pre, const char \*post, [vrna\\_md\\_t](#) \*md\_p)  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.*
- int [gmlRNA](#) (char \*string, char \*structure, char \*ssfile, char option)  
*Produce a secondary structure graph in Graph Meta Language (gml) and write it to a file.*
- int [ssv\\_rna\\_plot](#) (char \*string, char \*structure, char \*ssfile)

- Produce a secondary structure graph in SStructView format.*
- `int svg\_rna\_plot (char *string, char *structure, char *ssfile)`  
*Produce a secondary structure plot in SVG format and write it to a file.*
- `int xrna\_plot (char *string, char *structure, char *ssfile)`  
*Produce a secondary structure plot for further editing in XRNA.*
- `int PS\_rna\_plot (char *string, char *structure, char *file)`  
*Produce a secondary structure graph in PostScript and write it to 'filename'.*
- `int PS\_rna\_plot\_a (char *string, char *structure, char *file, char *pre, char *post)`  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.*
- `int PS\_rna\_plot\_a\_gquad (char *string, char *structure, char *ssfile, char *pre, char *post)`  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename' (detect and draw g-quadruplexes)*

## 16.75.2 Data Structure Documentation

### 16.75.2.1 struct vrna\_dotplot\_auxdata\_t

Collaboration diagram for vrna\_dotplot\_auxdata\_t:

## 16.75.3 Function Documentation

### 16.75.3.1 PS\_dot\_plot\_list()

```
int PS_dot_plot_list (
    char * seq,
    char * filename,
    vrna_ep_t * pl,
    vrna_ep_t * mf,
    char * comment )
#include <ViennaRNA/plotting/probabilities.h>
```

Produce a postscript dot-plot from two pair lists.

This function reads two plist structures (e.g. base pair probabilities and a secondary structure) as produced by [assign\\_plist\\_from\\_pr\(\)](#) and [assign\\_plist\\_from\\_db\(\)](#) and produces a postscript "dot plot" that is written to 'filename'. Using base pair probabilities in the first and mfe structure in the second plist, the resulting "dot plot" represents each base pairing probability by a square of corresponding area in a upper triangle matrix. The lower part of the matrix contains the minimum free energy structure.

See also

[assign\\_plist\\_from\\_pr\(\)](#), [assign\\_plist\\_from\\_db\(\)](#)

#### Parameters

|                 |                                      |
|-----------------|--------------------------------------|
| <i>seq</i>      | The RNA sequence                     |
| <i>filename</i> | A filename for the postscript output |
| <i>pl</i>       | The base pair probability pairlist   |
| <i>mf</i>       | The mfe secondary structure pairlist |
| <i>comment</i>  | A comment                            |

#### Returns

1 if postscript was successfully written, 0 otherwise



### 16.75.3.2 PS\_dot\_plot()

```
int PS_dot_plot (
    char * string,
    char * file )
#include <ViennaRNA/plotting/probabilities.h>
```

Produce postscript dot-plot.

Wrapper to PS\_dot\_plot\_list

Reads base pair probabilities produced by [pf\\_fold\(\)](#) from the global array [pr](#) and the pair list [base\\_pair](#) produced by [fold\(\)](#) and produces a postscript "dot plot" that is written to 'filename'. The "dot plot" represents each base pairing probability by a square of corresponding area in a upper triangle matrix. The lower part of the matrix contains the minimum free energy

#### Note

DO NOT USE THIS FUNCTION ANYMORE SINCE IT IS NOT THREADSAFE

**Deprecated** This function is deprecated and will be removed soon! Use [PS\\_dot\\_plot\\_list\(\)](#) instead!

### 16.75.3.3 vrna\_file\_PS\_rnaplot()

```
int vrna_file_PS_rnaplot (
    const char * seq,
    const char * structure,
    const char * file,
    vrna_md_t * md_p )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in PostScript and write it to 'filename'.

Note that this function has changed from previous versions and now expects the structure to be plotted in dot-bracket notation as an argument. It does not make use of the global [base\\_pair](#) array anymore.

#### Parameters

|                  |                                                                                          |
|------------------|------------------------------------------------------------------------------------------|
| <i>seq</i>       | The RNA sequence                                                                         |
| <i>structure</i> | The secondary structure in dot-bracket notation                                          |
| <i>file</i>      | The filename of the postscript output                                                    |
| <i>md_p</i>      | Model parameters used to generate a commandline option string in the output (Maybe NULL) |

#### Returns

1 on success, 0 otherwise

### 16.75.3.4 vrna\_file\_PS\_rnaplot\_a()

```
int vrna_file_PS_rnaplot_a (
    const char * seq,
    const char * structure,
    const char * file,
    const char * pre,
    const char * post,
    vrna_md_t * md_p )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'. Same as [vrna\\_file\\_PS\\_rnaplot\(\)](#) but adds extra PostScript macros for various annotations (see generated PS code). The 'pre' and 'post' variables contain PostScript code that is verbatim copied in the resulting PS file just before and

after the structure plot. If both arguments ('pre' and 'post') are NULL, no additional macros will be printed into the PostScript.

## Parameters

|                  |                                                                                          |
|------------------|------------------------------------------------------------------------------------------|
| <i>seq</i>       | The RNA sequence                                                                         |
| <i>structure</i> | The secondary structure in dot-bracket notation                                          |
| <i>file</i>      | The filename of the postscript output                                                    |
| <i>pre</i>       | PostScript code to appear before the secondary structure plot                            |
| <i>post</i>      | PostScript code to appear after the secondary structure plot                             |
| <i>md_p</i>      | Model parameters used to generate a commandline option string in the output (Maybe NULL) |

## Returns

1 on success, 0 otherwise

## 16.75.3.5 gmlRNA()

```
int gmlRNA (
    char * string,
    char * structure,
    char * ssfile,
    char option )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in Graph Meta Language (gml) and write it to a file.

If 'option' is an uppercase letter the RNA sequence is used to label nodes, if 'option' equals 'X' or 'x' the resulting file will contain coordinates for an initial layout of the graph.

## Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>string</i>    | The RNA sequence                                |
| <i>structure</i> | The secondary structure in dot-bracket notation |
| <i>ssfile</i>    | The filename of the gml output                  |
| <i>option</i>    | The option flag                                 |

## Returns

1 on success, 0 otherwise

## 16.75.3.6 ssv\_rna\_plot()

```
int ssv_rna_plot (
    char * string,
    char * structure,
    char * ssfile )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in SStructView format.

Write coord file for SStructView

## Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>string</i>    | The RNA sequence                                |
| <i>structure</i> | The secondary structure in dot-bracket notation |
| <i>ssfile</i>    | The filename of the ssv output                  |

**Returns**

1 on success, 0 otherwise

**16.75.3.7 svg\_rna\_plot()**

```
int svg_rna_plot (
    char * string,
    char * structure,
    char * ssfile )
#include <ViennaRNA/plotting/structures.h>
Produce a secondary structure plot in SVG format and write it to a file.
```

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>string</i>    | The RNA sequence                                |
| <i>structure</i> | The secondary structure in dot-bracket notation |
| <i>ssfile</i>    | The filename of the svg output                  |

**Returns**

1 on success, 0 otherwise

**16.75.3.8 xrna\_plot()**

```
int xrna_plot (
    char * string,
    char * structure,
    char * ssfile )
#include <ViennaRNA/plotting/structures.h>
Produce a secondary structure plot for further editing in XRNA.
```

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>string</i>    | The RNA sequence                                |
| <i>structure</i> | The secondary structure in dot-bracket notation |
| <i>ssfile</i>    | The filename of the xrna output                 |

**Returns**

1 on success, 0 otherwise

**16.75.3.9 PS\_rna\_plot()**

```
int PS_rna_plot (
    char * string,
    char * structure,
    char * file )
#include <ViennaRNA/plotting/structures.h>
Produce a secondary structure graph in PostScript and write it to 'filename'.
```

**Deprecated** Use `vrna_file_PS_rnaplot()` instead!

**16.75.3.10 PS\_rna\_plot\_a()**

```
int PS_rna_plot_a (
    char * string,
    char * structure,
    char * file,
    char * pre,
    char * post )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.

**Deprecated** Use [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#) instead!

**16.75.3.11 PS\_rna\_plot\_a\_gquad()**

```
int PS_rna_plot_a_gquad (
    char * string,
    char * structure,
    char * ssfile,
    char * pre,
    char * post )
#include <ViennaRNA/plotting/structures.h>
```

Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename' (detect and draw g-quadruplexes)

**Deprecated** Use [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#) instead!

**16.76 Layouts and Coordinates**

Functions to compute coordinate layouts for secondary structure plots.

**16.76.1 Detailed Description**

Functions to compute coordinate layouts for secondary structure plots.

Collaboration diagram for Layouts and Coordinates:

**Data Structures**

- struct [vrna\\_plot\\_layout\\_s](#)
- struct [vrna\\_plot\\_options\\_puzzler\\_t](#)

*Options data structure for RNApuzzler algorithm implementation. [More...](#)*

**Macros**

- #define [VRNA\\_PLOT\\_TYPE\\_SIMPLE](#) 0  
*Definition of Plot type simple*
- #define [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#) 1  
*Definition of Plot type Naview*
- #define [VRNA\\_PLOT\\_TYPE\\_CIRCULAR](#) 2  
*Definition of Plot type Circular*
- #define [VRNA\\_PLOT\\_TYPE\\_TURTLE](#) 3  
*Definition of Plot type Turtle [24].*
- #define [VRNA\\_PLOT\\_TYPE\\_PUZZLER](#) 4  
*Definition of Plot type RNApuzzler [24].*

## Typedefs

- typedef struct [vrna\\_plot\\_layout\\_s](#) [vrna\\_plot\\_layout\\_t](#)  
RNA secondary structure figure layout.

## Functions

- [vrna\\_plot\\_layout\\_t](#) \* [vrna\\_plot\\_layout](#) (const char \*structure, unsigned int plot\_type)  
Create a layout (coordinates, etc.) for a secondary structure plot.
- [vrna\\_plot\\_layout\\_t](#) \* [vrna\\_plot\\_layout\\_simple](#) (const char \*structure)  
Create a layout (coordinates, etc.) for a simple secondary structure plot.
- [vrna\\_plot\\_layout\\_t](#) \* [vrna\\_plot\\_layout\\_circular](#) (const char \*structure)  
Create a layout (coordinates, etc.) for a circular secondary structure plot.
- [vrna\\_plot\\_layout\\_t](#) \* [vrna\\_plot\\_layout\\_turtle](#) (const char \*structure)  
Create a layout (coordinates, etc.) for a secondary structure plot using the Turtle Algorithm [24].
- [vrna\\_plot\\_layout\\_t](#) \* [vrna\\_plot\\_layout\\_puzzler](#) (const char \*structure, [vrna\\_plot\\_options\\_puzzler\\_t](#) \*options)  
Create a layout (coordinates, etc.) for a secondary structure plot using the RNApuzzler Algorithm [24].
- void [vrna\\_plot\\_layout\\_free](#) ([vrna\\_plot\\_layout\\_t](#) \*layout)  
Free memory occupied by a figure layout data structure.
- int [vrna\\_plot\\_coords](#) (const char \*structure, float \*\*x, float \*\*y, int plot\_type)  
Compute nucleotide coordinates for secondary structure plot.
- int [vrna\\_plot\\_coords\\_pt](#) (const short \*pt, float \*\*x, float \*\*y, int plot\_type)  
Compute nucleotide coordinates for secondary structure plot.
- int [vrna\\_plot\\_coords\\_simple](#) (const char \*structure, float \*\*x, float \*\*y)  
Compute nucleotide coordinates for secondary structure plot the Simple way
- int [vrna\\_plot\\_coords\\_simple\\_pt](#) (const short \*pt, float \*\*x, float \*\*y)  
Compute nucleotide coordinates for secondary structure plot the Simple way
- int [vrna\\_plot\\_coords\\_circular](#) (const char \*structure, float \*\*x, float \*\*y)  
Compute coordinates of nucleotides mapped in equal distances onto a unit circle.
- int [vrna\\_plot\\_coords\\_circular\\_pt](#) (const short \*pt, float \*\*x, float \*\*y)  
Compute nucleotide coordinates for a Circular Plot
- int [vrna\\_plot\\_coords\\_puzzler](#) (const char \*structure, float \*\*x, float \*\*y, double \*\*arc\_coords, [vrna\\_plot\\_options\\_puzzler\\_t](#) \*options)  
Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].
- int [vrna\\_plot\\_coords\\_puzzler\\_pt](#) (short const \*const pair\_table, float \*\*x, float \*\*y, double \*\*arc\_coords, [vrna\\_plot\\_options\\_puzzler\\_t](#) \*puzzler)  
Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].
- [vrna\\_plot\\_options\\_puzzler\\_t](#) \* [vrna\\_plot\\_options\\_puzzler](#) (void)  
Create an RNApuzzler options data structure.
- void [vrna\\_plot\\_options\\_puzzler\\_free](#) ([vrna\\_plot\\_options\\_puzzler\\_t](#) \*options)  
Free memory occupied by an RNApuzzler options data structure.
- int [vrna\\_plot\\_coords\\_turtle](#) (const char \*structure, float \*\*x, float \*\*y, double \*\*arc\_coords)  
Compute nucleotide coordinates for secondary structure plot using the RNAturtle algorithm [24].
- int [vrna\\_plot\\_coords\\_turtle\\_pt](#) (short const \*const pair\_table, float \*\*x, float \*\*y, double \*\*arc\_coords)  
Compute nucleotide coordinates for secondary structure plot using the RNAturtle algorithm [24].

## 16.76.2 Data Structure Documentation

### 16.76.2.1 struct [vrna\\_plot\\_layout\\_s](#)

### 16.76.2.2 struct [vrna\\_plot\\_options\\_puzzler\\_t](#)

Options data structure for RNApuzzler algorithm implementation.

## 16.76.3 Macro Definition Documentation

### 16.76.3.1 VRNA\_PLOT\_TYPE\_SIMPLE

```
#define VRNA_PLOT_TYPE_SIMPLE 0
#include <ViennaRNA/plotting/layouts.h>
```

Definition of Plot type *simple*

This is the plot type definition for several RNA structure plotting functions telling them to use **Simple** plotting algorithm

See also

[rna\\_plot\\_type](#), [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#), [vrna\\_file\\_PS\\_rnaplot\(\)](#), [svg\\_rna\\_plot\(\)](#), [gmlRNA\(\)](#), [ssv\\_rna\\_plot\(\)](#), [xrna\\_plot\(\)](#)

### 16.76.3.2 VRNA\_PLOT\_TYPE\_NAVIEW

```
#define VRNA_PLOT_TYPE_NAVIEW 1
#include <ViennaRNA/plotting/layouts.h>
```

Definition of Plot type *Naview*

This is the plot type definition for several RNA structure plotting functions telling them to use **Naview** plotting algorithm [5].

See also

[rna\\_plot\\_type](#), [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#), [vrna\\_file\\_PS\\_rnaplot\(\)](#), [svg\\_rna\\_plot\(\)](#), [gmlRNA\(\)](#), [ssv\\_rna\\_plot\(\)](#), [xrna\\_plot\(\)](#)

### 16.76.3.3 VRNA\_PLOT\_TYPE\_CIRCULAR

```
#define VRNA_PLOT_TYPE_CIRCULAR 2
#include <ViennaRNA/plotting/layouts.h>
```

Definition of Plot type *Circular*

This is the plot type definition for several RNA structure plotting functions telling them to produce a **Circular plot**

See also

[rna\\_plot\\_type](#), [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#), [vrna\\_file\\_PS\\_rnaplot\(\)](#), [svg\\_rna\\_plot\(\)](#), [gmlRNA\(\)](#), [ssv\\_rna\\_plot\(\)](#), [xrna\\_plot\(\)](#)

## 16.76.4 Typedef Documentation

### 16.76.4.1 vrna\_plot\_layout\_t

```
typedef struct vrna_plot_layout_s vrna_plot_layout_t
#include <ViennaRNA/plotting/layouts.h>
```

RNA secondary structure figure layout.

See also

[vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_naview\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#)

## 16.76.5 Function Documentation

### 16.76.5.1 `vrna_plot_layout()`

```
vrna_plot_layout_t * vrna_plot_layout (
    const char * structure,
    unsigned int plot_type )
#include <ViennaRNA/plotting/layouts.h>
```

Create a layout (coordinates, etc.) for a secondary structure plot.

This function can be used to create a secondary structure nucleotide layout that is then further processed by an actual plotting function. The layout algorithm can be specified using the `plot_type` parameter, and the following algorithms are currently supported:

- [VRNA\\_PLOT\\_TYPE\\_SIMPLE](#)
- [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#)
- [VRNA\\_PLOT\\_TYPE\\_CIRCULAR](#)
- [VRNA\\_PLOT\\_TYPE\\_TURTLE](#)
- [VRNA\\_PLOT\\_TYPE\\_PUZZLER](#)

Passing an unsupported selection leads to the default algorithm [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#)

#### Note

If only X-Y coordinates of the corresponding structure layout are required, consider using [vrna\\_plot\\_coords\(\)](#) instead!

#### See also

[vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_naview\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#), [vrna\\_plot\\_coords\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)

#### Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
| <i>plot_type</i> | The layout algorithm to be used                 |

#### Returns

The layout data structure for the provided secondary structure

### 16.76.5.2 `vrna_plot_layout_simple()`

```
vrna_plot_layout_t * vrna_plot_layout_simple (
    const char * structure )
#include <ViennaRNA/plotting/layouts.h>
```

Create a layout (coordinates, etc.) for a *simple* secondary structure plot.

This function basically is a wrapper to [vrna\\_plot\\_layout\(\)](#) that passes the `plot_type` [VRNA\\_PLOT\\_TYPE\\_SIMPLE](#).

#### Note

If only X-Y coordinates of the corresponding structure layout are required, consider using [vrna\\_plot\\_coords\\_simple\(\)](#) instead!

#### See also

[vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_naview\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)



## Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

## Returns

The layout data structure for the provided secondary structure

**16.76.5.3 `vrna_plot_layout_circular()`**

```
vrna_plot_layout_t * vrna_plot_layout_circular (
    const char * structure )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Create a layout (coordinates, etc.) for a *circular* secondary structure plot.

This function basically is a wrapper to [vrna\\_plot\\_layout\(\)](#) that passes the `plot_type` `VRNA_PLOT_TYPE_CIRCULAR`.

## Note

If only X-Y coordinates of the corresponding structure layout are required, consider using [vrna\\_plot\\_coords\\_circular\(\)](#) instead!

## See also

[vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_navigate\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)

## Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

## Returns

The layout data structure for the provided secondary structure

**16.76.5.4 `vrna_plot_layout_turtle()`**

```
vrna_plot_layout_t * vrna_plot_layout_turtle (
    const char * structure )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Create a layout (coordinates, etc.) for a secondary structure plot using the *Turtle Algorithm* [24].

This function basically is a wrapper to [vrna\\_plot\\_layout\(\)](#) that passes the `plot_type` `VRNA_PLOT_TYPE_TURTLE`.

## Note

If only X-Y coordinates of the corresponding structure layout are required, consider using [vrna\\_plot\\_coords\\_turtle\(\)](#) instead!

## See also

[vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_navigate\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)

## Parameters

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

**Returns**

The layout data structure for the provided secondary structure

**16.76.5.5 vrna\_plot\_layout\_puzzler()**

```
vrna_plot_layout_t * vrna_plot_layout_puzzler (
    const char * structure,
    vrna_plot_options_puzzler_t * options )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Create a layout (coordinates, etc.) for a secondary structure plot using the *RNApuzzler Algorithm* [24].

This function basically is a wrapper to [vrna\\_plot\\_layout\(\)](#) that passes the `plot_type` `VRNA_PLOT_TYPE_PUZZLER`.

**Note**

If only X-Y coordinates of the corresponding structure layout are required, consider using [vrna\\_plot\\_coords\\_puzzler\(\)](#) instead!

**See also**

[vrna\\_plot\\_layout\\_free\(\)](#), [vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_navigate\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

**Returns**

The layout data structure for the provided secondary structure

**16.76.5.6 vrna\_plot\_layout\_free()**

```
void vrna_plot_layout_free (
    vrna_plot_layout_t * layout )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Free memory occupied by a figure layout data structure.

**See also**

[vrna\\_plot\\_layout\\_t](#), [vrna\\_plot\\_layout\(\)](#), [vrna\\_plot\\_layout\\_simple\(\)](#), [vrna\\_plot\\_layout\\_circular\(\)](#), [vrna\\_plot\\_layout\\_navigate\(\)](#), [vrna\\_plot\\_layout\\_turtle\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_layout\(\)](#)

**Parameters**

|               |                                   |
|---------------|-----------------------------------|
| <i>layout</i> | The layout data structure to free |
|---------------|-----------------------------------|

**16.76.5.7 vrna\_plot\_coords()**

```
int vrna_plot_coords (
    const char * structure,
    float ** x,
    float ** y,
    int plot_type )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Compute nucleotide coordinates for secondary structure plot.

This function takes a secondary structure and computes X-Y coordinates for each nucleotide that then can be used to create a structure plot. The parameter `plot_type` is used to select the underlying layout algorithm. Currently, the following selections are provided:

- [VRNA\\_PLOT\\_TYPE\\_SIMPLE](#)
- [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#)
- [VRNA\\_PLOT\\_TYPE\\_CIRCULAR](#)
- [VRNA\\_PLOT\\_TYPE\\_TURTLE](#)
- [VRNA\\_PLOT\\_TYPE\\_PUZZLER](#)

Passing an unsupported selection leads to the default algorithm [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#)

Here is a simple example how to use this function, assuming variable `structure` contains a valid dot-bracket string:

```
float *x, *y;
if (vrna_plot_coords(structure, &x, &y)) {
    printf("all fine");
} else {
    printf("some failure occurred!");
}
free(x);
free(y);
```

#### Note

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addresses `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

#### See also

[vrna\\_plot\\_coords\\_pt\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_plot\\_coords\\_naview\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#)

#### Parameters

|                |                  |                                                                                              |
|----------------|------------------|----------------------------------------------------------------------------------------------|
|                | <i>structure</i> | The secondary structure in dot-bracket notation                                              |
| <i>in, out</i> | <i>x</i>         | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| <i>in, out</i> | <i>y</i>         | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |
|                | <i>plot_type</i> | The layout algorithm to be used                                                              |

#### Returns

The length of the structure on success, 0 otherwise

#### 16.76.5.8 vrna\_plot\_coords\_pt()

```
int vrna_plot_coords_pt (
    const short * pt,
    float ** x,
    float ** y,
    int plot_type )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Compute nucleotide coordinates for secondary structure plot.

Same as [vrna\\_plot\\_coords\(\)](#) but takes a pair table with the structure information as input.

**Note**

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addressess `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\(\)](#), [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#), [vrna\\_plot\\_coords\\_navview\\_pt\(\)](#) [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#), [vrna\\_plot\\_coords\\_turtle\\_pt\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#)

**Parameters**

|         |                  |                                                                                              |
|---------|------------------|----------------------------------------------------------------------------------------------|
|         | <i>pt</i>        | The pair table that holds the secondary structure                                            |
| in, out | <i>x</i>         | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| in, out | <i>y</i>         | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |
|         | <i>plot_type</i> | The layout algorithm to be used                                                              |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.9 vrna\_plot\_coords\_simple()**

```
int vrna_plot_coords_simple (
    const char * structure,
    float ** x,
    float ** y )
```

#include <ViennaRNA/plotting/layouts.h>

Compute nucleotide coordinates for secondary structure plot the *Simple way*

This function basically is a wrapper to [vrna\\_plot\\_coords\(\)](#) that passes the `plot_type` `VRNA_PLOT_TYPE_SIMPLE`.

Here is a simple example how to use this function, assuming variable `structure` contains a valid dot-bracket string:

```
float *x, *y;
if (vrna_plot_coords_simple(structure, &x, &y)) {
    printf("all fine");
} else {
    printf("some failure occurred!");
}
free(x);
free(y);
```

**Note**

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addressess `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\(\)](#), [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_plot\\_coords\\_navview\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#)

**Parameters**

|         |                  |                                                                                              |
|---------|------------------|----------------------------------------------------------------------------------------------|
|         | <i>structure</i> | The secondary structure in dot-bracket notation                                              |
| in, out | <i>x</i>         | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| in, out | <i>y</i>         | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.10 vrna\_plot\_coords\_simple\_pt()**

```
int vrna_plot_coords_simple_pt (
    const short * pt,
    float ** x,
    float ** y )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Compute nucleotide coordinates for secondary structure plot the *Simple way*

Same as [vrna\\_plot\\_coords\\_simple\(\)](#) but takes a pair table with the structure information as input.

**Note**

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addressess `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\\_pt\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#), [vrna\\_plot\\_coords\\_naview\\_pt\(\)](#), [vrna\\_plot\\_coords\\_turtle\\_pt\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#)

**Parameters**

|                |           |                                                                                              |
|----------------|-----------|----------------------------------------------------------------------------------------------|
|                | <i>pt</i> | The pair table that holds the secondary structure                                            |
| <i>in, out</i> | <i>x</i>  | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| <i>in, out</i> | <i>y</i>  | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.11 vrna\_plot\_coords\_circular()**

```
int vrna_plot_coords_circular (
    const char * structure,
    float ** x,
    float ** y )
```

```
#include <ViennaRNA/plotting/layouts.h>
```

Compute coordinates of nucleotides mapped in equal distances onto a unit circle.

This function basically is a wrapper to [vrna\\_plot\\_coords\(\)](#) that passes the `plot_type` [VRNA\\_PLOT\\_TYPE\\_CIRCULAR](#).

In order to draw nice arcs using quadratic bezier curves that connect base pairs one may calculate a second tangential point  $P^t$  in addition to the actual  $R^2$  coordinates. the simplest way to do so may be to compute a radius scaling factor  $rs$  in the interval  $[0, 1]$  that weights the proportion of base pair span to the actual length of the sequence. This scaling factor can then be used to calculate the coordinates for  $P^t$ , i.e.

$$P_x^t[i] = X[i] * rs$$

and

$$P_y^t[i] = Y[i] * rs$$

.

**Note**

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addresses `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\(\)](#), [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_plot\\_coords\\_naview\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#)

**Parameters**

|                |                  |                                                                                              |
|----------------|------------------|----------------------------------------------------------------------------------------------|
|                | <i>structure</i> | The secondary structure in dot-bracket notation                                              |
| <i>in, out</i> | <i>x</i>         | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| <i>in, out</i> | <i>y</i>         | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.12 vrna\_plot\_coords\_circular\_pt()**

```
int vrna_plot_coords_circular_pt (
    const short * pt,
    float ** x,
    float ** y )
#include <ViennaRNA/plotting/layouts.h>
```

Compute nucleotide coordinates for a *Circular Plot*

Same as [vrna\\_plot\\_coords\\_circular\(\)](#) but takes a pair table with the structure information as input.

**Note**

On success, this function allocates memory for X and Y coordinates and assigns the pointers at addresses `x` and `y` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\\_pt\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#), [vrna\\_plot\\_coords\\_naview\\_pt\(\)](#), [vrna\\_plot\\_coords\\_turtle\\_pt\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#)

**Parameters**

|                |           |                                                                                              |
|----------------|-----------|----------------------------------------------------------------------------------------------|
|                | <i>pt</i> | The pair table that holds the secondary structure                                            |
| <i>in, out</i> | <i>x</i>  | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure) |
| <i>in, out</i> | <i>y</i>  | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.13 vrna\_plot\_coords\_puzzler()**

```
int vrna_plot_coords_puzzler (
```

```

    const char * structure,
    float ** x,
    float ** y,
    double ** arc_coords,
    vrna_plot_options_puzzler_t * options )
#include <ViennaRNA/plotting/RNApuzzler/RNApuzzler.h>
Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].
This function basically is a wrapper to vrna\_plot\_coords\(\) that passes the plot_type VRNA_PLOT_TYPE_PUZZLER.
Here is a simple example how to use this function, assuming variable structure contains a valid dot-bracket
string and using the default options (options = NULL):
float *x, *y;
double *arcs;
if (vrna_plot_coords_puzzler(structure, &x, &y, &arcs, NULL)) {
    printf("all fine");
} else {
    printf("some failure occurred!");
}
free(x);
free(y);
free(arcs);

```

#### Note

On success, this function allocates memory for X, Y and arc coordinates and assigns the pointers at addresses `x`, `y` and `arc_coords` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

#### See also

[vrna\\_plot\\_coords\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_navigate\(\)](#), [vrna\\_plot\\_options\\_puzzler\(\)](#)

#### Parameters

|         |                   |                                                                                                            |
|---------|-------------------|------------------------------------------------------------------------------------------------------------|
|         | <i>structure</i>  | The secondary structure in dot-bracket notation                                                            |
| in, out | <i>x</i>          | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure)               |
| in, out | <i>y</i>          | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure)               |
| in, out | <i>arc_coords</i> | The address of a pointer that will hold arc coordinates (pointer will point to memory, or NULL on failure) |
|         | <i>options</i>    | The options for the RNApuzzler algorithm (or NULL)                                                         |

#### Returns

The length of the structure on success, 0 otherwise

#### 16.76.5.14 vrna\_plot\_coords\_puzzler\_pt()

```

int vrna_plot_coords_puzzler_pt (
    short const *const pair_table,
    float ** x,
    float ** y,
    double ** arc_coords,
    vrna_plot_options_puzzler_t * puzzler )
#include <ViennaRNA/plotting/RNApuzzler/RNApuzzler.h>
Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].
Same as vrna\_plot\_coords\_puzzler\(\) but takes a pair table with the structure information as input.

```

**Note**

On success, this function allocates memory for X, Y and arc coordinates and assigns the pointers at addresses `x`, `y` and `arc_coords` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\\_pt\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#), [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#), [vrna\\_plot\\_coords\\_turtle\\_pt\(\)](#), [vrna\\_plot\\_coords\\_navview\\_pt\(\)](#)

**Parameters**

|                      |                   |                                                                                                            |
|----------------------|-------------------|------------------------------------------------------------------------------------------------------------|
|                      | <i>pt</i>         | The pair table that holds the secondary structure                                                          |
| <code>in, out</code> | <i>x</i>          | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure)               |
| <code>in, out</code> | <i>y</i>          | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure)               |
| <code>in, out</code> | <i>arc_coords</i> | The address of a pointer that will hold arc coordinates (pointer will point to memory, or NULL on failure) |
|                      | <i>options</i>    | The options for the RNApuzzler algorithm (or NULL)                                                         |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.15 vrna\_plot\_options\_puzzler()**

```
vrna_plot_options_puzzler_t * vrna_plot_options_puzzler (
    void )
#include <ViennaRNA/plotting/RNApuzzler/RNApuzzler.h>
```

Create an RNApuzzler options data structure.

**See also**

[vrna\\_plot\\_options\\_puzzler\\_free\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#)

**Returns**

An RNApuzzler options data structure with default settings

**16.76.5.16 vrna\_plot\_options\_puzzler\_free()**

```
void vrna_plot_options_puzzler_free (
    vrna_plot_options_puzzler_t * options )
#include <ViennaRNA/plotting/RNApuzzler/RNApuzzler.h>
```

Free memory occupied by an RNApuzzler options data structure.

**See also**

[vrna\\_plot\\_options\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#), [vrna\\_plot\\_layout\\_puzzler\(\)](#)

**Parameters**

|                |                                                 |
|----------------|-------------------------------------------------|
| <i>options</i> | A pointer to the options data structure to free |
|----------------|-------------------------------------------------|



**16.76.5.17 vrna\_plot\_coords\_turtle()**

```
int vrna_plot_coords_turtle (
    const char * structure,
    float ** x,
    float ** y,
    double ** arc_coords )
#include <ViennaRNA/plotting/RNApuzzler/RNAturtle.h>
```

Compute nucleotide coordinates for secondary structure plot using the *RNAturtle* algorithm [24].

This function basically is a wrapper to [vrna\\_plot\\_coords\(\)](#) that passes the `plot_type` [VRNA\\_PLOT\\_TYPE\\_TURTLE](#). Here is a simple example how to use this function, assuming variable `structure` contains a valid dot-bracket string:

```
float *x, *y;
double *arcs;
if (vrna_plot_coords_turtle(structure, &x, &y, &arcs)) {
    printf("all fine");
} else {
    printf("some failure occurred!");
}
free(x);
free(y);
free(arcs);
```

**Note**

On success, this function allocates memory for X, Y and arc coordinates and assigns the pointers at addresses `x`, `y` and `arc_coords` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\(\)](#), [vrna\\_plot\\_coords\\_turtle\\_pt\(\)](#), [vrna\\_plot\\_coords\\_circular\(\)](#), [vrna\\_plot\\_coords\\_simple\(\)](#), [vrna\\_plot\\_coords\\_navigate\(\)](#), [vrna\\_plot\\_coords\\_puzzler\(\)](#)

**Parameters**

|         |                   |                                                                                                            |
|---------|-------------------|------------------------------------------------------------------------------------------------------------|
|         | <i>structure</i>  | The secondary structure in dot-bracket notation                                                            |
| in, out | <i>x</i>          | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure)               |
| in, out | <i>y</i>          | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure)               |
| in, out | <i>arc_coords</i> | The address of a pointer that will hold arc coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

**16.76.5.18 vrna\_plot\_coords\_turtle\_pt()**

```
int vrna_plot_coords_turtle_pt (
    short const *const pair_table,
    float ** x,
    float ** y,
    double ** arc_coords )
#include <ViennaRNA/plotting/RNApuzzler/RNAturtle.h>
```

Compute nucleotide coordinates for secondary structure plot using the *RNAturtle* algorithm [24].

Same as [vrna\\_plot\\_coords\\_turtle\(\)](#) but takes a pair table with the structure information as input.

**Note**

On success, this function allocates memory for X, Y and arc coordinates and assigns the pointers at addresses `x`, `y` and `arc_coords` to the corresponding memory locations. It's the users responsibility to cleanup this memory after usage!

**See also**

[vrna\\_plot\\_coords\\_pt\(\)](#), [vrna\\_plot\\_coords\\_turtle\(\)](#), [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#), [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#), [vrna\\_plot\\_coords\\_puzzler\\_pt\(\)](#), [vrna\\_plot\\_coords\\_navigate\\_pt\(\)](#)

**Parameters**

|                      |                   |                                                                                                            |
|----------------------|-------------------|------------------------------------------------------------------------------------------------------------|
|                      | <i>pt</i>         | The pair table that holds the secondary structure                                                          |
| <code>in, out</code> | <i>x</i>          | The address of a pointer of X coordinates (pointer will point to memory, or NULL on failure)               |
| <code>in, out</code> | <i>y</i>          | The address of a pointer of Y coordinates (pointer will point to memory, or NULL on failure)               |
| <code>in, out</code> | <i>arc_coords</i> | The address of a pointer that will hold arc coordinates (pointer will point to memory, or NULL on failure) |

**Returns**

The length of the structure on success, 0 otherwise

## 16.77 Annotation

Functions to generate annotations for Secondary Structure Plots, Dot-Plots, and Others.

### 16.77.1 Detailed Description

Functions to generate annotations for Secondary Structure Plots, Dot-Plots, and Others.

Collaboration diagram for Annotation:

**Functions**

- `char ** vrna_annotate_covar_db` (const char \*\*alignment, const char \*structure, [vrna\\_md\\_t](#) \*md\_p)  
*Produce covariance annotation for an alignment given a secondary structure.*
- `vrna_cpair_t * vrna_annotate_covar_pairs` (const char \*\*alignment, [vrna\\_ep\\_t](#) \*pl, [vrna\\_ep\\_t](#) \*mfel, double threshold, [vrna\\_md\\_t](#) \*md)  
*Produce covariance annotation for an alignment given a set of base pairs.*

## 16.78 Alignment Plots

Functions to generate Alignment plots with annotated consensus structure.

### 16.78.1 Detailed Description

Functions to generate Alignment plots with annotated consensus structure.

Collaboration diagram for Alignment Plots:

**Functions**

- `int vrna_file_PS_aln` (const char \*filename, const char \*\*seqs, const char \*\*names, const char \*structure, unsigned int columns)

Create an annotated PostScript alignment plot.

- int [vrna\\_file\\_PS\\_aln\\_slice](#) (const char \*filename, const char \*\*seqs, const char \*\*names, const char \*structure, unsigned int start, unsigned int end, int offset, unsigned int columns)

Create an annotated PostScript alignment plot.

## 16.78.2 Function Documentation

### 16.78.2.1 vrna\_file\_PS\_aln()

```
int vrna_file_PS_aln (
    const char * filename,
    const char ** seqs,
    const char ** names,
    const char * structure,
    unsigned int columns )
#include <ViennaRNA/plotting/alignments.h>
```

Create an annotated PostScript alignment plot.

See also

[vrna\\_file\\_PS\\_aln\\_slice\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>filename</i>  | The output file name                                                                                      |
| <i>seqs</i>      | The aligned sequences                                                                                     |
| <i>names</i>     | The names of the sequences                                                                                |
| <i>structure</i> | The consensus structure in dot-bracket notation                                                           |
| <i>columns</i>   | The number of columns before the alignment is wrapped as a new block (a value of 0 indicates no wrapping) |

**SWIG Wrapper Notes** This function is available as overloaded function `file_PS_aln()` with three additional parameters `start`, `end`, and `offset` before the `columns` argument. Thus, it resembles the [vrna\\_file\\_PS\\_aln\\_slice\(\)](#) function. The last four arguments may be omitted, indicating the default of `start = 0`, `end = 0`, `offset = 0`, and `columns = 60`.

### 16.78.2.2 vrna\_file\_PS\_aln\_slice()

```
int vrna_file_PS_aln_slice (
    const char * filename,
    const char ** seqs,
    const char ** names,
    const char * structure,
    unsigned int start,
    unsigned int end,
    int offset,
    unsigned int columns )
#include <ViennaRNA/plotting/alignments.h>
```

Create an annotated PostScript alignment plot.

Similar to [vrna\\_file\\_PS\\_aln\(\)](#) but allows the user to print a particular slice of the alignment by specifying a `start` and `end` position. The additional `offset` parameter allows for adjusting the alignment position ruler value.

See also

[vrna\\_file\\_PS\\_aln\\_slice\(\)](#)

#### Parameters

|                  |                                                                                                                           |
|------------------|---------------------------------------------------------------------------------------------------------------------------|
| <i>filename</i>  | The output file name                                                                                                      |
| <i>seqs</i>      | The aligned sequences                                                                                                     |
| <i>names</i>     | The names of the sequences                                                                                                |
| <i>structure</i> | The consensus structure in dot-bracket notation                                                                           |
| <i>start</i>     | The start of the alignment slice (a value of 0 indicates the first position of the alignment, i.e. no slicing at 5' side) |
| <i>end</i>       | The end of the alignment slice (a value of 0 indicates the last position of the alignment, i.e. no slicing at 3' side)    |
| <i>offset</i>    | The alignment coordinate offset for the position ruler.                                                                   |
| <i>columns</i>   | The number of columns before the alignment is wrapped as a new block (a value of 0 indicates no wrapping)                 |

**SWIG Wrapper Notes** This function is available as overloaded function `file_PS_aln()` where the last four parameter may be omitted, indicating `start = 0`, `end = 0`, `offset = 0`, and `columns = 60`.

## 16.79 Search Algorithms

Implementations of various search algorithms to detect strings of objects within other strings of objects.

### 16.79.1 Detailed Description

Implementations of various search algorithms to detect strings of objects within other strings of objects.

Collaboration diagram for Search Algorithms:

#### Files

- file [BoyerMoore.h](#)

*Variants of the Boyer-Moore string search algorithm.*

#### Functions

- `const unsigned int * vrna_search_BMH_num` (`const unsigned int *needle`, `size_t needle_size`, `const unsigned int *haystack`, `size_t haystack_size`, `size_t start`, `size_t *badchars`, `unsigned char cyclic`)  
*Search for a string of elements in a larger string of elements using the Boyer-Moore-Horspool algorithm.*
- `const char * vrna_search_BMH` (`const char *needle`, `size_t needle_size`, `const char *haystack`, `size_t haystack_size`, `size_t start`, `size_t *badchars`, `unsigned char cyclic`)  
*Search for an ASCII pattern within a larger ASCII string using the Boyer-Moore-Horspool algorithm.*
- `size_t * vrna_search_BM_BCT_num` (`const unsigned int *pattern`, `size_t pattern_size`, `unsigned int num_max`)  
*Retrieve a Boyer-Moore Bad Character Table for a pattern of elements represented by natural numbers.*
- `size_t * vrna_search_BM_BCT` (`const char *pattern`)  
*Retrieve a Boyer-Moore Bad Character Table for a NULL-terminated pattern of ASCII characters.*

### 16.79.2 Function Documentation

**16.79.2.1 vrna\_search\_BMH\_num()**

```
const unsigned int * vrna_search_BMH_num (
    const unsigned int * needle,
    size_t needle_size,
    const unsigned int * haystack,
    size_t haystack_size,
    size_t start,
    size_t * badchars,
    unsigned char cyclic )
#include <ViennaRNA/search/BoyerMoore.h>
```

Search for a string of elements in a larger string of elements using the Boyer-Moore-Horspool algorithm. To speed-up subsequent searches with this function, the Bad Character Table should be precomputed and passed as argument `badchars`.

See also

[vrna\\_search\\_BM\\_BCT\\_num\(\)](#), [vrna\\_search\\_BMH\(\)](#)

**Parameters**

|                      |                                                                                                                                                            |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>needle</i>        | The pattern of object representations to search for                                                                                                        |
| <i>needle_size</i>   | The size (length) of the pattern provided in <code>needle</code>                                                                                           |
| <i>haystack</i>      | The string of objects the search will be performed on                                                                                                      |
| <i>haystack_size</i> | The size (length) of the <code>haystack</code> string                                                                                                      |
| <i>start</i>         | The position within <code>haystack</code> where to start the search                                                                                        |
| <i>badchars</i>      | A pre-computed Bad Character Table obtained from <a href="#">vrna_search_BM_BCT_num()</a> (If NULL, a Bad Character Table will be generated automatically) |
| <i>cyclic</i>        | Allow for cyclic matches if non-zero, stop search at end of haystack otherwise                                                                             |

**Returns**

A pointer to the first occurrence of `needle` within `haystack` after position `start`

**16.79.2.2 vrna\_search\_BMH()**

```
const char * vrna_search_BMH (
    const char * needle,
    size_t needle_size,
    const char * haystack,
    size_t haystack_size,
    size_t start,
    size_t * badchars,
    unsigned char cyclic )
#include <ViennaRNA/search/BoyerMoore.h>
```

Search for an ASCII pattern within a larger ASCII string using the Boyer-Moore-Horspool algorithm. To speed-up subsequent searches with this function, the Bad Character Table should be precomputed and passed as argument `badchars`. Furthermore, both, the lengths of `needle` and the length of `haystack` should be pre-computed and must be passed along with each call.

See also

[vrna\\_search\\_BM\\_BCT\(\)](#), [vrna\\_search\\_BMH\\_num\(\)](#)

## Parameters

|                      |                                                                                                                                                        |
|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>needle</i>        | The NULL-terminated ASCII pattern to search for                                                                                                        |
| <i>needle_size</i>   | The size (length) of the pattern provided in <i>needle</i>                                                                                             |
| <i>haystack</i>      | The NULL-terminated ASCII string of the search will be performed on                                                                                    |
| <i>haystack_size</i> | The size (length) of the <i>haystack</i> string                                                                                                        |
| <i>start</i>         | The position within <i>haystack</i> where to start the search                                                                                          |
| <i>badchars</i>      | A pre-computed Bad Character Table obtained from <a href="#">vrna_search_BM_BCT()</a> (If NULL, a Bad Character Table will be generated automatically) |
| <i>cyclic</i>        | Allow for cyclic matches if non-zero, stop search at end of haystack otherwise                                                                         |

## Returns

A pointer to the first occurrence of *needle* within *haystack* after position *start*

**16.79.2.3 vrna\_search\_BM\_BCT\_num()**

```
size_t * vrna_search_BM_BCT_num (
    const unsigned int * pattern,
    size_t pattern_size,
    unsigned int num_max )
#include <ViennaRNA/search/BoyerMoore.h>
```

Retrieve a Boyer-Moore Bad Character Table for a pattern of elements represented by natural numbers.

## Note

We store the maximum number representation of an element *num\_max* at position 0. So the actual bad character table *T* starts at *T*[1] for an element represented by number 0.

## See also

[vrna\\_search\\_BMH\\_num\(\)](#), [vrna\\_search\\_BM\\_BCT\(\)](#)

## Parameters

|                     |                                                                                |
|---------------------|--------------------------------------------------------------------------------|
| <i>pattern</i>      | The pattern of element representations used in the subsequent search           |
| <i>pattern_size</i> | The size (length) of the pattern provided in <i>pattern</i>                    |
| <i>num_max</i>      | The maximum number representation of an element, i.e. the size of the alphabet |

## Returns

A Bad Character Table for use in our Boyer-Moore search algorithm implementation(s)

**16.79.2.4 vrna\_search\_BM\_BCT()**

```
size_t * vrna_search_BM_BCT (
    const char * pattern )
#include <ViennaRNA/search/BoyerMoore.h>
```

Retrieve a Boyer-Moore Bad Character Table for a NULL-terminated pattern of ASCII characters.

## Note

We store the maximum number representation of an element, i.e. 127 at position 0. So the actual bad character table *T* starts at *T*[1] for an element represented by ASCII code 0.

See also

[vrna\\_search\\_BMH\(\)](#), [vrna\\_search\\_BM\\_BCT\\_num\(\)](#)

Parameters

|                |                                                                               |
|----------------|-------------------------------------------------------------------------------|
| <i>pattern</i> | The NULL-terminated pattern of ASCII characters used in the subsequent search |
|----------------|-------------------------------------------------------------------------------|

Returns

A Bad Character Table for use in our Boyer-Moore search algorithm implementation(s)

## 16.80 Combinatorics Algorithms

Implementations to solve various combinatorial aspects for strings of objects.

### 16.80.1 Detailed Description

Implementations to solve various combinatorial aspects for strings of objects.

Collaboration diagram for Combinatorics Algorithms:

### Files

- file [combinatorics.h](#)

*Various implementations that deal with combinatorial aspects of objects.*

### Functions

- unsigned int \*\* [vrna\\_enumerate\\_necklaces](#) (const unsigned int \*type\_counts)  
*Enumerate all necklaces with fixed content.*
- unsigned int [vrna\\_rotational\\_symmetry\\_num](#) (const unsigned int \*string, size\_t string\_length)  
*Determine the order of rotational symmetry for a string of objects represented by natural numbers.*
- unsigned int [vrna\\_rotational\\_symmetry\\_pos\\_num](#) (const unsigned int \*string, size\_t string\_length, unsigned int \*\*positions)  
*Determine the order of rotational symmetry for a string of objects represented by natural numbers.*
- unsigned int [vrna\\_rotational\\_symmetry](#) (const char \*string)  
*Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.*
- unsigned int [vrna\\_rotational\\_symmetry\\_pos](#) (const char \*string, unsigned int \*\*positions)  
*Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.*
- unsigned int [vrna\\_rotational\\_symmetry\\_db](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Determine the order of rotational symmetry for a dot-bracket structure.*
- unsigned int [vrna\\_rotational\\_symmetry\\_db\\_pos](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, unsigned int \*\*positions)  
*Determine the order of rotational symmetry for a dot-bracket structure.*
- unsigned int \*\* [vrna\\_n\\_multichoose\\_k](#) (size\_t n, size\_t k)  
*Obtain a list of k-combinations with repetition (n multichoose k)*
- unsigned int \* [vrna\\_boustrophedon](#) (size\_t start, size\_t end)  
*Generate a sequence of Boustrophedon distributed numbers.*
- unsigned int [vrna\\_boustrophedon\\_pos](#) (size\_t start, size\_t end, size\_t pos)  
*Obtain the i-th element in a Boustrophedon distributed interval of natural numbers.*

### 16.80.2 Function Documentation

### 16.80.2.1 `vrna_enumerate_necklaces()`

```
unsigned int ** vrna_enumerate_necklaces (
    const unsigned int * type_counts )
#include <ViennaRNA/combinatorics.h>
```

Enumerate all necklaces with fixed content.

This function implements *A fast algorithm to generate necklaces with fixed content* as published by Joe Sawada in 2003 [20].

The function receives a list of counts (the elements on the necklace) for each type of object within a necklace. The list starts at index 0 and ends with an entry that has a count of 0. The algorithm then enumerates all non-cyclic permutations of the content, returned as a list of necklaces. This list, again, is zero-terminated, i.e. the last entry of the list is a NULL pointer.

#### Parameters

|                          |                                      |
|--------------------------|--------------------------------------|
| <code>type_counts</code> | A 0-terminated list of entity counts |
|--------------------------|--------------------------------------|

#### Returns

A list of all non-cyclic permutations of the entities

**SWIG Wrapper Notes** This function is available as global function `enumerate_necklaces()` which accepts lists input, and produces list of lists output.

### 16.80.2.2 `vrna_rotational_symmetry_num()`

```
unsigned int vrna_rotational_symmetry_num (
    const unsigned int * string,
    size_t string_length )
#include <ViennaRNA/combinatorics.h>
```

Determine the order of rotational symmetry for a string of objects represented by natural numbers.

The algorithm applies a fast search of the provided string within itself, assuming the end of the string wraps around to connect with its start. For example, a string of the form 011011 has rotational symmetry of order 2

This is a simplified version of `vrna_rotational_symmetry_pos_num()` that may be useful if one is only interested in the degree of rotational symmetry but not the actual set of rotational symmetric strings.

#### See also

`vrna_rotational_symmetry_pos_num()`, `vrna_rotational_symmetry()`

#### Parameters

|                            |                                                   |
|----------------------------|---------------------------------------------------|
| <code>string</code>        | The string of elements encoded as natural numbers |
| <code>string_length</code> | The length of the string                          |

#### Returns

The order of rotational symmetry

**SWIG Wrapper Notes** This function is available as global function `rotational_symmetry()`. See `vrna_rotational_symmetry_pos()` for details. Note, that in the target language the length of the list `string` is always known a-priori, so the parameter `string_length` must be omitted.

### 16.80.2.3 `vrna_rotational_symmetry_pos_num()`

```
unsigned int vrna_rotational_symmetry_pos_num (
```



```

    const unsigned int * string,
    size_t string_length,
    unsigned int ** positions )
#include <ViennaRNA/combinatorics.h>

```

Determine the order of rotational symmetry for a string of objects represented by natural numbers.

The algorithm applies a fast search of the provided string within itself, assuming the end of the string wraps around to connect with it's start. For example, a string of the form 011011 has rotational symmetry of order 2

If the argument `positions` is not NULL, the function stores an array of string start positions for rotational shifts that map the string back onto itself. This array has length of order of rotational symmetry, i.e. the number returned by this function. The first element `positions[0]` always contains a shift value of 0 representing the trivial rotation.

#### Note

Do not forget to release the memory occupied by `positions` after a successful execution of this function.

#### See also

[vrna\\_rotational\\_symmetry\\_num\(\)](#), [vrna\\_rotational\\_symmetry\(\)](#), [vrna\\_rotational\\_symmetry\\_pos\(\)](#)

#### Parameters

|                      |                                                                                                                       |
|----------------------|-----------------------------------------------------------------------------------------------------------------------|
| <i>string</i>        | The string of elements encoded as natural numbers                                                                     |
| <i>string_length</i> | The length of the string                                                                                              |
| <i>positions</i>     | A pointer to an (undefined) list of alternative string start positions that lead to an identity mapping (may be NULL) |

#### Returns

The order of rotational symmetry

**SWIG Wrapper Notes** This function is available as global function **rotational\_symmetry()**. See [vrna\\_rotational\\_symmetry\\_pos\(\)](#) for details. Note, that in the target language the length of the list `string` is always known a-priori, so the parameter `string_length` must be omitted.

#### 16.80.2.4 vrna\_rotational\_symmetry()

```

unsigned int vrna_rotational_symmetry (
    const char * string )
#include <ViennaRNA/combinatorics.h>

```

Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.

The algorithm applies a fast search of the provided string within itself, assuming the end of the string wraps around to connect with it's start. For example, a string of the form AABAAB has rotational symmetry of order 2

This is a simplified version of [vrna\\_rotational\\_symmetry\\_pos\(\)](#) that may be useful if one is only interested in the degree of rotational symmetry but not the actual set of rotational symmetric strings.

#### See also

[vrna\\_rotational\\_symmetry\\_pos\(\)](#), [vrna\\_rotational\\_symmetry\\_num\(\)](#)

#### Parameters

|               |                                        |
|---------------|----------------------------------------|
| <i>string</i> | A NULL-terminated string of characters |
|---------------|----------------------------------------|

**Returns**

The order of rotational symmetry

**SWIG Wrapper Notes** This function is available as global function **rotational\_symmetry()**. See [vrna\\_rotational\\_symmetry\\_pos\(\)](#) for details.

**16.80.2.5 vrna\_rotational\_symmetry\_pos()**

```
unsigned int vrna_rotational_symmetry_pos (
    const char * string,
    unsigned int ** positions )
#include <ViennaRNA/combinatorics.h>
```

Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.

The algorithm applies a fast search of the provided string within itself, assuming the end of the string wraps around to connect with its start. For example, a string of the form **AABAAB** has rotational symmetry of order 2

If the argument `positions` is not NULL, the function stores an array of string start positions for rotational shifts that map the string back onto itself. This array has length of order of rotational symmetry, i.e. the number returned by this function. The first element `positions[0]` always contains a shift value of 0 representing the trivial rotation.

**Note**

Do not forget to release the memory occupied by `positions` after a successful execution of this function.

**See also**

[vrna\\_rotational\\_symmetry\(\)](#), [vrna\\_rotational\\_symmetry\\_num\(\)](#), [vrna\\_rotational\\_symmetry\\_num\\_pos\(\)](#)

**Parameters**

|                  |                                                                                                                       |
|------------------|-----------------------------------------------------------------------------------------------------------------------|
| <i>string</i>    | A NULL-terminated string of characters                                                                                |
| <i>positions</i> | A pointer to an (undefined) list of alternative string start positions that lead to an identity mapping (may be NULL) |

**Returns**

The order of rotational symmetry

**SWIG Wrapper Notes** This function is available as overloaded global function **rotational\_symmetry()**. It merges the functionalities of [vrna\\_rotational\\_symmetry\(\)](#), [vrna\\_rotational\\_symmetry\\_pos\(\)](#), [vrna\\_rotational\\_symmetry\\_num\(\)](#), and [vrna\\_rotational\\_symmetry\\_pos\\_num\(\)](#). In contrast to our C-implementation, this function doesn't return the order of rotational symmetry as a single value, but returns a list of cyclic permutation shifts that result in a rotationally symmetric string. The length of the list then determines the order of rotational symmetry.

**16.80.2.6 vrna\_rotational\_symmetry\_db()**

```
unsigned int vrna_rotational_symmetry_db (
    vrna_fold_compound_t * fc,
    const char * structure )
#include <ViennaRNA/combinatorics.h>
```

Determine the order of rotational symmetry for a dot-bracket structure.

Given a (permutation of multiple) RNA strand(s) and a particular secondary structure in dot-bracket notation, compute the degree of rotational symmetry. In case there is only a single linear RNA strand, the structure always has degree 1, as there are no rotational symmetries due to the direction of the nucleic acid sequence and the fixed positions of 5' and 3' ends. However, for circular RNAs, rotational symmetries might arise if the sequence consists of a concatenation of  $k$  identical subsequences.

This is a simplified version of [vrna\\_rotational\\_symmetry\\_db\\_pos\(\)](#) that may be useful if one is only interested in the degree of rotational symmetry but not the actual set of rotational symmetric strings.

See also

[vrna\\_rotational\\_symmetry\\_db\\_pos\(\)](#), [vrna\\_rotational\\_symmetry\(\)](#), [vrna\\_rotational\\_symmetry\\_num\(\)](#)

#### Parameters

|                  |                                                                                                         |
|------------------|---------------------------------------------------------------------------------------------------------|
| <i>fc</i>        | A fold_compound data structure containing the nucleic acid sequence(s), their order, and model settings |
| <i>structure</i> | The dot-bracket structure the degree of rotational symmetry is checked for                              |

#### Returns

The degree of rotational symmetry of the `structure` (0 in case of any errors)

**SWIG Wrapper Notes** This function is attached as method **rotational\_symmetry\_db()** to objects of type `fold_compound` (i.e. [vrna\\_fold\\_compound\\_t](#)). See [vrna\\_rotational\\_symmetry\\_db\\_pos\(\)](#) for details.

#### 16.80.2.7 vrna\_rotational\_symmetry\_db\_pos()

```
unsigned int vrna_rotational_symmetry_db_pos (
    vrna_fold_compound_t * fc,
    const char * structure,
    unsigned int ** positions )
```

```
#include <ViennaRNA/combinatorics.h>
```

Determine the order of rotational symmetry for a dot-bracket structure.

Given a (permutation of multiple) RNA strand(s) and a particular secondary structure in dot-bracket notation, compute the degree of rotational symmetry. In case there is only a single linear RNA strand, the structure always has degree 1, as there are no rotational symmetries due to the direction of the nucleic acid sequence and the fixed positions of 5' and 3' ends. However, for circular RNAs, rotational symmetries might arise if the sequence consists of a concatenation of  $k$  identical subsequences.

If the argument `positions` is not NULL, the function stores an array of string start positions for rotational shifts that map the string back onto itself. This array has length of order of rotational symmetry, i.e. the number returned by this function. The first element `positions[0]` always contains a shift value of 0 representing the trivial rotation.

#### Note

Do not forget to release the memory occupied by `positions` after a successful execution of this function.

See also

[vrna\\_rotational\\_symmetry\\_db\(\)](#), [vrna\\_rotational\\_symmetry\\_pos\(\)](#), [vrna\\_rotational\\_symmetry\\_pos\\_num\(\)](#)

#### Parameters

|                  |                                                                                                                       |
|------------------|-----------------------------------------------------------------------------------------------------------------------|
| <i>fc</i>        | A fold_compound data structure containing the nucleic acid sequence(s), their order, and model settings               |
| <i>structure</i> | The dot-bracket structure the degree of rotational symmetry is checked for                                            |
| <i>positions</i> | A pointer to an (undefined) list of alternative string start positions that lead to an identity mapping (may be NULL) |

## Returns

The degree of rotational symmetry of the `structure` (0 in case of any errors)

**SWIG Wrapper Notes** This function is attached as method **rotational\_symmetry\_db()** to objects of type `fold_compound` (i.e. `vrna_fold_compound_t`). Thus, the first argument must be omitted. In contrast to our C-implementation, this function doesn't simply return the order of rotational symmetry of the secondary structure, but returns the list `position` of cyclic permutation shifts that result in a rotationally symmetric structure. The length of the list then determines the order of rotational symmetry.

### 16.80.2.8 vrna\_n\_multichoose\_k()

```
unsigned int ** vrna_n_multichoose_k (
    size_t n,
    size_t k )
```

```
#include <ViennaRNA/combinatorics.h>
```

Obtain a list of k-combinations with repetition (n multichoose k)

This function compiles a list of k-combinations, or k-multicombination, i.e. a list of multisubsets of size k from a set of integer values from 0 to n - 1. For that purpose, we enumerate n + k - 1 choose k and decrease each index position i by i to obtain n multichoose k.

## Parameters

|          |                                                                      |
|----------|----------------------------------------------------------------------|
| <i>n</i> | Maximum number to choose from (interval of integers from 0 to n - 1) |
| <i>k</i> | Number of elements to choose, i.e. size of each multisubset          |

## Returns

A list of lists of elements of combinations (last entry is terminated by **NULL**)

### 16.80.2.9 vrna\_boustrophedon()

```
unsigned int vrna_boustrophedon (
    size_t start,
    size_t end )
```

```
#include <ViennaRNA/combinatorics.h>
```

Generate a sequence of Boustrophedon distributed numbers.

This function generates a sequence of positive natural numbers within the interval  $[start, end]$  in a Boustrophedon fashion. That is, the numbers  $start, \dots, end$  in the resulting list are alternating between left and right ends of the interval while progressing to the inside, i.e. the list consists of a sequence of natural numbers of the form:

$$start, end, start + 1, end - 1, start + 2, end - 2, \dots$$

The resulting list is 1-based and contains the length of the sequence of numbers at it's 0-th position.

Upon failure, the function returns **NULL**

## See also

[vrna\\_boustrophedon\\_pos\(\)](#)

## Parameters

|              |                                                          |
|--------------|----------------------------------------------------------|
| <i>start</i> | The first number of the list (left side of the interval) |
| <i>end</i>   | The last number of the list (right side of the interval) |

**Returns**

A list of alternating numbers from the interval  $[start, end]$  (or **NULL** on error)

**SWIG Wrapper Notes** This function is available as overloaded global function **boustrophedon()**.

**16.80.2.10 vrna\_boustrophedon\_pos()**

```
unsigned int vrna_boustrophedon_pos (
    size_t start,
    size_t end,
    size_t pos )
#include <ViennaRNA/combinatorics.h>
```

Obtain the *i*-th element in a Boustrophedon distributed interval of natural numbers.

**See also**

[vrna\\_boustrophedon\(\)](#)

**Parameters**

|              |                                                                                 |
|--------------|---------------------------------------------------------------------------------|
| <i>start</i> | The first number of the list (left side of the interval)                        |
| <i>end</i>   | The last number of the list (right side of the interval)                        |
| <i>pos</i>   | The index of the number within the Boustrophedon distributed sequence (1-based) |

**Returns**

The *pos*-th element in the Boustrophedon distributed sequence of natural numbers of the interval

**SWIG Wrapper Notes** This function is available as overloaded global function **boustrophedon()**. Omitting the *pos* argument yields the entire sequence from *start* to *end*.

**16.81 (Abstract) Data Structures**

All datastructures and typedefs shared among the ViennaRNA Package can be found here.

**16.81.1 Detailed Description**

All datastructures and typedefs shared among the ViennaRNA Package can be found here.

Collaboration diagram for (Abstract) Data Structures:

**Modules**

- [The Fold Compound](#)  
*This module provides interfaces that deal with the most basic data structure used in structure predicting and energy evaluating function of the RNAlib.*
- [The Dynamic Programming Matrices](#)  
*This module provides interfaces that deal with creation and destruction of dynamic programming matrices used within the RNAlib.*
- [Hash Tables](#)  
*Various implementations of hash table functions.*
- [Heaps](#)  
*Interface for an abstract implementation of a heap data structure.*
- [Buffers](#)  
*Functions that provide dynamically buffered stream-like data structures.*

## Files

- file [dp\\_matrices.h](#)  
*Functions to deal with standard dynamic programming (DP) matrices.*
- file [basic.h](#)  
*Various data structures and pre-processor macros.*

## Data Structures

- struct [vrna\\_basepair\\_s](#)  
*Base pair data structure used in subopt.c. [More...](#)*
- struct [vrna\\_cpair\\_s](#)  
*this datastructure is used as input parameter in functions of PS\_dot.c [More...](#)*
- struct [vrna\\_color\\_s](#)
- struct [vrna\\_data\\_linear\\_s](#)
- struct [vrna\\_sect\\_s](#)  
*Stack of partial structures for backtracking. [More...](#)*
- struct [vrna\\_bp\\_stack\\_s](#)  
*Base pair stack element. [More...](#)*
- struct [pu\\_contrib](#)  
*contributions to p\_u [More...](#)*
- struct [interact](#)  
*interaction data structure for RNAup [More...](#)*
- struct [pu\\_out](#)  
*Collection of all free\_energy of beeing unpaired values for output. [More...](#)*
- struct [constrain](#)  
*constraints for cofolding [More...](#)*
- struct [duplexT](#)  
*Data structure for RNAduplex. [More...](#)*
- struct [node](#)  
*Data structure for RNAsnoop (fold energy list) [More...](#)*
- struct [snoopT](#)  
*Data structure for RNAsnoop. [More...](#)*
- struct [dupVar](#)  
*Data structure used in RNApkplex. [More...](#)*

## Typedefs

- typedef struct [vrna\\_basepair\\_s](#) [vrna\\_basepair\\_t](#)  
*Typename for the base pair representing data structure [vrna\\_basepair\\_s](#).*
- typedef struct [vrna\\_elem\\_prob\\_s](#) [vrna\\_plist\\_t](#)  
*Typename for the base pair list representing data structure [vrna\\_elem\\_prob\\_s](#).*
- typedef struct [vrna\\_bp\\_stack\\_s](#) [vrna\\_bp\\_stack\\_t](#)  
*Typename for the base pair stack representing data structure [vrna\\_bp\\_stack\\_s](#).*
- typedef struct [vrna\\_cpair\\_s](#) [vrna\\_cpair\\_t](#)  
*Typename for data structure [vrna\\_cpair\\_s](#).*
- typedef struct [vrna\\_sect\\_s](#) [vrna\\_sect\\_t](#)  
*Typename for stack of partial structures [vrna\\_sect\\_s](#).*
- typedef double [FLT\\_OR\\_DBL](#)  
*Typename for floating point number in partition function computations.*
- typedef struct [vrna\\_basepair\\_s](#) [PAIR](#)  
*Old typename of [vrna\\_basepair\\_s](#).*

- typedef struct [vrna\\_elem\\_prob\\_s](#) plist  
*Old typename of [vrna\\_elem\\_prob\\_s](#).*
- typedef struct [vrna\\_cpair\\_s](#) cpair  
*Old typename of [vrna\\_cpair\\_s](#).*
- typedef struct [vrna\\_sect\\_s](#) sect  
*Old typename of [vrna\\_sect\\_s](#).*
- typedef struct [vrna\\_bp\\_stack\\_s](#) bondT  
*Old typename of [vrna\\_bp\\_stack\\_s](#).*
- typedef struct [pu\\_contrib](#) **pu\_contrib**  
*contributions to  $p_u$*
- typedef struct [interact](#) **interact**  
*interaction data structure for RNAup*
- typedef struct [pu\\_out](#) **pu\_out**  
*Collection of all free\_energy of beeing unpaired values for output.*
- typedef struct [constrain](#) **constrain**  
*constraints for cofolding*
- typedef struct [node](#) **folden**  
*Data structure for RNAsnoop (fold energy list)*
- typedef struct [dupVar](#) **dupVar**  
*Data structure used in RNApkplex.*

## Functions

- void [vrna\\_C11\\_features](#) (void)  
*Dummy symbol to check whether the library was build using C11/C++11 features.*

## 16.81.2 Data Structure Documentation

### 16.81.2.1 struct vrna\_basepair\_s

Base pair data structure used in subopt.c.

### 16.81.2.2 struct vrna\_cpair\_s

this datastructure is used as input parameter in functions of PS\_dot.c

### 16.81.2.3 struct vrna\_color\_s

### 16.81.2.4 struct vrna\_data\_linear\_s

Collaboration diagram for vrna\_data\_linear\_s:

### 16.81.2.5 struct vrna\_sect\_s

Stack of partial structures for backtracking.

### 16.81.2.6 struct vrna\_bp\_stack\_s

Base pair stack element.

### 16.81.2.7 struct pu\_contrib

contributions to  $p_u$

**Data Fields**

- double \*\* **H**  
*hairpin loops*
- double \*\* **I**  
*interior loops*
- double \*\* **M**  
*multi loops*
- double \*\* **E**  
*exterior loop*
- int **length**  
*length of the input sequence*
- int **w**  
*longest unpaired region*

**16.81.2.8 struct interact**

interaction data structure for RNAup

**Data Fields**

- double \* **Pi**  
*probabilities of interaction*
- double \* **Gi**  
*free energies of interaction*
- double **Gikjl**  
*full free energy for interaction between  $[k,i]$   $k < i$  in longer seq and  $[j,l]$   $j < l$  in shorter seq*
- double **Gikjl\_wo**  
*Gikjl without contributions for prob\_unpaired.*
- int **i**  
 *$k < i$  in longer seq*
- int **k**  
 *$k < i$  in longer seq*
- int **j**  
 *$j < l$  in shorter seq*
- int **l**  
 *$j < l$  in shorter seq*
- int **length**  
*length of longer sequence*

**16.81.2.9 struct pu\_out**

Collection of all free\_energy of beeing unpaired values for output.

**Data Fields**

- int **len**  
*sequence length*
- int **u\_vals**  
*number of different -u values*
- int **contribs**  
*[-c "SHIME"]*



- `char ** header`  
*header line*
- `double ** u_values`  
*(the -u values \* [-c "SHIME"]) \* seq len*

#### 16.81.2.10 struct constrain

constraints for cofolding

#### 16.81.2.11 struct duplexT

Data structure for RNA duplex.

#### 16.81.2.12 struct node

Data structure for RNAsnoop (fold energy list)  
 Collaboration diagram for node:

#### 16.81.2.13 struct snoopT

Data structure for RNAsnoop.

#### 16.81.2.14 struct dupVar

Data structure used in RNApplex.

### 16.81.3 Typedef Documentation

#### 16.81.3.1 PAIR

```
typedef struct vrna_basepair_s PAIR
#include <ViennaRNA/datastructures/basic.h>
Old typename of vrna_basepair_s.
```

**Deprecated** Use `vrna_basepair_t` instead!

#### 16.81.3.2 plist

```
typedef struct vrna_elem_prob_s plist
#include <ViennaRNA/datastructures/basic.h>
Old typename of vrna_elem_prob_s.
```

**Deprecated** Use `vrna_ep_t` or `vrna_elem_prob_s` instead!

#### 16.81.3.3 cpair

```
typedef struct vrna_cpair_s cpair
#include <ViennaRNA/datastructures/basic.h>
Old typename of vrna_cpair_s.
```

**Deprecated** Use `vrna_cpair_t` instead!

#### 16.81.3.4 sect

```
typedef struct vrna_sect_s sect
#include <ViennaRNA/datastructures/basic.h>
Old typename of vrna_sect_s.
```

**Deprecated** Use `vrna_sect_t` instead!

#### 16.81.3.5 bondT

```
typedef struct vrna_bp_stack_s bondT
#include <ViennaRNA/datastructures/basic.h>
Old typename of vrna_bp_stack_s.
```

**Deprecated** Use `vrna_bp_stack_t` instead!

### 16.81.4 Function Documentation

#### 16.81.4.1 vrna\_C11\_features()

```
void vrna_C11_features (
    void )
#include <ViennaRNA/datastructures/basic.h>
```

Dummy symbol to check whether the library was build using C11/C++11 features.

By default, several data structures of our new v3.0 API use C11/C++11 features, such as unnamed unions, unnamed structs. However, these features can be deactivated at compile time to allow building the library and executables with compilers that do not support these features.

Now, the problem arises that once our static library is compiled and a third-party application is supposed to link against it, it needs to know, at compile time, how to correctly address particular data structures. This is usually implicitly taken care of through the API exposed in our header files. Unfortunately, we had some preprocessor directives in our header files that changed the API depending on the capabilities of the compiler the third-party application is build with. This in turn prohibited the use of an RNAlib compiled without C11/C++11 support in a program that compiles/links with enabled C11/C++11 support and vice-versa.

Therefore, we introduce this dummy symbol which can be used to check, whether the static library was build with C11/C++11 features.

#### Note

If the symbol is present, the library was build with enabled C11/C++11 features support and no action is required. However, if the symbol is missing in RNAlib  $\geq 2.2.9$ , programs that link to RNAlib must define a pre-processor identifier `VRNA_DISABLE_C11_FEATURES` before including any ViennaRNA Package header file, for instance by adding a `CPPFLAG`

```
CPPFLAGS+=-DVRNA_DISABLE_C11_FEATURES
```

#### Since

v2.2.9

## 16.82 Messages

Functions to print various kind of messages.

### 16.82.1 Detailed Description

Functions to print various kind of messages.

Collaboration diagram for Messages:

## Functions

- void [vrna\\_message\\_error](#) (const char \*format,...)  
*Print an error message and die.*
- void [vrna\\_message\\_verror](#) (const char \*format, va\_list args)  
*Print an error message and die.*
- void [vrna\\_message\\_warning](#) (const char \*format,...)  
*Print a warning message.*
- void [vrna\\_message\\_vwarning](#) (const char \*format, va\_list args)  
*Print a warning message.*
- void [vrna\\_message\\_info](#) (FILE \*fp, const char \*format,...)  
*Print an info message.*
- void [vrna\\_message\\_vinfo](#) (FILE \*fp, const char \*format, va\_list args)  
*Print an info message.*
- void [vrna\\_message\\_input\\_seq\\_simple](#) (void)  
*Print a line to stdout that asks for an input sequence.*
- void [vrna\\_message\\_input\\_seq](#) (const char \*s)  
*Print a line with a user defined string and a ruler to stdout.*

## 16.82.2 Function Documentation

### 16.82.2.1 [vrna\\_message\\_error\(\)](#)

```
void vrna_message_error (
    const char * format,
    ... )
#include <ViennaRNA/utils/basic.h>
```

Print an error message and die.

This function is a wrapper to `fprintf(stderr, ...)` that puts a capital **ERROR:** in front of the message and then exits the calling program.

See also

[vrna\\_message\\_verror\(\)](#), [vrna\\_message\\_warning\(\)](#), [vrna\\_message\\_info\(\)](#)

#### Parameters

|               |                                                     |
|---------------|-----------------------------------------------------|
| <i>format</i> | The error message to be printed                     |
| ...           | Optional arguments for the formatted message string |

### 16.82.2.2 [vrna\\_message\\_verror\(\)](#)

```
void vrna_message_verror (
    const char * format,
    va_list args )
#include <ViennaRNA/utils/basic.h>
```

Print an error message and die.

This function is a wrapper to `vfprintf(stderr, ...)` that puts a capital **ERROR:** in front of the message and then exits the calling program.

See also

[vrna\\_message\\_error\(\)](#), [vrna\\_message\\_warning\(\)](#), [vrna\\_message\\_info\(\)](#)

Parameters

|               |                                                    |
|---------------|----------------------------------------------------|
| <i>format</i> | The error message to be printed                    |
| <i>args</i>   | The argument list for the formatted message string |

### 16.82.2.3 vrna\_message\_warning()

```
void vrna_message_warning (
    const char * format,
    ... )
#include <ViennaRNA/utils/basic.h>
```

Print a warning message.

This function is a wrapper to *fprintf(stderr, ...)* that puts a capital **WARNING:** in front of the message.

See also

[vrna\\_message\\_vwarning\(\)](#), [vrna\\_message\\_error\(\)](#), [vrna\\_message\\_info\(\)](#)

Parameters

|               |                                                     |
|---------------|-----------------------------------------------------|
| <i>format</i> | The warning message to be printed                   |
| ...           | Optional arguments for the formatted message string |

### 16.82.2.4 vrna\_message\_vwarning()

```
void vrna_message_vwarning (
    const char * format,
    va_list args )
#include <ViennaRNA/utils/basic.h>
```

Print a warning message.

This function is a wrapper to *fprintf(stderr, ...)* that puts a capital **WARNING:** in front of the message.

See also

[vrna\\_message\\_vwarning\(\)](#), [vrna\\_message\\_error\(\)](#), [vrna\\_message\\_info\(\)](#)

Parameters

|               |                                                    |
|---------------|----------------------------------------------------|
| <i>format</i> | The warning message to be printed                  |
| <i>args</i>   | The argument list for the formatted message string |

### 16.82.2.5 vrna\_message\_info()

```
void vrna_message_info (
    FILE * fp,
    const char * format,
    ... )
```

```
#include <ViennaRNA/utils/basic.h>
```

Print an info message.  
This function is a wrapper to *fprintf(...)*.

See also

[vrna\\_message\\_vinfo\(\)](#), [vrna\\_message\\_error\(\)](#), [vrna\\_message\\_warning\(\)](#)

#### Parameters

|               |                                                     |
|---------------|-----------------------------------------------------|
| <i>fp</i>     | The file pointer where the message is printed to    |
| <i>format</i> | The warning message to be printed                   |
| ...           | Optional arguments for the formatted message string |

#### 16.82.2.6 vrna\_message\_vinfo()

```
void vrna_message_vinfo (
    FILE * fp,
    const char * format,
    va_list args )
```

```
#include <ViennaRNA/utils/basic.h>
```

Print an info message.  
This function is a wrapper to *fprintf(...)*.

See also

[vrna\\_message\\_vinfo\(\)](#), [vrna\\_message\\_error\(\)](#), [vrna\\_message\\_warning\(\)](#)

#### Parameters

|               |                                                    |
|---------------|----------------------------------------------------|
| <i>fp</i>     | The file pointer where the message is printed to   |
| <i>format</i> | The info message to be printed                     |
| <i>args</i>   | The argument list for the formatted message string |

#### 16.82.2.7 vrna\_message\_input\_seq\_simple()

```
void vrna_message_input_seq_simple (
    void )
```

```
#include <ViennaRNA/utils/basic.h>
```

Print a line to *stdout* that asks for an input sequence.  
There will also be a ruler (scale line) printed that helps orientation of the sequence positions

#### 16.82.2.8 vrna\_message\_input\_seq()

```
void vrna_message_input_seq (
    const char * s )
```

```
#include <ViennaRNA/utils/basic.h>
```

Print a line with a user defined string and a ruler to *stdout*.  
(usually this is used to ask for user input) There will also be a ruler (scale line) printed that helps orientation of the sequence positions

#### Parameters

|          |                                                             |
|----------|-------------------------------------------------------------|
| <i>s</i> | A user defined string that will be printed to <i>stdout</i> |
|----------|-------------------------------------------------------------|

## 16.83 Unit Conversion

Functions to convert between various physical units.

### 16.83.1 Detailed Description

Functions to convert between various physical units.

Collaboration diagram for Unit Conversion:

#### Files

- file [units.h](#)

*Physical Units and Functions to convert them into each other.*

#### Enumerations

- enum [vrna\\_unit\\_energy\\_e](#) {  
[VRNA\\_UNIT\\_J](#), [VRNA\\_UNIT\\_KJ](#), [VRNA\\_UNIT\\_CAL\\_IT](#), [VRNA\\_UNIT\\_DACAL\\_IT](#),  
[VRNA\\_UNIT\\_KCAL\\_IT](#), [VRNA\\_UNIT\\_CAL](#), [VRNA\\_UNIT\\_DACAL](#), [VRNA\\_UNIT\\_KCAL](#),  
[VRNA\\_UNIT\\_G\\_TNT](#), [VRNA\\_UNIT\\_KG\\_TNT](#), [VRNA\\_UNIT\\_T\\_TNT](#), [VRNA\\_UNIT\\_EV](#),  
[VRNA\\_UNIT\\_WH](#), [VRNA\\_UNIT\\_KWH](#) }  
*Energy / Work Units.*
- enum [vrna\\_unit\\_temperature\\_e](#) {  
[VRNA\\_UNIT\\_K](#), [VRNA\\_UNIT\\_DEG\\_C](#), [VRNA\\_UNIT\\_DEG\\_F](#), [VRNA\\_UNIT\\_DEG\\_R](#),  
[VRNA\\_UNIT\\_DEG\\_N](#), [VRNA\\_UNIT\\_DEG\\_DE](#), [VRNA\\_UNIT\\_DEG\\_RE](#), [VRNA\\_UNIT\\_DEG\\_RO](#) }  
*Temperature Units.*

#### Functions

- double [vrna\\_convert\\_energy](#) (double energy, [vrna\\_unit\\_energy\\_e](#) from, [vrna\\_unit\\_energy\\_e](#) to)  
*Convert between energy / work units.*
- double [vrna\\_convert\\_temperature](#) (double temp, [vrna\\_unit\\_temperature\\_e](#) from, [vrna\\_unit\\_temperature\\_e](#) to)  
*Convert between temperature units.*
- int [vrna\\_convert\\_kcal\\_to\\_dcal](#) (double energy)  
*Convert floating point energy value into integer representation.*
- double [vrna\\_convert\\_dcal\\_to\\_kcal](#) (int energy)  
*Convert an integer representation of free energy in deka-cal/mol to kcal/mol.*

### 16.83.2 Enumeration Type Documentation

#### 16.83.2.1 vrna\_unit\_energy\_e

```
enum vrna_unit_energy_e
#include <ViennaRNA/utils/units.h>
Energy / Work Units.
```

See also

[vrna\\_convert\\_energy\(\)](#)

#### Enumerator

|             |                                                                    |
|-------------|--------------------------------------------------------------------|
| VRNA_UNIT_J | Joule ( $1\text{ J} = 1\text{ kg} \cdot \text{m}^2\text{s}^{-2}$ ) |
|-------------|--------------------------------------------------------------------|

## Enumerator

|                    |                                                                                                                          |
|--------------------|--------------------------------------------------------------------------------------------------------------------------|
| VRNA_UNIT_KJ       | Kilojoule ( $1 \text{ kJ} = 1,000 \text{ J}$ )                                                                           |
| VRNA_UNIT_CAL_IT   | Calorie (International (Steam) Table, $1 \text{ cal}_{IT} = 4.1868 \text{ J}$ )                                          |
| VRNA_UNIT_DACAL_IT | Decacalorie (International (Steam) Table, $1 \text{ dcal}_{IT} = 10 \text{ cal}_{IT} = 41.868 \text{ J}$ )               |
| VRNA_UNIT_KCAL_IT  | Kilocalorie (International (Steam) Table, $1 \text{ kcal}_{IT} = 4.1868 \text{ kJ}$ )                                    |
| VRNA_UNIT_CAL      | Calorie (Thermochemical, $1 \text{ cal}_{th} = 4.184 \text{ J}$ )                                                        |
| VRNA_UNIT_DACAL    | Decacalorie (Thermochemical, $1 \text{ dcal}_{th} = 10 \text{ cal}_{th} = 41.84 \text{ J}$ )                             |
| VRNA_UNIT_KCAL     | Kilocalorie (Thermochemical, $1 \text{ kcal}_{th} = 4.184 \text{ kJ}$ )                                                  |
| VRNA_UNIT_G_TNT    | g TNT ( $1 \text{ g TNT} = 1,000 \text{ cal}_{th} = 4,184 \text{ J}$ )                                                   |
| VRNA_UNIT_KG_TNT   | kg TNT ( $1 \text{ kg TNT} = 1,000 \text{ kcal}_{th} = 4,184 \text{ kJ}$ )                                               |
| VRNA_UNIT_T_TNT    | ton TNT ( $1 \text{ t TNT} = 1,000,000 \text{ kcal}_{th} = 4,184 \text{ MJ}$ )                                           |
| VRNA_UNIT_EV       | Electronvolt ( $1 \text{ eV} = 1.602176565 \times 10^{-19} \text{ J}$ )                                                  |
| VRNA_UNIT_WH       | Watt hour ( $1 \text{ W} \cdot \text{h} = 1 \text{ W} \cdot 3,600 \text{ s} = 3,600 \text{ J} = 3.6 \text{ kJ}$ )        |
| VRNA_UNIT_KWH      | Kilowatt hour ( $1 \text{ kW} \cdot \text{h} = 1 \text{ kW} \cdot 3,600 \text{ s} = 3,600 \text{ kJ} = 3.6 \text{ MJ}$ ) |

## 16.83.2.2 vrna\_unit\_temperature\_e

```
enum vrna_unit_temperature_e
#include <ViennaRNA/utils/units.h>
Temperature Units.
```

See also

[vrna\\_convert\\_temperature\(\)](#)

## Enumerator

|                  |                                                                                                            |
|------------------|------------------------------------------------------------------------------------------------------------|
| VRNA_UNIT_K      | Kelvin (K)                                                                                                 |
| VRNA_UNIT_DEG_C  | Degree Celcius ( $^{\circ}\text{C}$ ) ( $[^{\circ}\text{C}] = [K] - 273.15$ )                              |
| VRNA_UNIT_DEG_F  | Degree Fahrenheit ( $^{\circ}\text{F}$ ) ( $[^{\circ}\text{F}] = [K] \times \frac{9}{5} - 459.67$ )        |
| VRNA_UNIT_DEG_R  | Degree Rankine ( $^{\circ}\text{R}$ ) ( $[^{\circ}\text{R}] = [K] \times \frac{9}{5}$ )                    |
| VRNA_UNIT_DEG_N  | Degree Newton ( $^{\circ}\text{N}$ ) ( $[^{\circ}\text{N}] = ([K] - 273.15) \times \frac{33}{100}$ )       |
| VRNA_UNIT_DEG_DE | Degree Delisle ( $^{\circ}\text{De}$ ) ( $[^{\circ}\text{De}] = (373.15 - [K]) \times \frac{3}{2}$ )       |
| VRNA_UNIT_DEG_RE | Degree Réaumur ( $^{\circ}\text{Ré}$ ) ( $[^{\circ}\text{Ré}] = ([K] - 273.15) \times \frac{4}{5}$ )       |
| VRNA_UNIT_DEG_RO | Degree Rømer ( $^{\circ}\text{Rø}$ ) ( $[^{\circ}\text{Rø}] = ([K] - 273.15) \times \frac{21}{40} + 7.5$ ) |

## 16.83.3 Function Documentation

## 16.83.3.1 vrna\_convert\_energy()

```
double vrna_convert_energy (
    double energy,
    vrna_unit_energy_e from,
    vrna_unit_energy_e to )
#include <ViennaRNA/utils/units.h>
```

Convert between energy / work units.

See also

[vrna\\_unit\\_energy\\_e](#)

#### Parameters

|               |                    |
|---------------|--------------------|
| <i>energy</i> | Input energy value |
| <i>from</i>   | Input unit         |
| <i>to</i>     | Output unit        |

#### Returns

Energy value in Output unit

### 16.83.3.2 vrna\_convert\_temperature()

```
double vrna_convert_temperature (
    double temp,
    vrna_unit_temperature_e from,
    vrna_unit_temperature_e to )
#include <ViennaRNA/utils/units.h>
```

Convert between temperature units.

See also

[vrna\\_unit\\_temperature\\_e](#)

#### Parameters

|             |                         |
|-------------|-------------------------|
| <i>temp</i> | Input temperature value |
| <i>from</i> | Input unit              |
| <i>to</i>   | Output unit             |

#### Returns

Temperature value in Output unit

### 16.83.3.3 vrna\_convert\_kcal\_to\_dcal()

```
int vrna_convert_kcal_to_dcal (
    double energy )
#include <ViennaRNA/utils/units.h>
```

Convert floating point energy value into integer representation.

This function converts a floating point value in kcal/mol into its corresponding deka-cal/mol integer representation as used throughout RNAlib.

See also

[vrna\\_convert\\_dcal\\_to\\_kcal\(\)](#)



## Parameters

|               |                              |
|---------------|------------------------------|
| <i>energy</i> | The energy value in kcal/mol |
|---------------|------------------------------|

## Returns

The energy value in deka-cal/mol

**16.83.3.4 vrna\_convert\_dcal\_to\_kcal()**

```
double vrna_convert_dcal_to_kcal (
    int energy )
```

```
#include <ViennaRNA/utils/units.h>
```

Convert an integer representation of free energy in deka-cal/mol to kcal/mol.

This function converts a free energy value given as integer in deka-cal/mol into the corresponding floating point number in kcal/mol

## See also

[vrna\\_convert\\_kcal\\_to\\_dcal\(\)](#)

## Parameters

|               |                            |
|---------------|----------------------------|
| <i>energy</i> | The energy in deka-cal/mol |
|---------------|----------------------------|

## Returns

The energy in kcal/mol

## 16.84 The Fold Compound

This module provides interfaces that deal with the most basic data structure used in structure predicting and energy evaluating function of the RNAlib.

### 16.84.1 Detailed Description

This module provides interfaces that deal with the most basic data structure used in structure predicting and energy evaluating function of the RNAlib.

Throughout the entire RNAlib, the [vrna\\_fold\\_compound\\_t](#), is used to group information and data that is required for structure prediction and energy evaluation. Here, you'll find interface functions to create, modify, and delete [vrna\\_fold\\_compound\\_t](#) data structures. Collaboration diagram for The Fold Compound:

### Files

- file [fold\\_compound.h](#)  
*The Basic Fold Compound API.*

### Data Structures

- struct [vrna\\_fc\\_s](#)  
*The most basic data structure required by many functions throughout the RNAlib. [More...](#)*

### Macros

- #define [VRNA\\_STATUS\\_MFE\\_PRE](#) (unsigned char)1

- Status message indicating that MFE computations are about to begin.*

  - #define `VRNA_STATUS_MFE_POST` (unsigned char)2
- Status message indicating that MFE computations are finished.*

  - #define `VRNA_STATUS_PF_PRE` (unsigned char)3
- Status message indicating that Partition function computations are about to begin.*

  - #define `VRNA_STATUS_PF_POST` (unsigned char)4
- Status message indicating that Partition function computations are finished.*

  - #define `VRNA_OPTION_DEFAULT` 0U
- Option flag to specify default settings/requirements.*

  - #define `VRNA_OPTION_MFE` 1U
- Option flag to specify requirement of Minimum Free Energy (MFE) DP matrices and corresponding set of energy parameters.*

  - #define `VRNA_OPTION_PF` 2U
- Option flag to specify requirement of Partition Function (PF) DP matrices and corresponding set of Boltzmann factors.*

  - #define `VRNA_OPTION_HYBRID` 4U
- Option flag to specify requirement of dimer DP matrices.*

  - #define `VRNA_OPTION_EVAL_ONLY` 8U
- Option flag to specify that neither MFE, nor PF DP matrices are required.*

  - #define `VRNA_OPTION_WINDOW` 16U
- Option flag to specify requirement of DP matrices for local folding approaches.*

## Typedefs

- typedef struct `vrna_fc_s` `vrna_fold_compound_t`

*Typename for the `fold_compound` data structure `vrna_fc_s`.*
- typedef void() `vrna_callback_free_auxdata`(void \*data)

*Callback to free memory allocated for auxiliary user-provided data.*
- typedef void() `vrna_callback_recursion_status`(unsigned char status, void \*data)

*Callback to perform specific user-defined actions before, or after recursive computations.*

## Enumerations

- enum `vrna_fc_type_e` { `VRNA_FC_TYPE_SINGLE` , `VRNA_FC_TYPE_COMPARATIVE` }

*An enumerator that is used to specify the type of a `vrna_fold_compound_t`.*

## Functions

- `vrna_fold_compound_t * vrna_fold_compound` (const char \*sequence, const `vrna_md_t` \*md\_p, unsigned int options)

*Retrieve a `vrna_fold_compound_t` data structure for single sequences and hybridizing sequences.*
- `vrna_fold_compound_t * vrna_fold_compound_comparative` (const char \*\*sequences, `vrna_md_t` \*md\_p, unsigned int options)

*Retrieve a `vrna_fold_compound_t` data structure for sequence alignments.*
- void `vrna_fold_compound_free` (`vrna_fold_compound_t` \*fc)

*Free memory occupied by a `vrna_fold_compound_t`.*
- void `vrna_fold_compound_add_auxdata` (`vrna_fold_compound_t` \*fc, void \*data, `vrna_callback_free_auxdata` \*f)

*Add auxiliary data to the `vrna_fold_compound_t`.*
- void `vrna_fold_compound_add_callback` (`vrna_fold_compound_t` \*fc, `vrna_callback_recursion_status` \*f)

*Add a recursion status callback to the `vrna_fold_compound_t`.*

## 16.84.2 Data Structure Documentation

### 16.84.2.1 struct vrna\_fc\_s

The most basic data structure required by many functions throughout the RNAlib.

#### Note

Please read the documentation of this data structure carefully! Some attributes are only available for specific types this data structure can adopt.

#### Warning

Reading/Writing from/to attributes that are not within the scope of the current type usually result in undefined behavior!

#### See also

[vrna\\_fold\\_compound\\_t.type](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [VRNA\\_FC\\_TYPE\\_SINGLE](#), [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#)

**SWIG Wrapper Notes** This data structure is wrapped as an object **fold\_compound** with several related functions attached as methods.

A new **fold\_compound** can be obtained by calling one of its constructors:

- *fold\_compound(seq)* – Initialize with a single sequence, or two concatenated sequences separated by an ampersand character '&' (for cofolding)
- *fold\_compound(aln)* – Initialize with a sequence alignment *aln* stored as a list of sequences (with gap characters)

The resulting object has a list of attached methods which in most cases directly correspond to functions that mainly operate on the corresponding C data structure:

- *type()* – Get the type of the *fold\_compound* (See [vrna\\_fc\\_type\\_e](#))
- *length()* – Get the length of the sequence(s) or alignment stored within the *fold\_compound*

Collaboration diagram for vrna\_fc\_s:

#### Data Fields

##### Common data fields

- const [vrna\\_fc\\_type\\_e](#) type  
*The type of the [vrna\\_fold\\_compound\\_t](#).*
- unsigned int **length**  
*The length of the sequence (or sequence alignment)*
- int **cutpoint**  
*The position of the (cofold) cutpoint within the provided sequence. If there is no cutpoint, this field will be set to -1.*
- unsigned int \* **strand\_number**  
*The strand number a particular nucleotide is associated with.*
- unsigned int \* **strand\_order**  
*The strand order, i.e. permutation of current concatenated sequence.*
- unsigned int \* **strand\_order\_uniq**  
*The strand order array where identical sequences have the same ID.*
- unsigned int \* **strand\_start**  
*The start position of a particular strand within the current concatenated sequence.*
- unsigned int \* **strand\_end**  
*The end (last) position of a particular strand within the current concatenated sequence.*

- unsigned int **strands**  
*Number of interacting strands.*
- [vrna\\_seq\\_t](#) \* **nucleotides**  
*Set of nucleotide sequences.*
- [vrna\\_msa\\_t](#) \* **alignment**  
*Set of alignments.*
- [vrna\\_hc\\_t](#) \* **hc**  
*The hard constraints data structure used for structure prediction.*
- [vrna\\_mx\\_mfe\\_t](#) \* **matrices**  
*The MFE DP matrices.*
- [vrna\\_mx\\_pf\\_t](#) \* **exp\_matrices**  
*The PF DP matrices*
- [vrna\\_param\\_t](#) \* **params**  
*The precomputed free energy contributions for each type of loop.*
- [vrna\\_exp\\_param\\_t](#) \* **exp\_params**  
*The precomputed free energy contributions as Boltzmann factors*
- int \* **iindx**  
*DP matrix accessor*
- int \* **jindx**  
*DP matrix accessor*

### User-defined data fields

- [vrna\\_callback\\_recursion\\_status](#) \* **stat\_cb**  
*Recursion status callback (usually called just before, and after recursive computations in the library.*
- void \* **auxdata**  
*A pointer to auxiliary, user-defined data.*
- [vrna\\_callback\\_free\\_auxdata](#) \* **free\_auxdata**  
*A callback to free auxiliary user data whenever the fold\_compound itself is free'd.*

### Secondary Structure Decomposition (grammar) related data fields

- [vrna\\_sd\\_t](#) \* **domains\_struc**  
*Additional structured domains.*
- [vrna\\_ud\\_t](#) \* **domains\_up**  
*Additional unstructured domains.*
- [vrna\\_gr\\_aux\\_t](#) \* **aux\_grammar**  
*Additional decomposition grammar rules.*

### Data fields available for single/hybrid structure prediction

### Data fields for consensus structure prediction

### Additional data fields for Distance Class Partitioning

*These data fields are typically populated with meaningful data only if used in the context of Distance Class Partitioning*

- unsigned int **maxD1**  
*Maximum allowed base pair distance to first reference.*
- unsigned int **maxD2**  
*Maximum allowed base pair distance to second reference.*
- short \* **reference\_pt1**  
*A pairtable of the first reference structure.*
- short \* **reference\_pt2**  
*A pairtable of the second reference structure.*
- unsigned int \* **referenceBPs1**

- *Matrix containing number of basepairs of reference structure1 in interval [i,j].*  
unsigned int \* **referenceBPs2**
- *Matrix containing number of basepairs of reference structure2 in interval [i,j].*  
unsigned int \* **bpdist**
- *Matrix containing base pair distance of reference structure 1 and 2 on interval [i,j].*  
unsigned int \* **mm1**
- *Maximum matching matrix, reference struct 1 disallowed.*  
unsigned int \* **mm2**
- *Maximum matching matrix, reference struct 2 disallowed.*

#### Additional data fields for local folding

These data fields are typically populated with meaningful data only if used in the context of local folding

- int **window\_size**  
*window size for local folding sliding window approach*
- char \*\* **ptype\_local**  
*Pair type array (for local folding)*
- vrna\_zsc\_dat\_t **zscore\_data**  
*Data structure with settings for z-score computations.*

#### 16.84.2.1.1 Field Documentation

**16.84.2.1.1.1 type** const [vrna\\_fc\\_type\\_e](#) vrna\_fc\_s::type

The type of the [vrna\\_fold\\_compound\\_t](#).

Currently possible values are [VRNA\\_FC\\_TYPE\\_SINGLE](#), and [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#)

##### Warning

Do not edit this attribute, it will be automagically set by the corresponding `get()` methods for the [vrna\\_fold\\_compound\\_t](#). The value specified in this attribute dictates the set of other attributes to use within this data structure.

**16.84.2.1.1.2 stat\_cb** [vrna\\_callback\\_recursion\\_status\\*](#) vrna\_fc\_s::stat\_cb

Recursion status callback (usually called just before, and after recursive computations in the library).

See also

[vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_fold\\_compound\\_add\\_callback\(\)](#)

**16.84.2.1.1.3 auxdata** void\* vrna\_fc\_s::auxdata

A pointer to auxiliary, user-defined data.

See also

[vrna\\_fold\\_compound\\_add\\_auxdata\(\)](#), [vrna\\_fold\\_compound\\_t.free\\_auxdata](#)

**16.84.2.1.1.4 free\_auxdata** [vrna\\_callback\\_free\\_auxdata\\*](#) vrna\_fc\_s::free\_auxdata

A callback to free auxiliary user data whenever the fold\_compound itself is free'd.

See also

[vrna\\_fold\\_compound\\_t.auxdata](#), [vrna\\_callback\\_free\\_auxdata\(\)](#)

**16.84.2.1.1.5 sequence** `char* vrna_fc_s::sequence`

The input sequence string.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_SINGLE
```

**16.84.2.1.1.6 sequence\_encoding** `short* vrna_fc_s::sequence_encoding`

Numerical encoding of the input sequence.

**See also**

```
vrna_sequence_encode()
```

**Warning**

Only available if

```
type==VRNA_FC_TYPE_SINGLE
```

**16.84.2.1.1.7 ptype** `char* vrna_fc_s::ptype`

Pair type array.

Contains the numerical encoding of the pair type for each pair (i,j) used in MFE, Partition function and Evaluation computations.

**Note**

This array is always indexed via jindx, in contrast to previously different indexing between mfe and pf variants!

**Warning**

Only available if

```
type==VRNA_FC_TYPE_SINGLE
```

**See also**

```
vrna\_idx\_col\_wise\(\), vrna\_ptypes\(\)
```

**16.84.2.1.1.8 ptype\_pf\_compat** `char* vrna_fc_s::ptype_pf_compat`

ptype array indexed via iindx

**Deprecated** This attribute will vanish in the future! It's meant for backward compatibility only!

**Warning**

Only available if

```
type==VRNA_FC_TYPE_SINGLE
```

**16.84.2.1.1.9 sc** `vrna_sc_t* vrna_fc_s::sc`

The soft constraints for usage in structure prediction and evaluation.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_SINGLE
```

**16.84.2.1.1.10 sequences** `char** vrna_fc_s::sequences`

The aligned sequences.

**Note**

The end of the alignment is indicated by a NULL pointer in the second dimension

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.11 n\_seq** `unsigned int vrna_fc_s::n_seq`

The number of sequences in the alignment.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.12 cons\_seq** `char* vrna_fc_s::cons_seq`

The consensus sequence of the aligned sequences.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.13 S\_cons** `short* vrna_fc_s::S_cons`

Numerical encoding of the consensus sequence.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.14 S** `short** vrna_fc_s::S`

Numerical encoding of the sequences in the alignment.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.15 S5** `short** vrna_fc_s::S5`

S5[s][i] holds next base 5' of i in sequence s.

**Warning**

Only available if

```
type==VRNA_FC_TYPE_COMPARATIVE
```

**16.84.2.1.1.16 S3** `short** vrna_fc_s::S3`  
 Sl[s][i] holds next base 3' of i in sequence s.

**Warning**

Only available if

`type==VRNA_FC_TYPE_COMPARATIVE`

**16.84.2.1.1.17 pscore** `int* vrna_fc_s::pscore`  
 Precomputed array of pair types expressed as pairing scores.

**Warning**

Only available if

`type==VRNA_FC_TYPE_COMPARATIVE`

**16.84.2.1.1.18 pscore\_local** `int** vrna_fc_s::pscore_local`  
 Precomputed array of pair types expressed as pairing scores.

**Warning**

Only available if

`type==VRNA_FC_TYPE_COMPARATIVE`

**16.84.2.1.1.19 pscore\_pf\_compat** `short* vrna_fc_s::pscore_pf_compat`  
 Precomputed array of pair types expressed as pairing scores indexed via iindx.

**Deprecated** This attribute will vanish in the future!

**Warning**

Only available if

`type==VRNA_FC_TYPE_COMPARATIVE`

**16.84.2.1.1.20 scs** `vrna_sc_t** vrna_fc_s::scs`  
 A set of soft constraints (for each sequence in the alignment)

**Warning**

Only available if

`type==VRNA_FC_TYPE_COMPARATIVE`

## 16.84.3 Macro Definition Documentation

### 16.84.3.1 VRNA\_STATUS\_MFE\_PRE

```
#define VRNA_STATUS_MFE_PRE (unsigned char)1
#include <ViennaRNA/fold_compound.h>
```

Status message indicating that MFE computations are about to begin.

**See also**

[vrna\\_fold\\_compound\\_t.stat\\_cb](#), [vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_fold\(\)](#), [vrna\\_circfold\(\)](#),  
[vrna\\_alifold\(\)](#), [vrna\\_circalifold\(\)](#), [vrna\\_cofold\(\)](#)



### 16.84.3.2 VRNA\_STATUS\_MFE\_POST

```
#define VRNA_STATUS_MFE_POST (unsigned char)2
#include <ViennaRNA/fold_compound.h>
```

Status message indicating that MFE computations are finished.

See also

[vrna\\_fold\\_compound\\_t.stat\\_cb](#), [vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_fold\(\)](#), [vrna\\_circfold\(\)](#), [vrna\\_alifold\(\)](#), [vrna\\_circalifold\(\)](#), [vrna\\_cofold\(\)](#)

### 16.84.3.3 VRNA\_STATUS\_PF\_PRE

```
#define VRNA_STATUS_PF_PRE (unsigned char)3
#include <ViennaRNA/fold_compound.h>
```

Status message indicating that Partition function computations are about to begin.

See also

[vrna\\_fold\\_compound\\_t.stat\\_cb](#), [vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_pf\(\)](#)

### 16.84.3.4 VRNA\_STATUS\_PF\_POST

```
#define VRNA_STATUS_PF_POST (unsigned char)4
#include <ViennaRNA/fold_compound.h>
```

Status message indicating that Partition function computations are finished.

See also

[vrna\\_fold\\_compound\\_t.stat\\_cb](#), [vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_pf\(\)](#)

### 16.84.3.5 VRNA\_OPTION\_MFE

```
#define VRNA_OPTION_MFE 1U
#include <ViennaRNA/fold_compound.h>
```

Option flag to specify requirement of Minimum Free Energy (MFE) DP matrices and corresponding set of energy parameters.

See also

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [VRNA\\_OPTION\\_EVAL\\_ONLY](#)

### 16.84.3.6 VRNA\_OPTION\_PF

```
#define VRNA_OPTION_PF 2U
#include <ViennaRNA/fold_compound.h>
```

Option flag to specify requirement of Partition Function (PF) DP matrices and corresponding set of Boltzmann factors.

See also

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [VRNA\\_OPTION\\_EVAL\\_ONLY](#)

### 16.84.3.7 VRNA\_OPTION\_EVAL\_ONLY

```
#define VRNA_OPTION_EVAL_ONLY 8U
```

```
#include <ViennaRNA/fold_compound.h>
```

Option flag to specify that neither MFE, nor PF DP matrices are required.

Use this flag in conjunction with [VRNA\\_OPTION\\_MFE](#), and [VRNA\\_OPTION\\_PF](#) to save memory for a [vrna\\_fold\\_compound\\_t](#) obtained from [vrna\\_fold\\_compound\(\)](#), or [vrna\\_fold\\_compound\\_comparative\(\)](#) in cases where only energy evaluation but no structure prediction is required.

See also

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_eval\\_structure\(\)](#)

## 16.84.4 Typedef Documentation

### 16.84.4.1 vrna\_callback\_free\_auxdata

```
typedef void() vrna_callback_free_auxdata(void *data)
```

```
#include <ViennaRNA/fold_compound.h>
```

Callback to free memory allocated for auxiliary user-provided data.

This type of user-implemented function usually deletes auxiliary data structures. The user must take care to free all the memory occupied by the data structure passed.

**Notes on Callback Functions** This callback is supposed to free memory occupied by an auxiliary data structure. It will be called when the [vrna\\_fold\\_compound\\_t](#) is erased from memory through a call to [vrna\\_fold\\_compound\\_free\(\)](#) and will be passed the address of memory previously bound to the [vrna\\_fold\\_compound\\_t](#) via [vrna\\_fold\\_compound\\_add\\_auxdata\(\)](#).

See also

[vrna\\_fold\\_compound\\_add\\_auxdata\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_fold\\_compound\\_add\\_callback\(\)](#)

Parameters

|             |                                  |
|-------------|----------------------------------|
| <i>data</i> | The data that needs to be free'd |
|-------------|----------------------------------|

### 16.84.4.2 vrna\_callback\_recursion\_status

```
typedef void() vrna_callback_recursion_status(unsigned char status, void *data)
```

```
#include <ViennaRNA/fold_compound.h>
```

Callback to perform specific user-defined actions before, or after recursive computations.

**Notes on Callback Functions** This function will be called to notify a third-party implementation about the status of a currently ongoing recursion. The purpose of this callback mechanism is to provide users with a simple way to ensure pre- and post conditions for auxiliary mechanisms attached to our implementations.

See also

[vrna\\_fold\\_compound\\_add\\_auxdata\(\)](#), [vrna\\_fold\\_compound\\_add\\_callback\(\)](#), [vrna\\_mfe\(\)](#), [vrna\\_pf\(\)](#), [VRNA\\_STATUS\\_MFE\\_PRE](#), [VRNA\\_STATUS\\_MFE\\_POST](#), [VRNA\\_STATUS\\_PF\\_PRE](#), [VRNA\\_STATUS\\_PF\\_POST](#)

## Parameters

|               |                                                                                            |
|---------------|--------------------------------------------------------------------------------------------|
| <i>status</i> | The status indicator                                                                       |
| <i>data</i>   | The data structure that was assigned with <a href="#">vrna_fold_compound_add_auxdata()</a> |

## 16.84.5 Enumeration Type Documentation

### 16.84.5.1 vrna\_fc\_type\_e

```
enum vrna_fc_type_e
```

```
#include <ViennaRNA/fold_compound.h>
```

An enumerator that is used to specify the type of a [vrna\\_fold\\_compound\\_t](#).

## Enumerator

|                          |                                                                           |
|--------------------------|---------------------------------------------------------------------------|
| VRNA_FC_TYPE_SINGLE      | Type is suitable for single, and hybridizing sequences                    |
| VRNA_FC_TYPE_COMPARATIVE | Type is suitable for sequence alignments (consensus structure prediction) |

## 16.84.6 Function Documentation

### 16.84.6.1 vrna\_fold\_compound()

```
vrna_fold_compound_t * vrna_fold_compound (
    const char * sequence,
    const vrna_md_t * md_p,
    unsigned int options )
#include <ViennaRNA/fold_compound.h>
```

Retrieve a [vrna\\_fold\\_compound\\_t](#) data structure for single sequences and hybridizing sequences.

This function provides an easy interface to obtain a prefilled [vrna\\_fold\\_compound\\_t](#) by passing a single sequence, or two concatenated sequences as input. For the latter, sequences need to be separated by an '&' character like this:

```
char *sequence = "GGGG&CCCC";
```

The optional parameter `md_p` can be used to specify the model details for successive computations based on the content of the generated [vrna\\_fold\\_compound\\_t](#). Passing NULL will instruct the function to use default model details. The third parameter `options` may be used to specify dynamic programming (DP) matrix requirements.

## Options

- [VRNA\\_OPTION\\_DEFAULT](#) - Option flag to specify default settings/requirements.
- [VRNA\\_OPTION\\_MFE](#) - Option flag to specify requirement of Minimum Free Energy (MFE) DP matrices and corresponding set of energy parameters.
- [VRNA\\_OPTION\\_PF](#) - Option flag to specify requirement of Partition Function (PF) DP matrices and corresponding set of Boltzmann factors.
- [VRNA\\_OPTION\\_WINDOW](#) - Option flag to specify requirement of DP matrices for local folding approaches.

The above options may be OR-ed together.

If you just need the folding compound serving as a container for your data, you can simply pass [VRNA\\_OPTION\\_DEFAULT](#) to the `option` parameter. This creates a [vrna\\_fold\\_compound\\_t](#) without DP matrices, thus saving memory. Subsequent calls of any structure prediction function will then take care of allocating the memory required for the DP matrices. If you only intend to evaluate structures instead of actually predicting

them, you may use the `VRNA_OPTION_EVAL_ONLY` macro. This will seriously speedup the creation of the `vrna_fold_compound_t`.

#### Note

The sequence string must be uppercase, and should contain only RNA (resp. DNA) alphabet depending on what energy parameter set is used

#### See also

`vrna_fold_compound_free()`, `vrna_fold_compound_comparative()`, `vrna_md_t`

#### Parameters

|                 |                                                                                |
|-----------------|--------------------------------------------------------------------------------|
| <i>sequence</i> | A single sequence, or two concatenated sequences seperated by an '&' character |
| <i>md_p</i>     | An optional set of model details                                               |
| <i>options</i>  | The options for DP matrices memory allocation                                  |

#### Returns

A prefilled `vrna_fold_compound_t` ready to be used for computations (may be `NULL` on error)

### 16.84.6.2 `vrna_fold_compound_comparative()`

```
vrna_fold_compound_t * vrna_fold_compound_comparative (
    const char ** sequences,
    vrna_md_t * md_p,
    unsigned int options )
```

```
#include <ViennaRNA/fold_compound.h>
```

Retrieve a `vrna_fold_compound_t` data structure for sequence alignments.

This function provides an easy interface to obtain a prefilled `vrna_fold_compound_t` by passing an alignment of sequences.

The optional parameter `md_p` can be used to specify the model details for successive computations based on the content of the generated `vrna_fold_compound_t`. Passing `NULL` will instruct the function to use default model details. The third parameter `options` may be used to specify dynamic programming (DP) matrix requirements.

#### Options

- `VRNA_OPTION_DEFAULT` - Option flag to specify default settings/requirements.
- `VRNA_OPTION_MFE` - Option flag to specify requirement of Minimum Free Energy (MFE) DP matrices and corresponding set of energy parameters.
- `VRNA_OPTION_PF` - Option flag to specify requirement of Partition Function (PF) DP matrices and corresponding set of Boltzmann factors.
- `VRNA_OPTION_WINDOW` - Option flag to specify requirement of DP matrices for local folding approaches.

The above options may be OR-ed together.

If you just need the folding compound serving as a container for your data, you can simply pass `VRNA_OPTION_DEFAULT` to the `option` parameter. This creates a `vrna_fold_compound_t` without DP matrices, thus saving memory. Subsequent calls of any structure prediction function will then take care of allocating the memory required for the DP matrices. If you only intend to evaluate structures instead of actually predicting them, you may use the `VRNA_OPTION_EVAL_ONLY` macro. This will seriously speedup the creation of the `vrna_fold_compound_t`.

**Note**

The sequence strings must be uppercase, and should contain only RNA (resp. DNA) alphabet including gap characters depending on what energy parameter set is used.

**See also**

[vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_md\\_t](#), [VRNA\\_OPTION\\_MFE](#), [VRNA\\_OPTION\\_PF](#), [VRNA\\_OPTION\\_EVAL\\_ONLY](#), [read\\_clustal\(\)](#)

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>sequences</i> | A sequence alignment including 'gap' characters |
| <i>md_p</i>      | An optional set of model details                |
| <i>options</i>   | The options for DP matrices memory allocation   |

**Returns**

A prefilled `vrna_fold_compound_t` ready to be used for computations (may be `NULL` on error)

**16.84.6.3 vrna\_fold\_compound\_free()**

```
void vrna_fold_compound_free (
    vrna_fold_compound_t * fc )
#include <ViennaRNA/fold_compound.h>
Free memory occupied by a vrna\_fold\_compound\_t.
```

**See also**

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_mx\\_mfe\\_free\(\)](#), [vrna\\_mx\\_pf\\_free\(\)](#)

**Parameters**

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| <i>fc</i> | The <a href="#">vrna_fold_compound_t</a> that is to be erased from memory |
|-----------|---------------------------------------------------------------------------|

**16.84.6.4 vrna\_fold\_compound\_add\_auxdata()**

```
void vrna_fold_compound_add_auxdata (
    vrna_fold_compound_t * fc,
    void * data,
    vrna_callback_free_auxdata * f )
#include <ViennaRNA/fold_compound.h>
Add auxiliary data to the vrna\_fold\_compound\_t.
```

This function allows one to bind arbitrary data to a [vrna\\_fold\\_compound\\_t](#) which may later on be used by one of the callback functions, e.g. [vrna\\_callback\\_recursion\\_status\(\)](#). To allow for proper cleanup of the memory occupied by this auxiliary data, the user may also provide a pointer to a cleanup function that free's the corresponding memory. This function will be called automatically when the [vrna\\_fold\\_compound\\_t](#) is free'd with [vrna\\_fold\\_compound\\_free\(\)](#).

**Note**

Before attaching the arbitrary data pointer, this function will call the [vrna\\_callback\\_free\\_auxdata\(\)](#) on any pre-existing data that is already attached.

See also

[vrna\\_callback\\_free\\_auxdata\(\)](#)

#### Parameters

|             |                                                                                       |
|-------------|---------------------------------------------------------------------------------------|
| <i>fc</i>   | The fold_compound the arbitrary data pointer should be associated with                |
| <i>data</i> | A pointer to an arbitrary data structure                                              |
| <i>f</i>    | A pointer to function that free's memory occupied by the arbitrary data (May be NULL) |

#### 16.84.6.5 vrna\_fold\_compound\_add\_callback()

```
void vrna_fold_compound_add_callback (
    vrna_fold_compound_t * fc,
    vrna_callback_recursion_status * f )
```

```
#include <ViennaRNA/fold_compound.h>
```

Add a recursion status callback to the [vrna\\_fold\\_compound\\_t](#).

Binding a recursion status callback function to a [vrna\\_fold\\_compound\\_t](#) allows one to perform arbitrary operations just before, or after an actual recursive computations, e.g. MFE prediction, is performed by the RNAlib. The callback function will be provided with a pointer to its [vrna\\_fold\\_compound\\_t](#), and a status message. Hence, it has complete access to all variables that influence the recursive computations.

See also

[vrna\\_callback\\_recursion\\_status\(\)](#), [vrna\\_fold\\_compound\\_t](#), [VRNA\\_STATUS\\_MFE\\_PRE](#), [VRNA\\_STATUS\\_MFE\\_POST](#), [VRNA\\_STATUS\\_PF\\_PRE](#), [VRNA\\_STATUS\\_PF\\_POST](#)

#### Parameters

|           |                                                               |
|-----------|---------------------------------------------------------------|
| <i>fc</i> | The fold_compound the callback function should be attached to |
| <i>f</i>  | The pointer to the recursion status callback function         |

## 16.85 The Dynamic Programming Matrices

This module provides interfaces that deal with creation and destruction of dynamic programming matrices used within the RNAlib.

### 16.85.1 Detailed Description

This module provides interfaces that deal with creation and destruction of dynamic programming matrices used within the RNAlib.

Collaboration diagram for The Dynamic Programming Matrices:

### Data Structures

- struct [vrna\\_mx\\_mfe\\_s](#)

*Minimum Free Energy (MFE) Dynamic Programming (DP) matrices data structure required within the [vrna\\_fold\\_compound\\_t](#). More...*

- struct [vrna\\_mx\\_pf\\_s](#)

*Partition function (PF) Dynamic Programming (DP) matrices data structure required within the [vrna\\_fold\\_compound\\_t](#). More...*

## Typedefs

- typedef struct [vrna\\_mx\\_mfe\\_s](#) [vrna\\_mx\\_mfe\\_t](#)  
*Typename for the Minimum Free Energy (MFE) DP matrices data structure [vrna\\_mx\\_mfe\\_s](#).*
- typedef struct [vrna\\_mx\\_pf\\_s](#) [vrna\\_mx\\_pf\\_t](#)  
*Typename for the Partition Function (PF) DP matrices data structure [vrna\\_mx\\_pf\\_s](#).*

## Enumerations

- enum [vrna\\_mx\\_type\\_e](#) { [VRNA\\_MX\\_DEFAULT](#) , [VRNA\\_MX\\_WINDOW](#) , [VRNA\\_MX\\_2DFOLD](#) }  
*An enumerator that is used to specify the type of a polymorphic Dynamic Programming (DP) matrix data structure.*

## Functions

- int [vrna\\_mx\\_add](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_mx\\_type\\_e](#) type, unsigned int options)  
*Add Dynamic Programming (DP) matrices (allocate memory)*
- void [vrna\\_mx\\_mfe\\_free](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Free memory occupied by the Minimum Free Energy (MFE) Dynamic Programming (DP) matrices.*
- void [vrna\\_mx\\_pf\\_free](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Free memory occupied by the Partition Function (PF) Dynamic Programming (DP) matrices.*

## 16.85.2 Data Structure Documentation

### 16.85.2.1 struct [vrna\\_mx\\_mfe\\_s](#)

Minimum Free Energy (MFE) Dynamic Programming (DP) matrices data structure required within the [vrna\\_fold\\_compound\\_t](#).

#### Data Fields

##### Common fields for MFE matrices

- const [vrna\\_mx\\_type\\_e](#) type
- unsigned int **length**  
*Length of the sequence, therefore an indicator of the size of the DP matrices.*
- unsigned int [strands](#)

##### Default DP matrices

###### Note

*These data fields are available if*  
[vrna\\_mx\\_mfe\\_t.type](#) == [VRNA\\_MX\\_DEFAULT](#)

##### Local Folding DP matrices using window approach

###### Note

*These data fields are available if*  
[vrna\\_mx\\_mfe\\_t.type](#) == [VRNA\\_MX\\_WINDOW](#)

##### Distance Class DP matrices

###### Note

*These data fields are available if*  
[vrna\\_mx\\_mfe\\_t.type](#) == [VRNA\\_MX\\_2DFOLD](#)

### 16.85.2.1.1 Field Documentation

**16.85.2.1.1.1 type** const [vrna\\_mx\\_type\\_e](#) [vrna\\_mx\\_mfe\\_s::type](#)  
 Type of the DP matrices

**16.85.2.1.1.2 strands** unsigned int `vrna_mx_mfe_s::strands`  
 Number of strands

### 16.85.2.2 struct `vrna_mx_pf_s`

Partition function (PF) Dynamic Programming (DP) matrices data structure required within the `vrna_fold_compound_t`.

#### Data Fields

##### Common fields for DP matrices

- const `vrna_mx_type_e` type
- unsigned int `length`
- `FLT_OR_DBL` \* `scale`
- `FLT_OR_DBL` \* `expMLbase`

##### Default PF matrices

###### Note

*These data fields are available if*  
`vrna_mx_pf_t.type == VRNA_MX_DEFAULT`

##### Local Folding DP matrices using window approach

###### Note

*These data fields are available if*  
`vrna_mx_mfe_t.type == VRNA_MX_WINDOW`

##### Distance Class DP matrices

###### Note

*These data fields are available if*  
`vrna_mx_pf_t.type == VRNA_MX_2DFOLD`

### 16.85.2.2.1 Field Documentation

**16.85.2.2.1.1 type** const `vrna_mx_type_e` `vrna_mx_pf_s::type`  
 Type of the DP matrices

**16.85.2.2.1.2 length** unsigned int `vrna_mx_pf_s::length`  
 Size of the DP matrices (i.e. sequence length)

**16.85.2.2.1.3 scale** `FLT_OR_DBL`\* `vrna_mx_pf_s::scale`  
 Boltzmann factor scaling

**16.85.2.2.1.4 expMLbase** `FLT_OR_DBL`\* `vrna_mx_pf_s::expMLbase`  
 Boltzmann factors for unpaired bases in multibranch loop

## 16.85.3 Enumeration Type Documentation

### 16.85.3.1 `vrna_mx_type_e`

```
enum vrna_mx_type_e
#include <ViennaRNA/dp_matrices.h>
```

An enumerator that is used to specify the type of a polymorphic Dynamic Programming (DP) matrix data structure.

See also

`vrna_mx_mfe_t`, `vrna_mx_pf_t`



## Enumerator

|                 |                                                                                                                                                                                                         |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| VRNA_MX_DEFAULT | Default DP matrices.                                                                                                                                                                                    |
| VRNA_MX_WINDOW  | DP matrices suitable for local structure prediction using window approach.<br><br>See also<br><a href="#">vrna_mfe_window()</a> , <a href="#">vrna_mfe_window_zscore()</a> , <a href="#">pfl_fold()</a> |
| VRNA_MX_2DFOLD  | DP matrices suitable for distance class partitioned structure prediction.<br><br>See also<br><a href="#">vrna_mfe_TwoD()</a> , <a href="#">vrna_pf_TwoD()</a>                                           |

## 16.85.4 Function Documentation

16.85.4.1 `vrna_mx_add()`

```
int vrna_mx_add (
    vrna_fold_compound_t * vc,
    vrna_mx_type_e type,
    unsigned int options )
#include <ViennaRNA/dp_matrices.h>
```

Add Dynamic Programming (DP) matrices (allocate memory)

This function adds DP matrices of a specific type to the provided [vrna\\_fold\\_compound\\_t](#), such that successive DP recursion can be applied. The function caller has to specify which type of DP matrix is requested, see [vrna\\_mx\\_type\\_e](#), and what kind of recursive algorithm will be applied later on, using the parameters `type`, and `options`, respectively. For the latter, Minimum free energy (MFE), and Partition function (PF) computations are distinguished. A third option that may be passed is [VRNA\\_OPTION\\_HYBRID](#), indicating that auxiliary DP arrays are required for RNA-RNA interaction prediction.

## Note

Usually, there is no need to call this function, since the constructors of [vrna\\_fold\\_compound\\_t](#) are handling all the DP matrix memory allocation.

## See also

[vrna\\_mx\\_mfe\\_add\(\)](#), [vrna\\_mx\\_pf\\_add\(\)](#), [vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_mx\\_pf\\_free\(\)](#), [vrna\\_mx\\_mfe\\_free\(\)](#), [vrna\\_mx\\_type\\_e](#), [VRNA\\_OPTION\\_MFE](#), [VRNA\\_OPTION\\_PF](#), [VRNA\\_OPTION\\_HYBRID](#), [VRNA\\_OPTION\\_EVAL\\_ONLY](#)

## Parameters

|                |                                                                                                         |
|----------------|---------------------------------------------------------------------------------------------------------|
| <i>vc</i>      | The <a href="#">vrna_fold_compound_t</a> that holds pointers to the DP matrices                         |
| <i>type</i>    | The type of DP matrices requested                                                                       |
| <i>options</i> | Option flags that specify the kind of DP matrices, such as MFE or PF arrays, and auxiliary requirements |

**Returns**

1 if DP matrices were properly allocated and attached, 0 otherwise

**16.85.4.2 vrna\_mx\_mfe\_free()**

```
void vrna_mx_mfe_free (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/dp_matrices.h>
```

Free memory occupied by the Minimum Free Energy (MFE) Dynamic Programming (DP) matrices.

**See also**

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_mx\\_pf\\_free\(\)](#)

**Parameters**

|    |                                                                                                        |
|----|--------------------------------------------------------------------------------------------------------|
| vc | The <a href="#">vrna_fold_compound_t</a> storing the MFE DP matrices that are to be erased from memory |
|----|--------------------------------------------------------------------------------------------------------|

**16.85.4.3 vrna\_mx\_pf\_free()**

```
void vrna_mx_pf_free (
    vrna_fold_compound_t * vc )
#include <ViennaRNA/dp_matrices.h>
```

Free memory occupied by the Partition Function (PF) Dynamic Programming (DP) matrices.

**See also**

[vrna\\_fold\\_compound\(\)](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), [vrna\\_fold\\_compound\\_free\(\)](#), [vrna\\_mx\\_mfe\\_free\(\)](#)

**Parameters**

|    |                                                                                                       |
|----|-------------------------------------------------------------------------------------------------------|
| vc | The <a href="#">vrna_fold_compound_t</a> storing the PF DP matrices that are to be erased from memory |
|----|-------------------------------------------------------------------------------------------------------|

**16.86 Hash Tables**

Various implementations of hash table functions.

**16.86.1 Detailed Description**

Various implementations of hash table functions.

Hash tables are common data structures that allow for fast random access to the data that is stored within.

Here, we provide an abstract implementation of a hash table interface and a concrete implementation for pairs of secondary structure and corresponding free energy value. Collaboration diagram for Hash Tables:

**Files**

- file [hash\\_tables.h](#)

*Implementations of hash table functions.*

**Data Structures**

- struct [vrna\\_ht\\_entry\\_db\\_t](#)

Default hash table entry. [More...](#)

## Abstract interface

- typedef struct vrna\_hash\_table\_s \* [vrna\\_hash\\_table\\_t](#)  
A hash table object.
- typedef int() [vrna\\_callback\\_ht\\_compare\\_entries](#)(void \*x, void \*y)  
Callback function to compare two hash table entries.
- typedef unsigned int() [vrna\\_callback\\_ht\\_hash\\_function](#)(void \*x, unsigned long hashtable\_size)  
Callback function to generate a hash key, i.e. hash function.
- typedef int() [vrna\\_callback\\_ht\\_free\\_entry](#)(void \*x)  
Callback function to free a hash table entry.
- [vrna\\_hash\\_table\\_t](#) [vrna\\_ht\\_init](#) (unsigned int b, [vrna\\_callback\\_ht\\_compare\\_entries](#) \*compare\_function, [vrna\\_callback\\_ht\\_hash\\_function](#) \*hash\_function, [vrna\\_callback\\_ht\\_free\\_entry](#) \*free\_hash\_entry)  
Get an initialized hash table.
- unsigned long [vrna\\_ht\\_size](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Get the size of the hash table.
- unsigned long [vrna\\_ht\\_collisions](#) (struct vrna\_hash\_table\_s \*ht)  
Get the number of collisions in the hash table.
- void \* [vrna\\_ht\\_get](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Get an element from the hash table.
- int [vrna\\_ht\\_insert](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Insert an object into a hash table.
- void [vrna\\_ht\\_remove](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Remove an object from the hash table.
- void [vrna\\_ht\\_clear](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Clear the hash table.
- void [vrna\\_ht\\_free](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Free all memory occupied by the hash table.

## Dot-Bracket / Free Energy entries

- int [vrna\\_ht\\_db\\_comp](#) (void \*x, void \*y)  
Default hash table entry comparison.
- unsigned int [vrna\\_ht\\_db\\_hash\\_func](#) (void \*x, unsigned long hashtable\_size)  
Default hash function.
- int [vrna\\_ht\\_db\\_free\\_entry](#) (void \*hash\_entry)  
Default function to free memory occupied by a hash entry.

## 16.86.2 Data Structure Documentation

### 16.86.2.1 struct vrna\_ht\_entry\_db\_t

Default hash table entry.

See also

[vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_comp\(\)](#), [vrna\\_ht\\_db\\_hash\\_func\(\)](#), [vrna\\_ht\\_db\\_free\\_entry\(\)](#)

### Data Fields

- char \* [structure](#)
- float [energy](#)

### 16.86.2.1.1 Field Documentation

#### 16.86.2.1.1.1 **structure** `char* vrna_ht_entry_db_t::structure`

A secondary structure in dot-bracket notation

#### 16.86.2.1.1.2 **energy** `float vrna_ht_entry_db_t::energy`

The free energy of `structure`

### 16.86.3 Typedef Documentation

#### 16.86.3.1 **vrna\_hash\_table\_t**

```
typedef struct vrna_hash_table_s* vrna_hash_table_t
#include <ViennaRNA/datastructures/hash_tables.h>
```

A hash table object.

See also

[vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_free\(\)](#)

#### 16.86.3.2 **vrna\_callback\_ht\_compare\_entries**

```
typedef int() vrna_callback_ht_compare_entries(void *x, void *y)
#include <ViennaRNA/datastructures/hash_tables.h>
```

Callback function to compare two hash table entries.

See also

[vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_comp\(\)](#)

Parameters

|          |                    |
|----------|--------------------|
| <i>x</i> | A hash table entry |
| <i>y</i> | A hash table entry |

Returns

-1 if *x* is smaller, +1 if *x* is larger than *y*. 0 if *x* == *y*

#### 16.86.3.3 **vrna\_callback\_ht\_hash\_function**

```
typedef unsigned int() vrna_callback_ht_hash_function(void *x, unsigned long hashtable_size)
#include <ViennaRNA/datastructures/hash_tables.h>
```

Callback function to generate a hash key, i.e. hash function.

See also

[vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_hash\\_func\(\)](#)

Parameters

|                       |                            |
|-----------------------|----------------------------|
| <i>x</i>              | A hash table entry         |
| <i>hashtable_size</i> | The size of the hash table |

## Returns

The hash table key for entry  $x$

16.86.3.4 `vrna_callback_ht_free_entry`

```
typedef int() vrna_callback_ht_free_entry(void *x)
#include <ViennaRNA/datastructures/hash_tables.h>
Callback function to free a hash table entry.
```

## See also

[vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_free\\_entry\(\)](#)

## Parameters

|     |                    |
|-----|--------------------|
| $x$ | A hash table entry |
|-----|--------------------|

## Returns

0 on success

## 16.86.4 Function Documentation

16.86.4.1 `vrna_ht_init()`

```
vrna_hash_table_t vrna_ht_init (
    unsigned int b,
    vrna_callback_ht_compare_entries * compare_function,
    vrna_callback_ht_hash_function * hash_function,
    vrna_callback_ht_free_entry * free_hash_entry )
#include <ViennaRNA/datastructures/hash_tables.h>
```

Get an initialized hash table.

This function returns a ready-to-use hash table with pre-allocated memory for a particular number of entries.

## Note

If all function pointers are `NULL`, this function initializes the hash table with *default functions*, i.e.

- [vrna\\_ht\\_db\\_comp\(\)](#) for the `compare_function`,
- [vrna\\_ht\\_db\\_hash\\_func\(\)](#) for the `hash_function`, and
- [vrna\\_ht\\_db\\_free\\_entry\(\)](#) for the `free_hash_entry`

arguments.

## Warning

If `hash_bits` is larger than 27 you have to compile it with the flag `gcc -mmodel=large`.

## Parameters

|                               |                                                                                             |
|-------------------------------|---------------------------------------------------------------------------------------------|
| $b$                           | Number of bits for the hash table. This determines the size ( $2^b - 1$ ).                  |
| <code>compare_function</code> | A function pointer to compare any two entries in the hash table (may be <code>NULL</code> ) |
| <code>hash_function</code>    | A function pointer to retrieve the hash value of any entry (may be <code>NULL</code> )      |
| <code>free_hash_entry</code>  | A function pointer to free the memory occupied by any entry (may be <code>NULL</code> )     |

**Returns**

An initialized, empty hash table, or `NULL` on any error

**16.86.4.2 vrna\_ht\_size()**

```
unsigned long vrna_ht_size (
    vrna_hash_table_t ht )
#include <ViennaRNA/datastructures/hash_tables.h>
Get the size of the hash table.
```

**Parameters**

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
|-----------|----------------|

**Returns**

The size of the hash table, i.e. the maximum number of entries

**16.86.4.3 vrna\_ht\_collisions()**

```
unsigned long vrna_ht_collisions (
    struct vrna_hash_table_s * ht )
#include <ViennaRNA/datastructures/hash_tables.h>
Get the number of collisions in the hash table.
```

**Parameters**

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
|-----------|----------------|

**Returns**

The number of collisions in the hash table

**16.86.4.4 vrna\_ht\_get()**

```
void * vrna_ht_get (
    vrna_hash_table_t ht,
    void * x )
#include <ViennaRNA/datastructures/hash_tables.h>
Get an element from the hash table.
```

This function takes an object `x` and performs a look-up whether the object is stored within the hash table `ht`. If the object is already stored in `ht`, the function simply returns the entry, otherwise it returns `NULL`.

**See also**

[vrna\\_ht\\_insert\(\)](#), [vrna\\_hash\\_delete\(\)](#), [vrna\\_ht\\_init\(\)](#)

**Parameters**

|           |                           |
|-----------|---------------------------|
| <i>ht</i> | The hash table            |
| <i>x</i>  | The hash entry to look-up |

**Returns**

The entry `x` if it is stored in `ht`, `NULL` otherwise

**16.86.4.5 vrna\_ht\_insert()**

```
int vrna_ht_insert (
    vrna_hash_table_t ht,
    void * x )
#include <ViennaRNA/datastructures/hash_tables.h>
Insert an object into a hash table.
Writes the pointer to your hash entry into the table.
```

**Warning**

In case of collisions, this function simply increments the hash key until a free entry in the hash table is found.

**See also**

[vrna\\_ht\\_init\(\)](#), [vrna\\_hash\\_delete\(\)](#), [vrna\\_ht\\_clear\(\)](#)

**Parameters**

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
| <i>x</i>  | The hash entry |

**Returns**

0 on success, 1 if the value is already in the hash table, -1 on error.

**16.86.4.6 vrna\_ht\_remove()**

```
void vrna_ht_remove (
    vrna_hash_table_t ht,
    void * x )
#include <ViennaRNA/datastructures/hash_tables.h>
Remove an object from the hash table.
Deletes the pointer to your hash entry from the table.
```

**Note**

This function doesn't free any memory occupied by the hash entry.

**Parameters**

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
| <i>x</i>  | The hash entry |

**16.86.4.7 vrna\_ht\_clear()**

```
void vrna_ht_clear (
    vrna_hash_table_t ht )
#include <ViennaRNA/datastructures/hash_tables.h>
```

Clear the hash table.

This function removes all entries from the hash table and automatically free's the memory occupied by each entry using the bound [vrna\\_callback\\_ht\\_free\\_entry\(\)](#) function.

See also

[vrna\\_ht\\_free\(\)](#), [vrna\\_ht\\_init\(\)](#)

#### Parameters

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
|-----------|----------------|

#### 16.86.4.8 vrna\_ht\_free()

```
void vrna_ht_free (
    vrna_hash_table_t ht )
#include <ViennaRNA/datastructures/hash_tables.h>
```

Free all memory occupied by the hash table.

This function removes all entries from the hash table by calling the [vrna\\_callback\\_ht\\_free\\_entry\(\)](#) function for each entry. Finally, the memory occupied by the hash table itself is free'd as well.

#### Parameters

|           |                |
|-----------|----------------|
| <i>ht</i> | The hash table |
|-----------|----------------|

#### 16.86.4.9 vrna\_ht\_db\_comp()

```
int vrna_ht_db_comp (
    void * x,
    void * y )
#include <ViennaRNA/datastructures/hash_tables.h>
```

Default hash table entry comparison.

This is the default comparison function for hash table entries. It assumes the both entries *x* and *y* are of type [vrna\\_ht\\_entry\\_db\\_t](#) and compares the `structure` attribute of both entries

See also

[vrna\\_ht\\_entry\\_db\\_t](#), [vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_hash\\_func\(\)](#), [vrna\\_ht\\_db\\_free\\_entry\(\)](#)

#### Parameters

|          |                                                               |
|----------|---------------------------------------------------------------|
| <i>x</i> | A hash table entry of type <a href="#">vrna_ht_entry_db_t</a> |
| <i>y</i> | A hash table entry of type <a href="#">vrna_ht_entry_db_t</a> |

#### Returns

-1 if *x* is smaller, +1 if *x* is larger than *y*. 0 if both are equal.

#### 16.86.4.10 vrna\_ht\_db\_hash\_func()

```
unsigned int vrna_ht_db_hash_func (
    void * x,
    unsigned long hashtable_size )
```



```
#include <ViennaRNA/datastructures/hash_tables.h>
```

Default hash function.

This is the default hash function for hash table insertion/lookup. It assumes that entries are of type [vrna\\_ht\\_entry\\_db\\_t](#) and uses the Bob Jenkins 1996 mix function to create a hash key from the `structure` attribute of the hash entry.

See also

[vrna\\_ht\\_entry\\_db\\_t](#), [vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_comp\(\)](#), [vrna\\_ht\\_db\\_free\\_entry\(\)](#)

#### Parameters

|                             |                                           |
|-----------------------------|-------------------------------------------|
| <code>x</code>              | A hash table entry to compute the key for |
| <code>hashtable_size</code> | The size of the hash table                |

#### Returns

The hash key for entry `x`

#### 16.86.4.11 vrna\_ht\_db\_free\_entry()

```
int vrna_ht_db_free_entry (
    void * hash_entry )
```

```
#include <ViennaRNA/datastructures/hash_tables.h>
```

Default function to free memory occupied by a hash entry.

This function assumes that hash entries are of type [vrna\\_ht\\_entry\\_db\\_t](#) and free's the memory occupied by that entry.

See also

[vrna\\_ht\\_entry\\_db\\_t](#), [vrna\\_ht\\_init\(\)](#), [vrna\\_ht\\_db\\_comp\(\)](#), [vrna\\_ht\\_db\\_hash\\_func\(\)](#)

#### Parameters

|                         |                                      |
|-------------------------|--------------------------------------|
| <code>hash_entry</code> | The hash entry to remove from memory |
|-------------------------|--------------------------------------|

#### Returns

0 on success

## 16.87 Heaps

Interface for an abstract implementation of a heap data structure.

### 16.87.1 Detailed Description

Interface for an abstract implementation of a heap data structure.

Collaboration diagram for Heaps:

#### Files

- file [heap.h](#)

*Implementation of an abstract heap data structure.*

## Typedefs

- typedef struct vrna\_heap\_s \* [vrna\\_heap\\_t](#)  
*An abstract heap data structure.*
- typedef int() [vrna\\_callback\\_heap\\_cmp](#)(const void \*a, const void \*b, void \*data)  
*Heap compare function prototype.*
- typedef size\_t() [vrna\\_callback\\_heap\\_get\\_pos](#)(const void \*a, void \*data)  
*Retrieve the position of a particular heap entry within the heap.*
- typedef void() [vrna\\_callback\\_heap\\_set\\_pos](#)(const void \*a, size\_t pos, void \*data)  
*Store the position of a particular heap entry within the heap.*

## Functions

- [vrna\\_heap\\_t vrna\\_heap\\_init](#) (size\_t n, [vrna\\_callback\\_heap\\_cmp](#) \*cmp, [vrna\\_callback\\_heap\\_get\\_pos](#) \*get\_entry\_pos, [vrna\\_callback\\_heap\\_set\\_pos](#) \*set\_entry\_pos, void \*data)  
*Initialize a heap data structure.*
- void [vrna\\_heap\\_free](#) ([vrna\\_heap\\_t](#) h)  
*Free memory occupied by a heap data structure.*
- size\_t [vrna\\_heap\\_size](#) (struct vrna\_heap\_s \*h)  
*Get the size of a heap data structure, i.e. the number of stored elements.*
- void [vrna\\_heap\\_insert](#) ([vrna\\_heap\\_t](#) h, void \*v)  
*Insert an element into the heap.*
- void \* [vrna\\_heap\\_pop](#) ([vrna\\_heap\\_t](#) h)  
*Pop (remove and return) the object at the root of the heap.*
- const void \* [vrna\\_heap\\_top](#) ([vrna\\_heap\\_t](#) h)  
*Get the object at the root of the heap.*
- void \* [vrna\\_heap\\_remove](#) ([vrna\\_heap\\_t](#) h, const void \*v)  
*Remove an arbitrary element within the heap.*
- void \* [vrna\\_heap\\_update](#) ([vrna\\_heap\\_t](#) h, void \*v)  
*Update an arbitrary element within the heap.*

## 16.87.2 Typedef Documentation

### 16.87.2.1 vrna\_heap\_t

```
typedef struct vrna_heap_s* vrna\_heap\_t
#include <ViennaRNA/datastructures/heap.h>
```

An abstract heap data structure.

See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_heap\\_free\(\)](#), [vrna\\_heap\\_insert\(\)](#), [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_top\(\)](#), [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_update\(\)](#)

### 16.87.2.2 vrna\_callback\_heap\_cmp

```
typedef int() vrna\_callback\_heap\_cmp(const void *a, const void *b, void *data)
#include <ViennaRNA/datastructures/heap.h>
```

Heap compare function prototype.

Use this prototype to design the compare function for the heap implementation. The arbitrary data pointer `data` may be used to get access to further information required to actually compare the two values `a` and `b`.

**Note**

The heap implementation acts as a *min-heap*, therefore, the minimum element will be present at the heap's root. In case a *max-heap* is required, simply reverse the logic of this compare function.

**Parameters**

|             |                                                                       |
|-------------|-----------------------------------------------------------------------|
| <i>a</i>    | The first object to compare                                           |
| <i>b</i>    | The second object to compare                                          |
| <i>data</i> | An arbitrary data pointer passed through from the heap implementation |

**Returns**

A value less than zero if  $a < b$ , a value greater than zero if  $a > b$ , and 0 otherwise

**16.87.2.3 vrna\_callback\_heap\_get\_pos**

```
typedef size_t() vrna_callback_heap_get_pos(const void *a, void *data)
#include <ViennaRNA/datastructures/heap.h>
```

Retrieve the position of a particular heap entry within the heap.

**Parameters**

|             |                                                                       |
|-------------|-----------------------------------------------------------------------|
| <i>a</i>    | The object to look-up within the heap                                 |
| <i>data</i> | An arbitrary data pointer passed through from the heap implementation |

**Returns**

The position of the element *a* within the heap, or 0 if it is not in the heap

**16.87.2.4 vrna\_callback\_heap\_set\_pos**

```
typedef void() vrna_callback_heap_set_pos(const void *a, size_t pos, void *data)
#include <ViennaRNA/datastructures/heap.h>
```

Store the position of a particular heap entry within the heap.

**Parameters**

|             |                                                                                |
|-------------|--------------------------------------------------------------------------------|
| <i>a</i>    | The object whose position shall be stored                                      |
| <i>pos</i>  | The current position of <i>a</i> within the heap, or 0 if <i>a</i> was deleted |
| <i>data</i> | An arbitrary data pointer passed through from the heap implementation          |

**16.87.3 Function Documentation****16.87.3.1 vrna\_heap\_init()**

```
vrna_heap_t vrna_heap_init (
    size_t n,
    vrna_callback_heap_cmp * cmp,
    vrna_callback_heap_get_pos * get_entry_pos,
    vrna_callback_heap_set_pos * set_entry_pos,
    void * data )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Initialize a heap data structure.

This function initializes a heap data structure. The implementation is based on a *min-heap*, i.e. the minimal element is located at the root of the heap. However, by reversing the logic of the compare function, one can easily transform this into a *max-heap* implementation.

Beside the regular operations on a heap data structure, we implement removal and update of arbitrary elements within the heap. For that purpose, however, one requires a reverse-index lookup system that, (i) for a given element stores the current position in the heap, and (ii) allows for fast lookup of an elements current position within the heap. The corresponding getter- and setter- functions may be provided through the arguments `get_entry_pos` and `set_entry_pos`, respectively.

Sometimes, it is difficult to simply compare two data structures without any context. Therefore, the compare function is provided with a user-defined data pointer that can hold any context required.

#### Warning

If any of the arguments `get_entry_pos` or `set_entry_pos` is NULL, the operations `vrna_heap_update()` and `vrna_heap_remove()` won't work.

#### See also

[vrna\\_heap\\_free\(\)](#), [vrna\\_heap\\_insert\(\)](#), [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_top\(\)](#), [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_update\(\)](#), [vrna\\_heap\\_t](#), [vrna\\_callback\\_heap\\_cmp](#), [vrna\\_callback\\_heap\\_get\\_pos](#), [vrna\\_callback\\_heap\\_set\\_pos](#)

#### Parameters

|                      |                                                                                                                                                                       |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>n</i>             | The initial size of the heap, i.e. the number of elements to store                                                                                                    |
| <i>cmp</i>           | The address of a compare function that will be used to fulfill the partial order requirement                                                                          |
| <i>get_entry_pos</i> | The address of a function that retrieves the position of an element within the heap (or NULL)                                                                         |
| <i>set_entry_pos</i> | The address of a function that stores the position of an element within the heap (or NULL)                                                                            |
| <i>data</i>          | An arbitrary data pointer passed through to the compare function <code>cmp</code> , and the set/get functions <code>get_entry_pos</code> / <code>set_entry_pos</code> |

#### Returns

An initialized heap data structure, or NULL on error

#### 16.87.3.2 vrna\_heap\_free()

```
void vrna_heap_free (
    vrna_heap_t h )
#include <ViennaRNA/datastructures/heap.h>
Free memory occupied by a heap data structure.
```

#### See also

[vrna\\_heap\\_init\(\)](#)

#### Parameters

|          |                                |
|----------|--------------------------------|
| <i>h</i> | The heap that should be free'd |
|----------|--------------------------------|

#### 16.87.3.3 vrna\_heap\_size()

```
size_t vrna_heap_size (
    struct vrna_heap_s * h )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Get the size of a heap data structure, i.e. the number of stored elements.

#### Parameters

|          |                         |
|----------|-------------------------|
| <i>h</i> | The heap data structure |
|----------|-------------------------|

#### Returns

The number of elements currently stored in the heap, or 0 upon any error

### 16.87.3.4 vrna\_heap\_insert()

```
void vrna_heap_insert (
    vrna_heap_t h,
    void * v )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Insert an element into the heap.

#### See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_top\(\)](#), [vrna\\_heap\\_free\(\)](#), [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_update\(\)](#)

#### Parameters

|          |                                                                    |
|----------|--------------------------------------------------------------------|
| <i>h</i> | The heap data structure                                            |
| <i>v</i> | A pointer to the object that is about to be inserted into the heap |

### 16.87.3.5 vrna\_heap\_pop()

```
void * vrna_heap_pop (
    vrna_heap_t h )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Pop (remove and return) the object at the root of the heap.

This function removes the root from the heap and returns it to the caller.

#### See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_heap\\_top\(\)](#), [vrna\\_heap\\_insert\(\)](#), [vrna\\_heap\\_free\(\)](#), [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_update\(\)](#)

#### Parameters

|          |                         |
|----------|-------------------------|
| <i>h</i> | The heap data structure |
|----------|-------------------------|

#### Returns

The object at the root of the heap, i.e. the minimal element (or NULL if (a) the heap is empty or (b) any error occurred)

### 16.87.3.6 vrna\_heap\_top()

```
const void * vrna_heap_top (
    vrna_heap_t h )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Get the object at the root of the heap.

See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_insert\(\)](#), [vrna\\_heap\\_free\(\)](#) [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_update\(\)](#)

Parameters

|          |                         |
|----------|-------------------------|
| <i>h</i> | The heap data structure |
|----------|-------------------------|

Returns

The object at the root of the heap, i.e. the minimal element (or NULL if (a) the heap is empty or (b) any error occurred)

### 16.87.3.7 vrna\_heap\_remove()

```
void * vrna_heap_remove (
    vrna_heap_t h,
    const void * v )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Remove an arbitrary element within the heap.

See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_callback\\_heap\\_get\\_pos](#), [vrna\\_callback\\_heap\\_set\\_pos](#), [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_free\(\)](#)

Warning

This function won't work if the heap was not properly initialized with callback functions for fast reverse-index mapping!

Parameters

|          |                                    |
|----------|------------------------------------|
| <i>h</i> | The heap data structure            |
| <i>v</i> | The object to remove from the heap |

Returns

The object that was removed from the heap (or NULL if (a) it wasn't found or (b) any error occurred)

### 16.87.3.8 vrna\_heap\_update()

```
void * vrna_heap_update (
    vrna_heap_t h,
    void * v )
```

```
#include <ViennaRNA/datastructures/heap.h>
```

Update an arbitrary element within the heap.

Note

If the object that is to be updated is not currently stored in the heap, it will be inserted. In this case, the function returns NULL.

### Warning

This function won't work if the heap was not properly initialized with callback functions for fast reverse-index mapping!

### See also

[vrna\\_heap\\_init\(\)](#), [vrna\\_callback\\_heap\\_get\\_pos](#), [vrna\\_callback\\_heap\\_set\\_pos](#) [vrna\\_heap\\_pop\(\)](#), [vrna\\_heap\\_remove\(\)](#), [vrna\\_heap\\_free\(\)](#)

### Parameters

|          |                         |
|----------|-------------------------|
| <i>h</i> | The heap data structure |
| <i>v</i> | The object to update    |

### Returns

The 'previous' object within the heap that now got replaced by *v* (or NULL if (a) it wasn't found or (b) any error occurred)

## 16.88 Buffers

Functions that provide dynamically buffered stream-like data structures.

### 16.88.1 Detailed Description

Functions that provide dynamically buffered stream-like data structures.  
Collaboration diagram for Buffers:

### Files

- file [char\\_stream.h](#)  
*Implementation of a dynamic, buffered character stream.*
- file [stream\\_output.h](#)  
*An implementation of a buffered, ordered stream output data structure.*

### Typedefs

- typedef struct vrna\_ordered\_stream\_s \* **vrna\_ostream\_t**  
*An ordered output stream structure with unordered insert capabilities.*
- typedef void() [vrna\\_callback\\_stream\\_output](#)(void \*auxdata, unsigned int i, void \*data)  
*Ordered stream processing callback.*

### Functions

- vrna\_cstr\_t [vrna\\_cstr](#) (size\_t size, FILE \*output)  
*Create a dynamic char \* stream data structure.*
- void [vrna\\_cstr\\_discard](#) (struct vrna\_cstr\_s \*buf)  
*Discard the current content of the dynamic char \* stream data structure.*
- void [vrna\\_cstr\\_free](#) (vrna\_cstr\_t buf)  
*Free the memory occupied by a dynamic char \* stream data structure.*
- void [vrna\\_cstr\\_close](#) (vrna\_cstr\_t buf)  
*Free the memory occupied by a dynamic char \* stream and close the output stream.*
- void [vrna\\_cstr\\_fflush](#) (struct vrna\_cstr\_s \*buf)



*Flush the dynamic char \* output stream.*

- [vrna\\_ostream\\_t vrna\\_ostream\\_init](#) ([vrna\\_callback\\_stream\\_output](#) \*output, void \*auxdata)

*Get an initialized ordered output stream.*

- void [vrna\\_ostream\\_free](#) ([vrna\\_ostream\\_t](#) dat)

*Free an initialized ordered output stream.*

- void [vrna\\_ostream\\_request](#) ([vrna\\_ostream\\_t](#) dat, unsigned int num)

*Request index in ordered output stream.*

- void [vrna\\_ostream\\_provide](#) ([vrna\\_ostream\\_t](#) dat, unsigned int i, void \*data)

*Provide output stream data for a particular index.*

## 16.88.2 Typedef Documentation

### 16.88.2.1 vrna\_callback\_stream\_output

```
typedef void() vrna_callback_stream_output(void *auxdata, unsigned int i, void *data)
```

```
#include <ViennaRNA/datastructures/stream_output.h>
```

Ordered stream processing callback.

This callback will be processed in sequential order as soon as sequential data in the output stream becomes available.

#### Note

The callback must also release the memory occupied by the data passed since the stream will lose any reference to it after the callback has been executed.

#### Parameters

|                |                                                                                                           |
|----------------|-----------------------------------------------------------------------------------------------------------|
| <i>auxdata</i> | A shared pointer for all calls, as provided by the second argument to <a href="#">vrna_ostream_init()</a> |
| <i>i</i>       | The index number of the data passed to <i>data</i>                                                        |
| <i>data</i>    | A block of data ready for processing                                                                      |

## 16.88.3 Function Documentation

### 16.88.3.1 vrna\_cstr()

```
vrna_cstr_t vrna_cstr (
    size_t size,
    FILE * output )
```

```
#include <ViennaRNA/datastructures/char_stream.h>
```

Create a dynamic char \* stream data structure.

#### See also

[vrna\\_cstr\\_free\(\)](#), [vrna\\_cstr\\_close\(\)](#), [vrna\\_cstr\\_fflush\(\)](#), [vrna\\_cstr\\_discard\(\)](#), [vrna\\_cstr\\_printf\(\)](#)

#### Parameters

|               |                                                                                                                               |
|---------------|-------------------------------------------------------------------------------------------------------------------------------|
| <i>size</i>   | The initial size of the buffer in characters                                                                                  |
| <i>output</i> | An optional output file stream handle that is used to write the collected data to (defaults to <i>stdout</i> if <i>NULL</i> ) |

### 16.88.3.2 vrna\_cstr\_discard()

```
void vrna_cstr_discard (
    struct vrna_cstr_s * buf )
#include <ViennaRNA/datastructures/char_stream.h>
```

Discard the current content of the dynamic char \* stream data structure.

See also

[vrna\\_cstr\\_free\(\)](#), [vrna\\_cstr\\_close\(\)](#), [vrna\\_cstr\\_fflush\(\)](#), [vrna\\_cstr\\_printf\(\)](#)

#### Parameters

|            |                                                  |
|------------|--------------------------------------------------|
| <i>buf</i> | The dynamic char * stream data structure to free |
|------------|--------------------------------------------------|

### 16.88.3.3 vrna\_cstr\_free()

```
void vrna_cstr_free (
    vrna_cstr_t buf )
#include <ViennaRNA/datastructures/char_stream.h>
```

Free the memory occupied by a dynamic char \* stream data structure.  
This function first flushes any remaining character data within the stream and then free's the memory occupied by the data structure.

See also

[vrna\\_cstr\\_close\(\)](#), [vrna\\_cstr\\_fflush\(\)](#), [vrna\\_cstr\(\)](#)

#### Parameters

|            |                                                  |
|------------|--------------------------------------------------|
| <i>buf</i> | The dynamic char * stream data structure to free |
|------------|--------------------------------------------------|

### 16.88.3.4 vrna\_cstr\_close()

```
void vrna_cstr_close (
    vrna_cstr_t buf )
#include <ViennaRNA/datastructures/char_stream.h>
```

Free the memory occupied by a dynamic char \* stream and close the output stream.  
This function first flushes any remaining character data within the stream then closes the attached output file stream (if any), and finally free's the memory occupied by the data structure.

See also

[vrna\\_cstr\\_free\(\)](#), [vrna\\_cstr\\_fflush\(\)](#), [vrna\\_cstr\(\)](#)

#### Parameters

|            |                                                  |
|------------|--------------------------------------------------|
| <i>buf</i> | The dynamic char * stream data structure to free |
|------------|--------------------------------------------------|

### 16.88.3.5 vrna\_cstr\_fflush()

```
void vrna_cstr_fflush (
    struct vrna_cstr_s * buf )
```

```
#include <ViennaRNA/datastructures/char_stream.h>
```

Flush the dynamic char \* output stream.

This function flushes the collected char \* stream, either by writing to the attached file handle, or simply by writing to *stdout* if no file handle has been attached upon construction using [vrna\\_cstr\(\)](#).

#### Postcondition

The stream buffer is empty after execution of this function

#### See also

[vrna\\_cstr\(\)](#), [vrna\\_cstr\\_close\(\)](#), [vrna\\_cstr\\_free\(\)](#)

#### Parameters

|            |                                                   |
|------------|---------------------------------------------------|
| <i>buf</i> | The dynamic char * stream data structure to flush |
|------------|---------------------------------------------------|

### 16.88.3.6 vrna\_ostream\_init()

```
vrna_ostream_t vrna_ostream_init (
    vrna_callback_stream_output * output,
    void * auxdata )
```

```
#include <ViennaRNA/datastructures/stream_output.h>
```

Get an initialized ordered output stream.

#### See also

[vrna\\_ostream\\_free\(\)](#), [vrna\\_ostream\\_request\(\)](#), [vrna\\_ostream\\_provide\(\)](#)

#### Parameters

|                |                                                                                    |
|----------------|------------------------------------------------------------------------------------|
| <i>output</i>  | A callback function that processes and releases data in the stream                 |
| <i>auxdata</i> | A pointer to auxiliary data passed as first argument to the <i>output</i> callback |

#### Returns

An initialized ordered output stream

### 16.88.3.7 vrna\_ostream\_free()

```
void vrna_ostream_free (
    vrna_ostream_t dat )
```

```
#include <ViennaRNA/datastructures/stream_output.h>
```

Free an initialized ordered output stream.

#### See also

[vrna\\_ostream\\_init\(\)](#)

#### Parameters

|            |                                                              |
|------------|--------------------------------------------------------------|
| <i>dat</i> | The output stream for which occupied memory should be free'd |
|------------|--------------------------------------------------------------|

### 16.88.3.8 vrna\_ostream\_request()

```
void vrna_ostream_request (
    vrna_ostream_t dat,
    unsigned int num )
#include <ViennaRNA/datastructures/stream_output.h>
```

Request index in ordered output stream.

This function must be called prior to [vrna\\_ostream\\_provide\(\)](#) to indicate that data associated with a certain index number is expected to be inserted into the stream in the future.

See also

[vrna\\_ostream\\_init\(\)](#), [vrna\\_ostream\\_provide\(\)](#), [vrna\\_ostream\\_free\(\)](#)

#### Parameters

|            |                                                    |
|------------|----------------------------------------------------|
| <i>dat</i> | The output stream for which the index is requested |
| <i>num</i> | The index to request data for                      |

### 16.88.3.9 vrna\_ostream\_provide()

```
void vrna_ostream_provide (
    vrna_ostream_t dat,
    unsigned int i,
    void * data )
#include <ViennaRNA/datastructures/stream_output.h>
```

Provide output stream data for a particular index.

#### Precondition

The index data is provided for must have been requested using [vrna\\_ostream\\_request\(\)](#) beforehand.

See also

[vrna\\_ostream\\_request\(\)](#)

#### Parameters

|             |                                              |
|-------------|----------------------------------------------|
| <i>dat</i>  | The output stream for which data is provided |
| <i>i</i>    | The index of the provided data               |
| <i>data</i> | The data provided                            |

## 16.89 Deprecated Interface for Global MFE Prediction

### 16.89.1 Detailed Description

Collaboration diagram for Deprecated Interface for Global MFE Prediction:

#### Files

- file [alifold.h](#)  
*Functions for comparative structure prediction using RNA sequence alignments.*
- file [cofold.h](#)  
*MFE implementations for RNA-RNA interaction.*

- file [fold.h](#)

*MFE calculations for single RNA sequences.*

## Functions

- float [cofold](#) (const char \*sequence, char \*structure)  
*Compute the minimum free energy of two interacting RNA molecules.*
- float [cofold\\_par](#) (const char \*string, char \*structure, [vrna\\_param\\_t](#) \*parameters, int is\_constrained)  
*Compute the minimum free energy of two interacting RNA molecules.*
- void [free\\_co\\_arrays](#) (void)  
*Free memory occupied by [cofold\(\)](#)*
- void [update\\_cofold\\_params](#) (void)  
*Recalculate parameters.*
- void [update\\_cofold\\_params\\_par](#) ([vrna\\_param\\_t](#) \*parameters)  
*Recalculate parameters.*
- void [export\\_cofold\\_arrays\\_gq](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*ggg\_p, int \*\*indx\_p, char \*\*ptype\_p)  
*Export the arrays of partition function cofold (with gquadruplex support)*
- void [export\\_cofold\\_arrays](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*indx\_p, char \*\*ptype\_p)  
*Export the arrays of partition function cofold.*
- void [initialize\\_cofold](#) (int length)
- float [fold\\_par](#) (const char \*sequence, char \*structure, [vrna\\_param\\_t](#) \*parameters, int is\_constrained, int is\_circular)  
*Compute minimum free energy and an appropriate secondary structure of an RNA sequence.*
- float [fold](#) (const char \*sequence, char \*structure)  
*Compute minimum free energy and an appropriate secondary structure of an RNA sequence.*
- float [circfold](#) (const char \*sequence, char \*structure)  
*Compute minimum free energy and an appropriate secondary structure of a circular RNA sequence.*
- void [free\\_arrays](#) (void)  
*Free arrays for mfe folding.*
- void [update\\_fold\\_params](#) (void)  
*Recalculate energy parameters.*
- void [update\\_fold\\_params\\_par](#) ([vrna\\_param\\_t](#) \*parameters)  
*Recalculate energy parameters.*
- void [export\\_fold\\_arrays](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)
- void [export\\_fold\\_arrays\\_par](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, [vrna\\_param\\_t](#) \*\*P\_p)
- void [export\\_circfold\\_arrays](#) (int \*Fc\_p, int \*FcH\_p, int \*FcI\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)
- void [export\\_circfold\\_arrays\\_par](#) (int \*Fc\_p, int \*FcH\_p, int \*FcI\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, [vrna\\_param\\_t](#) \*\*P\_p)
- int [LoopEnergy](#) (int n1, int n2, int type, int type\_2, int si1, int sj1, int sp1, int sq1)
- int [HairpinE](#) (int size, int type, int si1, int sj1, const char \*string)
- void [initialize\\_fold](#) (int length)
- float [alifold](#) (const char \*\*strings, char \*structure)  
*Compute MFE and according consensus structure of an alignment of sequences.*
- float [circalifold](#) (const char \*\*strings, char \*structure)  
*Compute MFE and according structure of an alignment of sequences assuming the sequences are circular instead of linear.*
- void [free\\_alifold\\_arrays](#) (void)  
*Free the memory occupied by MFE alifold functions.*

## 16.89.2 Function Documentation

### 16.89.2.1 alifold()

```
float alifold (
    const char ** strings,
    char * structure )
#include <ViennaRNA/alifold.h>
```

Compute MFE and according consensus structure of an alignment of sequences.

This function predicts the consensus structure for the aligned 'sequences' and returns the minimum free energy; the mfe structure in bracket notation is returned in 'structure'.

Sufficient space must be allocated for 'structure' before calling [alifold\(\)](#).

**Deprecated** Usage of this function is discouraged! Use [vrna\\_alifold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

See also

[vrna\\_alifold\(\)](#), [vrna\\_mfe\(\)](#)

#### Parameters

|                  |                                                                                                                                                         |
|------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>strings</i>   | A pointer to a NULL terminated array of character arrays                                                                                                |
| <i>structure</i> | A pointer to a character array that may contain a constraining consensus structure (will be overwritten by a consensus structure that exhibits the MFE) |

#### Returns

The free energy score in kcal/mol

### 16.89.2.2 cofold()

```
float cofold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/cofold.h>
```

Compute the minimum free energy of two interacting RNA molecules.

The code is analog to the [fold\(\)](#) function. If [cut\\_point](#) == -1 results should be the same as with [fold\(\)](#).

**Deprecated** use [vrna\\_mfe\\_dimer\(\)](#) instead

#### Parameters

|                  |                                                           |
|------------------|-----------------------------------------------------------|
| <i>sequence</i>  | The two sequences concatenated                            |
| <i>structure</i> | Will hold the barcket dot structure of the dimer molecule |

#### Returns

minimum free energy of the structure

### 16.89.2.3 cofold\_par()

```
float cofold_par (
```

```
    const char * string,  
    char * structure,  
    vrna_param_t * parameters,  
    int is_constrained )  
#include <ViennaRNA/cofold.h>  
Compute the minimum free energy of two interacting RNA molecules.
```

**Deprecated** use `vrna_mfe_dimer()` instead

#### 16.89.2.4 free\_co\_arrays()

```
void free_co_arrays (  
    void )  
#include <ViennaRNA/cofold.h>  
Free memory occupied by cofold()
```

**Deprecated** This function will only free memory allocated by a prior call of `cofold()` or `cofold_par()`. See `vrna_mfe_dimer()` for how to use the new API

#### Note

folding matrices now reside in the fold compound, and should be free'd there

#### See also

`vrna_fc_destroy()`, `vrna_mfe_dimer()`

#### 16.89.2.5 update\_cofold\_params()

```
void update_cofold_params (  
    void )  
#include <ViennaRNA/cofold.h>  
Recalculate parameters.
```

**Deprecated** See `vrna_params_subst()` for an alternative using the new API

#### 16.89.2.6 update\_cofold\_params\_par()

```
void update_cofold_params_par (  
    vrna_param_t * parameters )  
#include <ViennaRNA/cofold.h>  
Recalculate parameters.
```

**Deprecated** See `vrna_params_subst()` for an alternative using the new API

#### 16.89.2.7 export\_cofold\_arrays\_gq()

```
void export_cofold_arrays_gq (  
    int ** f5_p,  
    int ** c_p,  
    int ** fML_p,  
    int ** fM1_p,  
    int ** fC_p,
```

```

    int ** ggg_p,
    int ** indx_p,
    char ** ptype_p )
#include <ViennaRNA/cofold.h>

```

Export the arrays of partition function cofold (with gquadruplex support)

Export the cofold arrays for use e.g. in the concentration Computations or suboptimal secondary structure backtracking

**Deprecated** folding matrices now reside within the fold compound. Thus, this function will only work in conjunction with a prior call to [cofold\(\)](#) or [cofold\\_par\(\)](#)

See also

[vrna\\_mfe\\_dimer\(\)](#) for the new API

#### Parameters

|                |                                                                                                                                        |
|----------------|----------------------------------------------------------------------------------------------------------------------------------------|
| <i>f5_p</i>    | A pointer to the 'f5' array, i.e. array containing best free energy in interval [1..j]                                                 |
| <i>c_p</i>     | A pointer to the 'c' array, i.e. array containing best free energy in interval [i..j] given that i pairs with j                        |
| <i>fML_p</i>   | A pointer to the 'M' array, i.e. array containing best free energy in interval [i..j] for any multiloop segment with at least one stem |
| <i>fM1_p</i>   | A pointer to the 'M1' array, i.e. array containing best free energy in interval [i..j] for multiloop segment with exactly one stem     |
| <i>fc_p</i>    | A pointer to the 'fc' array, i.e. array ...                                                                                            |
| <i>ggg_p</i>   | A pointer to the 'ggg' array, i.e. array containing best free energy of a gquadruplex delimited by [i..j]                              |
| <i>indx_p</i>  | A pointer to the indexing array used for accessing the energy matrices                                                                 |
| <i>ptype_p</i> | A pointer to the ptype array containing the base pair types for each possibility (i,j)                                                 |

#### 16.89.2.8 export\_cofold\_arrays()

```

void export_cofold_arrays (
    int ** f5_p,
    int ** c_p,
    int ** fML_p,
    int ** fM1_p,
    int ** fc_p,
    int ** indx_p,
    char ** ptype_p )
#include <ViennaRNA/cofold.h>

```

Export the arrays of partition function cofold.

Export the cofold arrays for use e.g. in the concentration Computations or suboptimal secondary structure backtracking

**Deprecated** folding matrices now reside within the [vrna\\_fold\\_compound\\_t](#). Thus, this function will only work in conjunction with a prior call to the deprecated functions [cofold\(\)](#) or [cofold\\_par\(\)](#)

See also

[vrna\\_mfe\\_dimer\(\)](#) for the new API

#### Parameters

|             |                                                                                        |
|-------------|----------------------------------------------------------------------------------------|
| <i>f5_p</i> | A pointer to the 'f5' array, i.e. array containing best free energy in interval [1..j] |
|-------------|----------------------------------------------------------------------------------------|



## Parameters

|                  |                                                                                                                                       |
|------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| <i>c_p</i>       | A pointer to the 'c' array, i.e. array containing best free energy in interval [i,j] given that i pairs with j                        |
| <i>fML_p</i>     | A pointer to the 'M' array, i.e. array containing best free energy in interval [i,j] for any multiloop segment with at least one stem |
| <i>fM1_p</i>     | A pointer to the 'M1' array, i.e. array containing best free energy in interval [i,j] for multiloop segment with exactly one stem     |
| <i>fc_p</i>      | A pointer to the 'fc' array, i.e. array ...                                                                                           |
| <i>indx_p</i>    | A pointer to the indexing array used for accessing the energy matrices                                                                |
| <i>pptype←_p</i> | A pointer to the ptype array containing the base pair types for each possibility (i,j)                                                |

**16.89.2.9 initialize\_cofold()**

```
void initialize_cofold (
    int length )
#include <ViennaRNA/cofold.h>
allocate arrays for folding
```

**Deprecated** {This function is obsolete and will be removed soon!}

**16.89.2.10 fold\_par()**

```
float fold_par (
    const char * sequence,
    char * structure,
    vrna_param_t * parameters,
    int is_constrained,
    int is_circular )
#include <ViennaRNA/fold.h>
```

Compute minimum free energy and an appropriate secondary structure of an RNA sequence.

The first parameter given, the RNA sequence, must be *uppercase* and should only contain an alphabet  $\Sigma$  that is understood by the RNAlib

(e.g.  $\Sigma = \{A, U, C, G\}$ )

The second parameter, *structure*, must always point to an allocated block of memory with a size of at least  $\text{strlen}(\text{sequence}) + 1$

If the third parameter is NULL, global model detail settings are assumed for the folding recursions. Otherwise, the provided parameters are used.

The fourth parameter indicates whether a secondary structure constraint in enhanced dot-bracket notation is passed through the structure parameter or not. If so, the characters " $| x < >$ " are recognized to mark bases that are paired, unpaired, paired upstream, or downstream, respectively. Matching brackets " $( )$ " denote base pairs, dots "." are used for unconstrained bases.

To indicate that the RNA sequence is circular and thus has to be post-processed, set the last parameter to non-zero. After a successful call of `fold_par()`, a backtracked secondary structure (in dot-bracket notation) that exhibits the minimum of free energy will be written to the memory *structure* is pointing to. The function returns the minimum of free energy for any fold of the sequence given.

## Note

OpenMP: Passing NULL to the 'parameters' argument involves access to several global model detail variables and thus is not to be considered threadsafe

**Deprecated** use `vrna_mfe()` instead!

See also

[vrna\\_mfe\(\)](#), [fold\(\)](#), [circfold\(\)](#), [vrna\\_md\\_t](#), [set\\_energy\\_model\(\)](#), [get\\_scaled\\_parameters\(\)](#)

Parameters

|                       |                                                                                                                                     |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------|
| <i>sequence</i>       | RNA sequence                                                                                                                        |
| <i>structure</i>      | A pointer to the character array where the secondary structure in dot-bracket notation will be written to                           |
| <i>parameters</i>     | A data structure containing the pre-scaled energy contributions and the model details. (NULL may be passed, see OpenMP notes above) |
| <i>is_constrained</i> | Switch to indicate that a structure constraint is passed via the structure argument (0==off)                                        |
| <i>is_circular</i>    | Switch to (de-)activate post-processing steps in case RNA sequence is circular (0==off)                                             |

Returns

the minimum free energy (MFE) in kcal/mol

### 16.89.2.11 fold()

```
float fold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/fold.h>
```

Compute minimum free energy and an appropriate secondary structure of an RNA sequence.

This function essentially does the same thing as [fold\\_par\(\)](#). However, it takes its model details, i.e. [temperature](#), [dangles](#), [tetra\\_loop](#), [noGU](#), [no\\_closingGU](#), [fold\\_constrained](#), [noLonelyPairs](#) from the current global settings within the library

**Deprecated** use [vrna\\_fold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

See also

[fold\\_par\(\)](#), [circfold\(\)](#)

Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | RNA sequence                                                                                              |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

Returns

the minimum free energy (MFE) in kcal/mol

### 16.89.2.12 circfold()

```
float circfold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/fold.h>
```

Compute minimum free energy and an appropriate secondary structure of a circular RNA sequence.

This function essentially does the same thing as [fold\\_par\(\)](#). However, it takes its model details, i.e. [temperature](#), [dangles](#), [tetra\\_loop](#), [noGU](#), [no\\_closingGU](#), [fold\\_constrained](#), [noLonelyPairs](#) from the current global settings within the library

**Deprecated** Use [vrna\\_circfold\(\)](#), or [vrna\\_mfe\(\)](#) instead!

See also

[fold\\_par\(\)](#), [circfold\(\)](#)

#### Parameters

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | RNA sequence                                                                                              |
| <i>structure</i> | A pointer to the character array where the secondary structure in dot-bracket notation will be written to |

#### Returns

the minimum free energy (MFE) in kcal/mol

#### 16.89.2.13 free\_arrays()

```
void free_arrays (
    void )
#include <ViennaRNA/fold.h>
Free arrays for mfe folding.
```

**Deprecated** See [vrna\\_fold\(\)](#), [vrna\\_circfold\(\)](#), or [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

#### 16.89.2.14 update\_fold\_params()

```
void update_fold_params (
    void )
#include <ViennaRNA/fold.h>
Recalculate energy parameters.
```

**Deprecated** For non-default model settings use the new API with [vrna\\_params\\_subst\(\)](#) and [vrna\\_mfe\(\)](#) instead!

#### 16.89.2.15 update\_fold\_params\_par()

```
void update_fold_params_par (
    vrna_param_t * parameters )
#include <ViennaRNA/fold.h>
Recalculate energy parameters.
```

**Deprecated** For non-default model settings use the new API with [vrna\\_params\\_subst\(\)](#) and [vrna\\_mfe\(\)](#) instead!

#### 16.89.2.16 export\_fold\_arrays()

```
void export_fold_arrays (
    int ** f5_p,
    int ** c_p,
    int ** fML_p,
    int ** fMl_p,
    int ** indx_p,
    char ** ptype_p )
#include <ViennaRNA/fold.h>
```

**Deprecated** See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

#### 16.89.2.17 export\_fold\_arrays\_par()

```
void export_fold_arrays_par (
    int ** f5_p,
    int ** c_p,
    int ** fML_p,
    int ** fM1_p,
    int ** indx_p,
    char ** ptype_p,
    vrna_param_t ** P_p )
#include <ViennaRNA/fold.h>
```

**Deprecated** See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

#### 16.89.2.18 export\_circfold\_arrays()

```
void export_circfold_arrays (
    int * Fc_p,
    int * FcH_p,
    int * FcI_p,
    int * FcM_p,
    int ** fM2_p,
    int ** f5_p,
    int ** c_p,
    int ** fML_p,
    int ** fM1_p,
    int ** indx_p,
    char ** ptype_p )
#include <ViennaRNA/fold.h>
```

**Deprecated** See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

#### 16.89.2.19 export\_circfold\_arrays\_par()

```
void export_circfold_arrays_par (
    int * Fc_p,
    int * FcH_p,
    int * FcI_p,
    int * FcM_p,
    int ** fM2_p,
    int ** f5_p,
    int ** c_p,
    int ** fML_p,
    int ** fM1_p,
    int ** indx_p,
    char ** ptype_p,
    vrna_param_t ** P_p )
#include <ViennaRNA/fold.h>
```

**Deprecated** See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

**16.89.2.20 LoopEnergy()**

```
int LoopEnergy (
    int n1,
    int n2,
    int type,
    int type_2,
    int sil,
    int sj1,
    int sp1,
    int sq1 )
#include <ViennaRNA/fold.h>
```

**Deprecated** {This function is deprecated and will be removed soon. Use [E\\_IntLoop\(\)](#) instead!}

**16.89.2.21 HairpinE()**

```
int HairpinE (
    int size,
    int type,
    int sil,
    int sj1,
    const char * string )
#include <ViennaRNA/fold.h>
```

**Deprecated** {This function is deprecated and will be removed soon. Use [E\\_Hairpin\(\)](#) instead!}

**16.89.2.22 initialize\_fold()**

```
void initialize_fold (
    int length )
#include <ViennaRNA/fold.h>
Allocate arrays for folding
```

**Deprecated** See [vrna\\_mfe\(\)](#) and [vrna\\_fold\\_compound\\_t](#) for the usage of the new API!

**16.89.2.23 circalifold()**

```
float circalifold (
    const char ** strings,
    char * structure )
#include <ViennaRNA/alifold.h>
```

Compute MFE and according structure of an alignment of sequences assuming the sequences are circular instead of linear.

**Deprecated** Usage of this function is discouraged! Use [vrna\\_alicircfold\(\)](#), and [vrna\\_mfe\(\)](#) instead!

See also

[vrna\\_alicircfold\(\)](#), [vrna\\_alifold\(\)](#), [vrna\\_mfe\(\)](#)

**Parameters**

|                  |                                                                                                                                                         |
|------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>strings</i>   | A pointer to a NULL terminated array of character arrays                                                                                                |
| <i>structure</i> | A pointer to a character array that may contain a constraining consensus structure (will be overwritten by a consensus structure that exhibits the MFE) |

### Returns

The free energy score in kcal/mol

#### 16.89.2.24 free\_alifold\_arrays()

```
void free_alifold_arrays (
    void )
#include <ViennaRNA/alifold.h>
Free the memory occupied by MFE alifold functions.
```

**Deprecated** Usage of this function is discouraged! It only affects memory being free'd that was allocated by an old API function before. Release of memory occupied by the newly introduced [vrna\\_fold\\_compound\\_t](#) is handled by [vrna\\_fold\\_compound\\_free\(\)](#)

### See also

[vrna\\_fold\\_compound\\_free\(\)](#)

## 16.90 Deprecated Interface for Local (Sliding Window) MFE Prediction

### 16.90.1 Detailed Description

Collaboration diagram for Deprecated Interface for Local (Sliding Window) MFE Prediction:

### Files

- file [Lfold.h](#)  
*Functions for locally optimal MFE structure prediction.*

### Functions

- float [Lfold](#) (const char \*string, const char \*structure, int maxdist)  
*The local analog to [fold\(\)](#).*
- float [Lfoldz](#) (const char \*string, const char \*structure, int maxdist, int zsc, double min\_z)

### 16.90.2 Function Documentation

#### 16.90.2.1 Lfold()

```
float Lfold (
    const char * string,
    const char * structure,
    int maxdist )
#include <ViennaRNA/Lfold.h>
```

The local analog to [fold\(\)](#).

Computes the minimum free energy structure including only base pairs with a span smaller than 'maxdist'

**Deprecated** Use [vrna\\_mfe\\_window\(\)](#) instead!

### 16.90.2.2 Lfoldz()

```
float Lfoldz (
    const char * string,
    const char * structure,
    int maxdist,
    int zsc,
    double min_z )
#include <ViennaRNA/Lfold.h>
```

**Deprecated** Use `vrna_mfe_window_zscore()` instead!

## 16.91 Deprecated Interface for Global Partition Function Computation

### 16.91.1 Detailed Description

Collaboration diagram for Deprecated Interface for Global Partition Function Computation:

#### Files

- file [part\\_func\\_co.h](#)  
*Partition function for two RNA sequences.*

#### Functions

- float [pf\\_fold\\_par](#) (const char \*sequence, char \*structure, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_↔  
bppm, int is\_constrained, int is\_circular)  
*Compute the partition function  $Q$  for a given RNA sequence.*
- float [pf\\_fold](#) (const char \*sequence, char \*structure)  
*Compute the partition function  $Q$  of an RNA sequence.*
- float [pf\\_circ\\_fold](#) (const char \*sequence, char \*structure)  
*Compute the partition function of a circular RNA sequence.*
- void [free\\_pf\\_arrays](#) (void)  
*Free arrays for the partition function recursions.*
- void [update\\_pf\\_params](#) (int length)  
*Recalculate energy parameters.*
- void [update\\_pf\\_params\\_par](#) (int length, [vrna\\_exp\\_param\\_t](#) \*parameters)  
*Recalculate energy parameters.*
- [FLT\\_OR\\_DBL](#) \* [export\\_bppm](#) (void)  
*Get a pointer to the base pair probability array.*
- int [get\\_pf\\_arrays](#) (short \*\*S\_p, short \*\*S1\_p, char \*\*ptype\_p, [FLT\\_OR\\_DBL](#) \*\*qb\_p, [FLT\\_OR\\_DBL](#) \*\*qm↔  
\_p, [FLT\\_OR\\_DBL](#) \*\*q1k\_p, [FLT\\_OR\\_DBL](#) \*\*q1n\_p)  
*Get the pointers to (almost) all relevant computation arrays used in partition function computation.*
- double [get\\_subseq\\_F](#) (int i, int j)  
*Get the free energy of a subsequence from the  $q[]$  array.*
- double [mean\\_bp\\_distance](#) (int length)  
*Get the mean base pair distance of the last partition function computation.*
- double [mean\\_bp\\_distance\\_pr](#) (int length, [FLT\\_OR\\_DBL](#) \*pr)  
*Get the mean base pair distance in the thermodynamic ensemble.*
- [vrna\\_ep\\_t](#) \* [stackProb](#) (double cutoff)  
*Get the probability of stacks.*
- void [init\\_pf\\_fold](#) (int length)  
*Allocate space for [pf\\_fold\(\)](#)*
- [vrna\\_dimer\\_pf\\_t](#) co\_pf\_fold (char \*sequence, char \*structure)

- Calculate partition function and base pair probabilities.*
- [vrna\\_dimer\\_pf\\_t co\\_pf\\_fold\\_par](#) (char \*sequence, char \*structure, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_bppm, int is\_constrained)
- Calculate partition function and base pair probabilities.*
- void [compute\\_probabilities](#) (double FAB, double FEA, double FEB, [vrna\\_ep\\_t](#) \*prAB, [vrna\\_ep\\_t](#) \*prA, [vrna\\_ep\\_t](#) \*prB, int Alength)
- Compute Boltzmann probabilities of dimerization without homodimers.*
- void [init\\_co\\_pf\\_fold](#) (int length)
- [FLT\\_OR\\_DBL](#) \* [export\\_co\\_bppm](#) (void)
- Get a pointer to the base pair probability array.*
- void [free\\_co\\_pf\\_arrays](#) (void)
- Free the memory occupied by [co\\_pf\\_fold\(\)](#)*
- void [update\\_co\\_pf\\_params](#) (int length)
- Recalculate energy parameters.*
- void [update\\_co\\_pf\\_params\\_par](#) (int length, [vrna\\_exp\\_param\\_t](#) \*parameters)
- Recalculate energy parameters.*
- void [assign\\_plist\\_from\\_db](#) ([vrna\\_ep\\_t](#) \*\*pl, const char \*struc, float pr)
- Create a [vrna\\_ep\\_t](#) from a dot-bracket string.*
- void [assign\\_plist\\_from\\_pr](#) ([vrna\\_ep\\_t](#) \*\*pl, [FLT\\_OR\\_DBL](#) \*probs, int length, double cutoff)
- Create a [vrna\\_ep\\_t](#) from a probability matrix.*
- float [alipf\\_fold\\_par](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_bppm, int is\_constrained, int is\_circular)
- float [alipf\\_fold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)
- The partition function version of [alifold\(\)](#) works in analogy to [pf\\_fold\(\)](#). Pair probabilities and information about sequence covariations are returned via the 'pi' variable as a list of [vrna\\_pinfo\\_t](#) structs. The list is terminated by the first entry with  $pi.i = 0$ .*
- float [alipf\\_circ\\_fold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)
- [FLT\\_OR\\_DBL](#) \* [export\\_ali\\_bppm](#) (void)
- Get a pointer to the base pair probability array.*
- void [free\\_alipf\\_arrays](#) (void)
- Free the memory occupied by folding matrices allocated by [alipf\\_fold](#), [alipf\\_circ\\_fold](#), etc.*
- char \* [alipbacktrack](#) (double \*prob)
- Sample a consensus secondary structure from the Boltzmann ensemble according its probability.*
- int [get\\_alipf\\_arrays](#) (short \*\*\*S\_p, short \*\*\*S5\_p, short \*\*\*S3\_p, unsigned short \*\*\*a2s\_p, char \*\*\*Ss←\_p, [FLT\\_OR\\_DBL](#) \*\*qb\_p, [FLT\\_OR\\_DBL](#) \*\*qm\_p, [FLT\\_OR\\_DBL](#) \*\*q1k\_p, [FLT\\_OR\\_DBL](#) \*\*qln\_p, short \*\*pscore)
- Get pointers to (almost) all relevant arrays used in [alifold](#)'s partition function computation.*

## 16.91.2 Function Documentation

### 16.91.2.1 alipf\_fold\_par()

```
float alipf_fold_par (
    const char ** sequences,
    char * structure,
    vrna_ep_t ** pl,
    vrna_exp_param_t * parameters,
    int calculate_bppm,
    int is_constrained,
    int is_circular )
#include <ViennaRNA/alifold.h>
```

**Deprecated** Use [vrna\\_pf\(\)](#) instead



## Parameters

|                       |  |
|-----------------------|--|
| <i>sequences</i>      |  |
| <i>structure</i>      |  |
| <i>pl</i>             |  |
| <i>parameters</i>     |  |
| <i>calculate_bppm</i> |  |
| <i>is_constrained</i> |  |
| <i>is_circular</i>    |  |

## Returns

## 16.91.2.2 pf\_fold\_par()

```
float pf_fold_par (
    const char * sequence,
    char * structure,
    vrna_exp_param_t * parameters,
    int calculate_bppm,
    int is_constrained,
    int is_circular )
```

```
#include <ViennaRNA/part_func.h>
```

Compute the partition function  $Q$  for a given RNA sequence.

If *structure* is not a NULL pointer on input, it contains on return a string consisting of the letters " . , | { } ( ) " denoting bases that are essentially unpaired, weakly paired, strongly paired without preference, weakly upstream (downstream) paired, or strongly up- (down-)stream paired bases, respectively. If *fold\_constrained* is not 0, the *structure* string is interpreted on input as a list of constraints for the folding. The character "x" marks bases that must be unpaired, matching brackets " ( ) " denote base pairs, all other characters are ignored. Any pairs conflicting with the constraint will be forbidden. This is usually sufficient to ensure the constraints are honored. If the parameter *calculate\_bppm* is set to 0 base pairing probabilities will not be computed (saving CPU time), otherwise after calculations took place *pr* will contain the probability that bases  $i$  and  $j$  pair.

**Deprecated** Use [vrna\\_pf\(\)](#) instead

## Note

The global array [pr](#) is deprecated and the user who wants the calculated base pair probabilities for further computations is advised to use the function [export\\_bppm\(\)](#)

## Postcondition

After successful run the hidden folding matrices are filled with the appropriate Boltzmann factors. Depending on whether the global variable [do\\_backtrack](#) was set the base pair probabilities are already computed and may be accessed for further usage via the [export\\_bppm\(\)](#) function. A call of [free\\_pf\\_arrays\(\)](#) will free all memory allocated by this function. Successive calls will first free previously allocated memory before starting the computation.

## See also

[vrna\\_pf\(\)](#), [bppm\\_to\\_structure\(\)](#), [export\\_bppm\(\)](#), [vrna\\_exp\\_params\(\)](#), [free\\_pf\\_arrays\(\)](#)

## Parameters

|           |                 |                        |
|-----------|-----------------|------------------------|
| <i>in</i> | <i>sequence</i> | The RNA sequence input |
|-----------|-----------------|------------------------|

## Parameters

|         |                       |                                                                                                                                       |
|---------|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| in, out | <i>structure</i>      | A pointer to a char array where a base pair probability information can be stored in a pseudo-dot-bracket notation (may be NULL, too) |
| in      | <i>parameters</i>     | Data structure containing the precalculated Boltzmann factors                                                                         |
| in      | <i>calculate_bppm</i> | Switch to Base pair probability calculations on/off (0==off)                                                                          |
| in      | <i>is_constrained</i> | Switch to indicate that a structure constraint is passed via the structure argument (0==off)                                          |
| in      | <i>is_circular</i>    | Switch to (de-)activate postprocessing steps in case RNA sequence is circular (0==off)                                                |

## Returns

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

## 16.91.2.3 pf\_fold()

```
float pf_fold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/part_func.h>
```

Compute the partition function  $Q$  of an RNA sequence.

If *structure* is not a NULL pointer on input, it contains on return a string consisting of the letters ". , | { } ( ) " denoting bases that are essentially unpaired, weakly paired, strongly paired without preference, weakly upstream (downstream) paired, or strongly up- (down-)stream paired bases, respectively. If *fold\_constrained* is not 0, the *structure* string is interpreted on input as a list of constraints for the folding. The character "x" marks bases that must be unpaired, matching brackets " ( ) " denote base pairs, all other characters are ignored. Any pairs conflicting with the constraint will be forbidden. This is usually sufficient to ensure the constraints are honored. If *do\_backtrack* has been set to 0 base pairing probabilities will not be computed (saving CPU time), otherwise *pr* will contain the probability that bases  $i$  and  $j$  pair.

## Note

The global array *pr* is deprecated and the user who wants the calculated base pair probabilities for further computations is advised to use the function *export\_bppm()*.

**OpenMP:** This function is not entirely threadsafe. While the recursions are working on their own copies of data the model details for the recursions are determined from the global settings just before entering the recursions. Consider using *pf\_fold\_par()* for a really threadsafe implementation.

## Precondition

This function takes its model details from the global variables provided in *RNAlib*

## Postcondition

After successful run the hidden folding matrices are filled with the appropriate Boltzmann factors. Depending on whether the global variable *do\_backtrack* was set the base pair probabilities are already computed and may be accessed for further usage via the *export\_bppm()* function. A call of *free\_pf\_arrays()* will free all memory allocated by this function. Successive calls will first free previously allocated memory before starting the computation.

## See also

*pf\_fold\_par()*, *pf\_circ\_fold()*, *bppm\_to\_structure()*, *export\_bppm()*

## Parameters

|                  |                                                                                                                                       |
|------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| <i>sequence</i>  | The RNA sequence input                                                                                                                |
| <i>structure</i> | A pointer to a char array where a base pair probability information can be stored in a pseudo-dot-bracket notation (may be NULL, too) |

## Returns

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

## 16.91.2.4 pf\_circ\_fold()

```
float pf_circ_fold (
    const char * sequence,
    char * structure )
#include <ViennaRNA/part_func.h>
```

Compute the partition function of a circular RNA sequence.

## Note

The global array `pr` is deprecated and the user who wants the calculated base pair probabilities for further computations is advised to use the function `export_bppm()`.

**OpenMP:** This function is not entirely threadsafe. While the recursions are working on their own copies of data the model details for the recursions are determined from the global settings just before entering the recursions. Consider using `pf_fold_par()` for a really threadsafe implementation.

## Precondition

This function takes its model details from the global variables provided in *RNAlib*

## Postcondition

After successful run the hidden folding matrices are filled with the appropriate Boltzmann factors. Depending on whether the global variable `do_backtrack` was set the base pair probabilities are already computed and may be accessed for further usage via the `export_bppm()` function. A call of `free_pf_arrays()` will free all memory allocated by this function. Successive calls will first free previously allocated memory before starting the computation.

## See also

`vrna_pf()`

**Deprecated** Use `vrna_pf()` instead!

## Parameters

|                |                  |                                                                                                                                       |
|----------------|------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| <i>in</i>      | <i>sequence</i>  | The RNA sequence input                                                                                                                |
| <i>in, out</i> | <i>structure</i> | A pointer to a char array where a base pair probability information can be stored in a pseudo-dot-bracket notation (may be NULL, too) |

## Returns

The ensemble free energy  $G = -RT \cdot \log(Q)$  in kcal/mol

### 16.91.2.5 free\_pf\_arrays()

```
void free_pf_arrays (
    void )
#include <ViennaRNA/part_func.h>
```

Free arrays for the partition function recursions.

Call this function if you want to free all allocated memory associated with the partition function forward recursion.

#### Note

Successive calls of [pf\\_fold\(\)](#), [pf\\_circ\\_fold\(\)](#) already check if they should free any memory from a previous run.

#### OpenMP notice:

This function should be called before leaving a thread in order to avoid leaking memory

**Deprecated** See [vrna\\_fold\\_compound\\_t](#) and its related functions for how to free memory occupied by the dynamic programming matrices

#### Postcondition

All memory allocated by [pf\\_fold\\_par\(\)](#), [pf\\_fold\(\)](#) or [pf\\_circ\\_fold\(\)](#) will be free'd

#### See also

[pf\\_fold\\_par\(\)](#), [pf\\_fold\(\)](#), [pf\\_circ\\_fold\(\)](#)

### 16.91.2.6 update\_pf\_params()

```
void update_pf_params (
    int length )
#include <ViennaRNA/part_func.h>
```

Recalculate energy parameters.

Call this function to recalculate the pair matrix and energy parameters after a change in folding parameters like [temperature](#)

**Deprecated** Use [vrna\\_exp\\_params\\_subst\(\)](#) instead

### 16.91.2.7 update\_pf\_params\_par()

```
void update_pf_params_par (
    int length,
    vrna_exp_param_t * parameters )
#include <ViennaRNA/part_func.h>
```

Recalculate energy parameters.

**Deprecated** Use [vrna\\_exp\\_params\\_subst\(\)](#) instead

### 16.91.2.8 export\_bppm()

```
FLT_OR_DBL * export_bppm (
    void )
#include <ViennaRNA/part_func.h>
```

Get a pointer to the base pair probability array.

Accessing the base pair probabilities for a pair (i,j) is achieved by

```
FLT_OR_DBL *pr = export_bppm();
pr_ij          = pr[iindx[i]-j];
```

**Precondition**

Call [pf\\_fold\\_par\(\)](#), [pf\\_fold\(\)](#) or [pf\\_circ\\_fold\(\)](#) first to fill the base pair probability array

**See also**

[pf\\_fold\(\)](#), [pf\\_circ\\_fold\(\)](#), [vrna\\_idx\\_row\\_wise\(\)](#)

**Returns**

A pointer to the base pair probability array

**16.91.2.9 get\_pf\_arrays()**

```
int get_pf_arrays (
    short ** S_p,
    short ** S1_p,
    char ** ptype_p,
    FLT_OR_DBL ** qb_p,
    FLT_OR_DBL ** qm_p,
    FLT_OR_DBL ** q1k_p,
    FLT_OR_DBL ** qln_p )
#include <ViennaRNA/part_func.h>
```

Get the pointers to (almost) all relevant computation arrays used in partition function computation.

**Precondition**

In order to assign meaningful pointers, you have to call [pf\\_fold\\_par\(\)](#) or [pf\\_fold\(\)](#) first!

**See also**

[pf\\_fold\\_par\(\)](#), [pf\\_fold\(\)](#), [pf\\_circ\\_fold\(\)](#)

**Parameters**

|     |                                        |                                                                         |
|-----|----------------------------------------|-------------------------------------------------------------------------|
| out | <i>S_p</i>                             | A pointer to the 'S' array (integer representation of nucleotides)      |
| out | <i>S1_p</i>                            | A pointer to the 'S1' array (2nd integer representation of nucleotides) |
| out | <i>ptype</i> <sub>↔</sub><br><i>_p</i> | A pointer to the pair type matrix                                       |
| out | <i>qb_p</i>                            | A pointer to the $Q^B$ matrix                                           |
| out | <i>qm_p</i>                            | A pointer to the $Q^M$ matrix                                           |
| out | <i>q1k_p</i>                           | A pointer to the 5' slice of the Q matrix ( $q1k(k) = Q(1, k)$ )        |
| out | <i>qln_p</i>                           | A pointer to the 3' slice of the Q matrix ( $qln(l) = Q(l, n)$ )        |

**Returns**

Non Zero if everything went fine, 0 otherwise

**16.91.2.10 mean\_bp\_distance()**

```
double mean_bp_distance (
    int length )
#include <ViennaRNA/part_func.h>
```

Get the mean base pair distance of the last partition function computation.

**Deprecated** Use `vrna_mean_bp_distance()` or `vrna_mean_bp_distance_pr()` instead!

See also

`vrna_mean_bp_distance()`, `vrna_mean_bp_distance_pr()`

Parameters

|               |  |
|---------------|--|
| <i>length</i> |  |
|---------------|--|

Returns

mean base pair distance in thermodynamic ensemble

#### 16.91.2.11 mean\_bp\_distance\_pr()

```
double mean_bp_distance_pr (
    int length,
    FLT_OR_DBL * pr )
#include <ViennaRNA/part_func.h>
```

Get the mean base pair distance in the thermodynamic ensemble.  
This is a threadsafe implementation of `mean_bp_dist()` !  
 $\langle d \rangle = \sum_{a,b} p_a p_b d(S_a, S_b)$   
this can be computed from the pair probs  $p_{ij}$  as  
 $\langle d \rangle = \sum_{ij} p_{ij} (1 - p_{ij})$

**Deprecated** Use `vrna_mean_bp_distance()` or `vrna_mean_bp_distance_pr()` instead!

Parameters

|               |                                                   |
|---------------|---------------------------------------------------|
| <i>length</i> | The length of the sequence                        |
| <i>pr</i>     | The matrix containing the base pair probabilities |

Returns

The mean pair distance of the structure ensemble

#### 16.91.2.12 stackProb()

```
vrna_ep_t * stackProb (
    double cutoff )
#include <ViennaRNA/part_func.h>
```

Get the probability of stacks.

**Deprecated** Use `vrna_stack_prob()` instead!

#### 16.91.2.13 init\_pf\_fold()

```
void init_pf_fold (
    int length )
#include <ViennaRNA/part_func.h>
```

Allocate space for `pf_fold()`

**Deprecated** This function is obsolete and will be removed soon!

#### 16.91.2.14 co\_pf\_fold()

```
vrna_dimer_pf_t co_pf_fold (
    char * sequence,
    char * structure )
#include <ViennaRNA/part_func_co.h>
```

Calculate partition function and base pair probabilities.

This is the cofold partition function folding. The second molecule starts at the [cut\\_point](#) nucleotide.

##### Note

OpenMP: Since this function relies on the global parameters [do\\_backtrack](#), [dangles](#), [temperature](#) and [pf\\_scale](#) it is not threadsafe according to concurrent changes in these variables! Use [co\\_pf\\_fold\\_par\(\)](#) instead to circumvent this issue.

**Deprecated** {Use [vrna\\_pf\\_dimer\(\)](#) instead!}

##### Parameters

|                  |                                        |
|------------------|----------------------------------------|
| <i>sequence</i>  | Concatenated RNA sequences             |
| <i>structure</i> | Will hold the structure or constraints |

##### Returns

[vrna\\_dimer\\_pf\\_t](#) structure containing a set of energies needed for concentration computations.

#### 16.91.2.15 co\_pf\_fold\_par()

```
vrna_dimer_pf_t co_pf_fold_par (
    char * sequence,
    char * structure,
    vrna_exp_param_t * parameters,
    int calculate_bppm,
    int is_constrained )
#include <ViennaRNA/part_func_co.h>
```

Calculate partition function and base pair probabilities.

This is the cofold partition function folding. The second molecule starts at the [cut\\_point](#) nucleotide.

**Deprecated** Use [vrna\\_pf\\_dimer\(\)](#) instead!

##### See also

[get\\_boltzmann\\_factors\(\)](#), [co\\_pf\\_fold\(\)](#)

##### Parameters

|                       |                                                                                              |
|-----------------------|----------------------------------------------------------------------------------------------|
| <i>sequence</i>       | Concatenated RNA sequences                                                                   |
| <i>structure</i>      | Pointer to the structure constraint                                                          |
| <i>parameters</i>     | Data structure containing the precalculated Boltzmann factors                                |
| <i>calculate_bppm</i> | Switch to turn Base pair probability calculations on/off (0==off)                            |
| <i>is_constrained</i> | Switch to indicate that a structure constraint is passed via the structure argument (0==off) |

## Returns

`vrna_dimer_pf_t` structure containing a set of energies needed for concentration computations.

**16.91.2.16 compute\_probabilities()**

```
void compute_probabilities (
    double FAB,
    double FEA,
    double FEB,
    vrna_ep_t * prAB,
    vrna_ep_t * prA,
    vrna_ep_t * prB,
    int Alength )
```

```
#include <ViennaRNA/part_func_co.h>
```

Compute Boltzmann probabilities of dimerization without homodimers.

Given the pair probabilities and free energies (in the null model) for a dimer AB and the two constituent monomers A and B, compute the conditional pair probabilities given that a dimer AB actually forms. Null model pair probabilities are given as a list as produced by [assign\\_plist\\_from\\_pr\(\)](#), the dimer probabilities 'prAB' are modified in place.

**Deprecated** { Use [vrna\\_pf\\_dimer\\_probs\(\)](#) instead!}

## Parameters

|                |                              |
|----------------|------------------------------|
| <i>FAB</i>     | free energy of dimer AB      |
| <i>FEA</i>     | free energy of monomer A     |
| <i>FEB</i>     | free energy of monomer B     |
| <i>prAB</i>    | pair probabilities for dimer |
| <i>prA</i>     | pair probabilities monomer   |
| <i>prB</i>     | pair probabilities monomer   |
| <i>Alength</i> | Length of molecule A         |

**16.91.2.17 init\_co\_pf\_fold()**

```
void init_co_pf_fold (
    int length )
#include <ViennaRNA/part_func_co.h>
DO NOT USE THIS FUNCTION ANYMORE
```

**Deprecated** { This function is deprecated and will be removed soon!}

**16.91.2.18 export\_co\_bppm()**

```
FLT_OR_DBL * export_co_bppm (
    void )
#include <ViennaRNA/part_func_co.h>
Get a pointer to the base pair probability array.
Accessing the base pair probabilities for a pair (i,j) is achieved by
FLT_OR_DBL *pr = export_bppm(); pr_ij = pr[iindx[i]-j];
```

**Deprecated** This function is deprecated and will be removed soon! The base pair probability array is available through the [vrna\\_fold\\_compound\\_t](#) data structure, and its associated [vrna\\_mx\\_pf\\_t](#) member.



See also

[vrna\\_idx\\_row\\_wise\(\)](#)

Returns

A pointer to the base pair probability array

#### 16.91.2.19 free\_co\_pf\_arrays()

```
void free_co_pf_arrays (
    void )
#include <ViennaRNA/part_func_co.h>
Free the memory occupied by co\_pf\_fold\(\)
```

**Deprecated** This function will be removed for the new API soon! See [vrna\\_pf\\_dimer\(\)](#), [vrna\\_fold\\_compound\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) for an alternative

#### 16.91.2.20 update\_co\_pf\_params()

```
void update_co_pf_params (
    int length )
#include <ViennaRNA/part_func_co.h>
Recalculate energy parameters.
This function recalculates all energy parameters given the current model settings.
```

**Deprecated** Use [vrna\\_exp\\_params\\_subst\(\)](#) instead!

Parameters

|               |                                    |
|---------------|------------------------------------|
| <i>length</i> | Length of the current RNA sequence |
|---------------|------------------------------------|

#### 16.91.2.21 update\_co\_pf\_params\_par()

```
void update_co_pf_params_par (
    int length,
    vrna_exp_param_t * parameters )
#include <ViennaRNA/part_func_co.h>
Recalculate energy parameters.
```

This function recalculates all energy parameters given the current model settings. Its second argument can either be NULL or a data structure containing the precomputed Boltzmann factors. In the first scenario, the necessary data structure will be created automatically according to the current global model settings, i.e. this mode might not be threadsafe. However, if the provided data structure is not NULL, threadsafety for the model parameters [dangles](#), [pf\\_scale](#) and [temperature](#) is regained, since their values are taken from this data structure during subsequent calculations.

**Deprecated** Use [vrna\\_exp\\_params\\_subst\(\)](#) instead!

Parameters

|                   |                                                             |
|-------------------|-------------------------------------------------------------|
| <i>length</i>     | Length of the current RNA sequence                          |
| <i>parameters</i> | data structure containing the precomputed Boltzmann factors |

### 16.91.2.22 assign\_plist\_from\_db()

```
void assign_plist_from_db (
    vrna_ep_t ** pl,
    const char * struc,
    float pr )
#include <ViennaRNA/utils/structures.h>
```

Create a `vrna_ep_t` from a dot-bracket string.

The dot-bracket string is parsed and for each base pair an entry in the plist is created. The probability of each pair in the list is set by a function parameter.

The end of the plist is marked by sequence positions *i* as well as *j* equal to 0. This condition should be used to stop looping over its entries

**Deprecated** Use `vrna_plist()` instead

#### Parameters

|              |                                                               |
|--------------|---------------------------------------------------------------|
| <i>pl</i>    | A pointer to the <code>vrna_ep_t</code> that is to be created |
| <i>struc</i> | The secondary structure in dot-bracket notation               |
| <i>pr</i>    | The probability for each base pair                            |

### 16.91.2.23 assign\_plist\_from\_pr()

```
void assign_plist_from_pr (
    vrna_ep_t ** pl,
    FLT_OR_DBL * probs,
    int length,
    double cutoff )
#include <ViennaRNA/utils/structures.h>
```

Create a `vrna_ep_t` from a probability matrix.

The probability matrix given is parsed and all pair probabilities above the given threshold are used to create an entry in the plist

The end of the plist is marked by sequence positions *i* as well as *j* equal to 0. This condition should be used to stop looping over its entries

#### Note

This function is threadsafe

**Deprecated** Use `vrna_plist_from_probs()` instead!

#### Parameters

|     |               |                                                               |
|-----|---------------|---------------------------------------------------------------|
| out | <i>pl</i>     | A pointer to the <code>vrna_ep_t</code> that is to be created |
| in  | <i>probs</i>  | The probability matrix used for creating the plist            |
| in  | <i>length</i> | The length of the RNA sequence                                |
| in  | <i>cutoff</i> | The cutoff value                                              |

### 16.91.2.24 alipf\_fold()

```
float alipf_fold (
```

```

    const char ** sequences,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/alifold.h>

```

The partition function version of [alifold\(\)](#) works in analogy to [pf\\_fold\(\)](#). Pair probabilities and information about sequence covariations are returned via the 'pi' variable as a list of [vrna\\_pinfo\\_t](#) structs. The list is terminated by the first entry with pi.i = 0.

**Deprecated** Use [vrna\\_pf\(\)](#) instead

#### Parameters

|                  |  |
|------------------|--|
| <i>sequences</i> |  |
| <i>structure</i> |  |
| <i>pl</i>        |  |

#### Returns

#### 16.91.2.25 alipf\_circ\_fold()

```

float alipf_circ_fold (
    const char ** sequences,
    char * structure,
    vrna_ep_t ** pl )
#include <ViennaRNA/alifold.h>

```

**Deprecated** Use [vrna\\_pf\(\)](#) instead

#### Parameters

|                  |  |
|------------------|--|
| <i>sequences</i> |  |
| <i>structure</i> |  |
| <i>pl</i>        |  |

#### Returns

#### 16.91.2.26 export\_ali\_bppm()

```

FLT_OR_DBL * export_ali_bppm (
    void )
#include <ViennaRNA/alifold.h>

```

Get a pointer to the base pair probability array.  
 Accessing the base pair probabilities for a pair (i,j) is achieved by

```

FLT_OR_DBL *pr = export_bppm(); pr_ij = pr[iindx[i]-j];

```

**Deprecated** Usage of this function is discouraged! The new [vrna\\_fold\\_compound\\_t](#) allows direct access to the folding matrices, including the pair probabilities! The pair probability array returned here reflects the one of the latest call to [vrna\\_pf\(\)](#), or any of the old API calls for consensus structure partition function folding.

See also

[vrna\\_fold\\_compound\\_t](#), [vrna\\_fold\\_compound\\_comparative\(\)](#), and [vrna\\_pf\(\)](#)

Returns

A pointer to the base pair probability array

#### 16.91.2.27 free\_alipf\_arrays()

```
void free_alipf_arrays (
    void )
```

```
#include <ViennaRNA/alifold.h>
```

Free the memory occupied by folding matrices allocated by `alipf_fold`, `alipf_circ_fold`, etc.

**Deprecated** Usage of this function is discouraged! This function only free's memory allocated by old API function calls. Memory allocated by any of the new API calls (starting with `vrna_`) will be not affected!

See also

[vrna\\_fold\\_compound\\_t](#), [vrna\\_vrna\\_fold\\_compound\\_free\(\)](#)

#### 16.91.2.28 alipbacktrack()

```
char * alipbacktrack (
    double * prob )
```

```
#include <ViennaRNA/alifold.h>
```

Sample a consensus secondary structure from the Boltzmann ensemble according its probability.

**Deprecated** Use [vrna\\_pbacktrack\(\)](#) instead!

Parameters

|             |                         |
|-------------|-------------------------|
| <i>prob</i> | to be described (berni) |
|-------------|-------------------------|

Returns

A sampled consensus secondary structure in dot-bracket notation

#### 16.91.2.29 get\_alipf\_arrays()

```
int get_alipf_arrays (
    short *** S_p,
    short *** S5_p,
    short *** S3_p,
    unsigned short *** a2s_p,
    char *** Ss_p,
    FLT_OR_DBL ** qb_p,
    FLT_OR_DBL ** qm_p,
    FLT_OR_DBL ** qlk_p,
    FLT_OR_DBL ** qln_p,
    short ** pscore )
```

```
#include <ViennaRNA/alifold.h>
```

Get pointers to (almost) all relevant arrays used in alifold's partition function computation.

**Note**

To obtain meaningful pointers, call `alipf_fold` first!

**See also**

`pf_alifold()`, `alipf_circ_fold()`

**Deprecated** It is discouraged to use this function! The new `vrna_fold_compound_t` allows direct access to all necessary consensus structure prediction related variables!

**See also**

`vrna_fold_compound_t`, `vrna_fold_compound_comparative()`, `vrna_pf()`

**Parameters**

|                          |                                                                      |
|--------------------------|----------------------------------------------------------------------|
| <code>S_p</code>         | A pointer to the 'S' array (integer representation of nucleotides)   |
| <code>S5_p</code>        | A pointer to the 'S5' array                                          |
| <code>S3_p</code>        | A pointer to the 'S3' array                                          |
| <code>a2s↔<br/>_p</code> | A pointer to the alignment-column to sequence position mapping array |
| <code>Ss_p</code>        | A pointer to the 'Ss' array                                          |
| <code>qb_p</code>        | A pointer to the $Q^B$ matrix                                        |
| <code>qm_p</code>        | A pointer to the $Q^M$ matrix                                        |
| <code>q1k↔<br/>_p</code> | A pointer to the 5' slice of the Q matrix ( $q1k(k) = Q(1, k)$ )     |
| <code>qln_p</code>       | A pointer to the 3' slice of the Q matrix ( $qln(l) = Q(l, n)$ )     |
| <code>pscore</code>      | A pointer to the start of a pscore list                              |

**Returns**

Non Zero if everything went fine, 0 otherwise

## 16.92 Deprecated Interface for Local (Sliding Window) Partition Function Computation

### 16.92.1 Detailed Description

Collaboration diagram for Deprecated Interface for Local (Sliding Window) Partition Function Computation:

**Files**

- file `LPfold.h`

*Partition function and equilibrium probability implementation for the sliding window algorithm.*

**Functions**

- void `update_pf_paramsLP` (int length)
- `vrna_ep_t * pfl_fold` (char \*sequence, int winSize, int pairSize, float cutoffb, double \*\*pU, `vrna_ep_t` \*\*dpp2, FILE \*pUfp, FILE \*spup)  
*Compute partition functions for locally stable secondary structures.*
- `vrna_ep_t * pfl_fold_par` (char \*sequence, int winSize, int pairSize, float cutoffb, double \*\*pU, `vrna_ep_t` \*\*dpp2, FILE \*pUfp, FILE \*spup, `vrna_exp_param_t` \*parameters)

*Compute partition functions for locally stable secondary structures.*

- void [putoutpU\\_prob](#) (double \*\*pU, int length, int ulength, FILE \*fp, int energies)  
*Writes the unpaired probabilities (pU) or opening energies into a file.*
- void [putoutpU\\_prob\\_bin](#) (double \*\*pU, int length, int ulength, FILE \*fp, int energies)  
*Writes the unpaired probabilities (pU) or opening energies into a binary file.*

## 16.92.2 Function Documentation

### 16.92.2.1 update\_pf\_paramsLP()

```
void update_pf_paramsLP (
    int length )
#include <ViennaRNA/LPfold.h>
```

Parameters

|               |  |
|---------------|--|
| <i>length</i> |  |
|---------------|--|

### 16.92.2.2 pfl\_fold()

```
vrna_ep_t * pfl_fold (
    char * sequence,
    int winSize,
    int pairSize,
    float cutoffb,
    double ** pU,
    vrna_ep_t ** dpp2,
    FILE * pUfp,
    FILE * spup )
#include <ViennaRNA/LPfold.h>
```

Compute partition functions for locally stable secondary structures.

`pfl_fold` computes partition functions for every window of size 'winSize' possible in a RNA molecule, allowing only pairs with a span smaller than 'pairSize'. It returns the mean pair probabilities averaged over all windows containing the pair in 'pl'. 'winSize' should always be  $\geq$  'pairSize'. Note that in contrast to [Lfold\(\)](#), bases outside of the window do not influence the structure at all. Only probabilities higher than 'cutoffb' are kept.

If 'pU' is supplied (i.e. is not the NULL pointer), [pfl\\_fold\(\)](#) will also compute the mean probability that regions of length 'u' and smaller are unpaired. The parameter 'u' is supplied in 'pup[0][0]'. On return the 'pup' array will contain these probabilities, with the entry on 'pup[x][y]' containing the mean probability that x and the y-1 preceding bases are unpaired. The 'pU' array needs to be large enough to hold  $n+1$  float\* entries, where n is the sequence length.

If an array dpp2 is supplied, the probability of base pair (i,j) given that there already exists a base pair (i+1,j-1) is also computed and saved in this array. If pUfp is given (i.e. not NULL), pU is not saved but put out immediately. If spup is given (i.e. is not NULL), the pair probabilities in pl are not saved but put out immediately.

Parameters

|                 |                                          |
|-----------------|------------------------------------------|
| <i>sequence</i> | RNA sequence                             |
| <i>winSize</i>  | size of the window                       |
| <i>pairSize</i> | maximum size of base pair                |
| <i>cutoffb</i>  | cutoffb for base pairs                   |
| <i>pU</i>       | array holding all unpaired probabilities |
| <i>dpp2</i>     | array of dependent pair probabilities    |
| <i>pUfp</i>     | file pointer for pU                      |
| <i>spup</i>     | file pointer for pair probabilities      |

**Returns**

list of pair probabilities

**16.92.2.3 putoutpU\_prob()**

```
void putoutpU_prob (
    double ** pU,
    int length,
    int ulength,
    FILE * fp,
    int energies )
#include <ViennaRNA/LPfold.h>
```

Writes the unpaired probabilities (pU) or opening energies into a file.

Can write either the unpaired probabilities (accessibilities) pU or the opening energies -log(pU)kT into a file

**Parameters**

|                 |                                       |
|-----------------|---------------------------------------|
| <i>pU</i>       | pair probabilities                    |
| <i>length</i>   | length of RNA sequence                |
| <i>ulength</i>  | maximum length of unpaired stretch    |
| <i>fp</i>       | file pointer of destination file      |
| <i>energies</i> | switch to put out as opening energies |

**16.92.2.4 putoutpU\_prob\_bin()**

```
void putoutpU_prob_bin (
    double ** pU,
    int length,
    int ulength,
    FILE * fp,
    int energies )
#include <ViennaRNA/LPfold.h>
```

Writes the unpaired probabilities (pU) or opening energies into a binary file.

Can write either the unpaired probabilities (accessibilities) pU or the opening energies -log(pU)kT into a file

**Parameters**

|                 |                                       |
|-----------------|---------------------------------------|
| <i>pU</i>       | pair probabilities                    |
| <i>length</i>   | length of RNA sequence                |
| <i>ulength</i>  | maximum length of unpaired stretch    |
| <i>fp</i>       | file pointer of destination file      |
| <i>energies</i> | switch to put out as opening energies |

**16.93 Deprecated Interface for Stochastic Backtracking****16.93.1 Detailed Description**

Collaboration diagram for Deprecated Interface for Stochastic Backtracking:

## Functions

- char \* [pbacktrack](#) (char \*sequence)  
*Sample a secondary structure from the Boltzmann ensemble according its probability.*
- char \* [pbacktrack5](#) (char \*sequence, int length)  
*Sample a sub-structure from the Boltzmann ensemble according its probability.*
- char \* [pbacktrack\\_circ](#) (char \*sequence)  
*Sample a secondary structure of a circular RNA from the Boltzmann ensemble according its probability.*

## Variables

- int [st\\_back](#)  
*Flag indicating that auxiliary arrays are needed throughout the computations. This is essential for stochastic backtracking.*

## 16.93.2 Function Documentation

### 16.93.2.1 [pbacktrack\(\)](#)

```
char * pbacktrack (
    char * sequence )
#include <ViennaRNA/part_func.h>
Sample a secondary structure from the Boltzmann ensemble according its probability.
```

#### Precondition

[st\\_back](#) has to be set to 1 before calling [pf\\_fold\(\)](#) or [pf\\_fold\\_par\(\)](#)  
[pf\\_fold\\_par\(\)](#) or [pf\\_fold\(\)](#) have to be called first to fill the partition function matrices

#### Parameters

|                          |                  |
|--------------------------|------------------|
| <a href="#">sequence</a> | The RNA sequence |
|--------------------------|------------------|

#### Returns

A sampled secondary structure in dot-bracket notation

### 16.93.2.2 [pbacktrack\\_circ\(\)](#)

```
char * pbacktrack_circ (
    char * sequence )
#include <ViennaRNA/part_func.h>
Sample a secondary structure of a circular RNA from the Boltzmann ensemble according its probability.
This function does the same as pbacktrack\(\) but assumes the RNA molecule to be circular
```

#### Precondition

[st\\_back](#) has to be set to 1 before calling [pf\\_fold\(\)](#) or [pf\\_fold\\_par\(\)](#)  
[pf\\_fold\\_par\(\)](#) or [pf\\_circ\\_fold\(\)](#) have to be called first to fill the partition function matrices

**Deprecated** Use [vrna\\_pbacktrack\(\)](#) instead.



## Parameters

|                       |                  |
|-----------------------|------------------|
| <code>sequence</code> | The RNA sequence |
|-----------------------|------------------|

## Returns

A sampled secondary structure in dot-bracket notation

### 16.93.3 Variable Documentation

#### 16.93.3.1 `st_back`

```
int st_back [extern]
#include <ViennaRNA/part_func.h>
```

Flag indicating that auxiliary arrays are needed throughout the computations. This is essential for stochastic backtracking.

Set this variable to 1 prior to a call of `pf_fold()` to ensure that all matrices needed for stochastic backtracking are filled in the forward recursions

**Deprecated** set the `uniq_ML` flag in `vrna_md_t` before passing it to `vrna_fold_compound()`.

## See also

[pbacktrack\(\)](#), [pbacktrack\\_circ](#)

## 16.94 Deprecated Interface for Multiple Sequence Alignment Utilities

### 16.94.1 Detailed Description

Collaboration diagram for Deprecated Interface for Multiple Sequence Alignment Utilities:

#### Typedefs

- typedef struct [vrna\\_pinfo\\_s](#) `pair_info`  
*Old typename of [vrna\\_pinfo\\_s](#).*

#### Functions

- int [get\\_mpi](#) (char \*Aseq[], int n\_seq, int length, int \*mini)  
*Get the mean pairwise identity in steps from ?to?(ident)*
- void [encode\\_al\\_i\\_sequence](#) (const char \*sequence, short \*S, short \*s5, short \*s3, char \*ss, unsigned short \*as, int [circ](#))  
*Get arrays with encoded sequence of the alignment.*
- void [alloc\\_sequence\\_arrays](#) (const char \*\*sequences, short \*\*\*S, short \*\*\*S5, short \*\*\*S3, unsigned short \*\*\*a2s, char \*\*\*Ss, int [circ](#))  
*Allocate memory for sequence array used to deal with aligned sequences.*
- void [free\\_sequence\\_arrays](#) (unsigned int n\_seq, short \*\*\*S, short \*\*\*S5, short \*\*\*S3, unsigned short \*\*\*a2s, char \*\*\*Ss)  
*Free the memory of the sequence arrays used to deal with aligned sequences.*

### 16.94.2 Typedef Documentation

### 16.94.2.1 pair\_info

```
typedef struct vrna_pinfo_s pair_info
#include <ViennaRNA/utils/alignments.h>
Old typename of vrna_pinfo_s.
```

**Deprecated** Use `vrna_pinfo_t` instead!

## 16.94.3 Function Documentation

### 16.94.3.1 get\_mpi()

```
int get_mpi (
    char * Alseq[],
    int n_seq,
    int length,
    int * mini )
#include <ViennaRNA/utils/alignments.h>
Get the mean pairwise identity in steps from ?to?(ident)
```

**Deprecated** Use `vrna_aln_mpi()` as a replacement

#### Parameters

|               |                                          |
|---------------|------------------------------------------|
| <i>Alseq</i>  |                                          |
| <i>n_seq</i>  | The number of sequences in the alignment |
| <i>length</i> | The length of the alignment              |
| <i>mini</i>   |                                          |

#### Returns

The mean pairwise identity

### 16.94.3.2 encode\_al\_sequence()

```
void encode_al_sequence (
    const char * sequence,
    short * S,
    short * s5,
    short * s3,
    char * ss,
    unsigned short * as,
    int circ )
#include <ViennaRNA/utils/alignments.h>
```

Get arrays with encoded sequence of the alignment.

this function assumes that in S, S5, s3, ss and as enough space is already allocated (size must be at least sequence length+2)

#### Parameters

|                 |                                                                         |
|-----------------|-------------------------------------------------------------------------|
| <i>sequence</i> | The gapped sequence from the alignment                                  |
| <i>S</i>        | pointer to an array that holds encoded sequence                         |
| <i>s5</i>       | pointer to an array that holds the next base 5' of alignment position i |
| <i>s3</i>       | pointer to an array that holds the next base 3' of alignment position i |

## Parameters

|             |                                                                |
|-------------|----------------------------------------------------------------|
| <i>ss</i>   |                                                                |
| <i>as</i>   |                                                                |
| <i>circ</i> | assume the molecules to be circular instead of linear (circ=0) |

**16.94.3.3 alloc\_sequence\_arrays()**

```
void alloc_sequence_arrays (
    const char ** sequences,
    short *** S,
    short *** S5,
    short *** S3,
    unsigned short *** a2s,
    char *** Ss,
    int circ )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Allocate memory for sequence array used to deal with aligned sequences.

Note that these arrays will also be initialized according to the sequence alignment given

See also

[free\\_sequence\\_arrays\(\)](#)

## Parameters

|                  |                                                                                    |
|------------------|------------------------------------------------------------------------------------|
| <i>sequences</i> | The aligned sequences                                                              |
| <i>S</i>         | A pointer to the array of encoded sequences                                        |
| <i>S5</i>        | A pointer to the array that contains the next 5' nucleotide of a sequence position |
| <i>S3</i>        | A pointer to the array that contains the next 3' nucleotide of a sequence position |
| <i>a2s</i>       | A pointer to the array that contains the alignment to sequence position mapping    |
| <i>Ss</i>        | A pointer to the array that contains the ungapped sequence                         |
| <i>circ</i>      | assume the molecules to be circular instead of linear (circ=0)                     |

**16.94.3.4 free\_sequence\_arrays()**

```
void free_sequence_arrays (
    unsigned int n_seq,
    short *** S,
    short *** S5,
    short *** S3,
    unsigned short *** a2s,
    char *** Ss )
```

```
#include <ViennaRNA/utils/alignments.h>
```

Free the memory of the sequence arrays used to deal with aligned sequences.

This function frees the memory previously allocated with [alloc\\_sequence\\_arrays\(\)](#)

See also

[alloc\\_sequence\\_arrays\(\)](#)

## Parameters

|              |                                                                                    |
|--------------|------------------------------------------------------------------------------------|
| <i>n_seq</i> | The number of aligned sequences                                                    |
| <i>S</i>     | A pointer to the array of encoded sequences                                        |
| <i>S5</i>    | A pointer to the array that contains the next 5' nucleotide of a sequence position |
| <i>S3</i>    | A pointer to the array that contains the next 3' nucleotide of a sequence position |
| <i>a2s</i>   | A pointer to the array that contains the alignment to sequence position mapping    |
| <i>Ss</i>    | A pointer to the array that contains the ungapped sequence                         |

## 16.95 Deprecated Interface for Secondary Structure Utilities

### 16.95.1 Detailed Description

Collaboration diagram for Deprecated Interface for Secondary Structure Utilities:

#### Files

- file [RNAstruct.h](#)  
*Parsing and Coarse Graining of Structures.*

#### Functions

- char \* [b2HIT](#) (const char \*structure)  
*Converts the full structure from bracket notation to the HIT notation including root.*
- char \* [b2C](#) (const char \*structure)  
*Converts the full structure from bracket notation to the a coarse grained notation using the 'H' 'B' 'I' 'M' and 'R' identifiers.*
- char \* [b2Shapiro](#) (const char \*structure)  
*Converts the full structure from bracket notation to the weighted coarse grained notation using the 'H' 'B' 'I' 'M' 'S' 'E' and 'R' identifiers.*
- char \* [add\\_root](#) (const char \*structure)  
*Adds a root to an un-rooted tree in any except bracket notation.*
- char \* [expand\\_Shapiro](#) (const char \*coarse)  
*Inserts missing 'S' identifiers in unweighted coarse grained structures as obtained from [b2C\(\)](#).*
- char \* [expand\\_Full](#) (const char \*structure)  
*Convert the full structure from bracket notation to the expanded notation including root.*
- char \* [unexpand\\_Full](#) (const char \*ffull)  
*Restores the bracket notation from an expanded full or HIT tree, that is any tree using only identifiers 'U' 'P' and 'R'.*
- char \* [unweight](#) (const char \*wcoarse)  
*Strip weights from any weighted tree.*
- void [unexpand\\_aligned\\_F](#) (char \*align[2])  
*Converts two aligned structures in expanded notation.*
- void [parse\\_structure](#) (const char \*structure)  
*Collects a statistic of structure elements of the full structure in bracket notation.*
- char \* [pack\\_structure](#) (const char \*struc)  
*Pack secondary secondary structure, 5:1 compression using base 3 encoding.*
- char \* [unpack\\_structure](#) (const char \*packed)  
*Unpack secondary structure previously packed with [pack\\_structure\(\)](#)*
- short \* [make\\_pair\\_table](#) (const char \*structure)  
*Create a pair table of a secondary structure.*
- short \* [copy\\_pair\\_table](#) (const short \*pt)

*Get an exact copy of a pair table.*

- short \* [alimake\\_pair\\_table](#) (const char \*structure)
- short \* [make\\_pair\\_table\\_snoop](#) (const char \*structure)
- int [bp\\_distance](#) (const char \*str1, const char \*str2)

*Compute the "base pair" distance between two secondary structures s1 and s2.*

- unsigned int \* [make\\_referenceBP\\_array](#) (short \*reference\_pt, unsigned int turn)

*Make a reference base pair count matrix.*

- unsigned int \* [compute\\_BPdifferences](#) (short \*pt1, short \*pt2, unsigned int turn)

*Make a reference base pair distance matrix.*

- void [parenthesis\\_structure](#) (char \*structure, [vrna\\_bp\\_stack\\_t](#) \*bp, int length)

*Create a dot-bracket/parenthesis structure from backtracking stack.*

- void [parenthesis\\_zuker](#) (char \*structure, [vrna\\_bp\\_stack\\_t](#) \*bp, int length)

*Create a dot-bracket/parenthesis structure from backtracking stack obtained by zuker suboptimal calculation in cofold.c.*

- void [bppm\\_to\\_structure](#) (char \*structure, [FLT\\_OR\\_DBL](#) \*pr, unsigned int length)

*Create a dot-bracket like structure string from base pair probability matrix.*

- char [bppm\\_symbol](#) (const float \*x)

*Get a pseudo dot bracket notation for a given probability information.*

## Variables

- int **loop\_size** [2000]  
*contains a list of all loop sizes. loop\_size[0] contains the number of external bases.*
- int **helix\_size** [2000]  
*contains a list of all stack sizes.*
- int **loop\_degree** [2000]  
*contains the corresponding list of loop degrees.*
- int **loops**  
*contains the number of loops ( and therefore of stacks ).*
- int **unpaired**  
*contains the number of unpaired bases.*
- int **pairs**  
*contains the number of base pairs in the last parsed structure.*

## 16.95.2 Function Documentation

### 16.95.2.1 b2HIT()

```
char * b2HIT (
    const char * structure )
#include <ViennaRNA/RNAstruct.h>
```

Converts the full structure from bracket notation to the HIT notation including root.

**Deprecated** See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_HIT](#) for a replacement

#### Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

## Returns

### 16.95.2.2 b2C()

```
char * b2C (
    const char * structure )
#include <ViennaRNA/RNAstruct.h>
```

Converts the full structure from bracket notation to the a coarse grained notation using the 'H' 'B' 'I' 'M' and 'R' identifiers.

**Deprecated** See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_SHORT](#) for a replacement

## Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

## Returns

### 16.95.2.3 b2Shapiro()

```
char * b2Shapiro (
    const char * structure )
#include <ViennaRNA/RNAstruct.h>
```

Converts the full structure from bracket notation to the *weighted* coarse grained notation using the 'H' 'B' 'I' 'M' 'S' 'E' and 'R' identifiers.

**Deprecated** See [vrna\\_db\\_to\\_tree\\_string\(\)](#) and [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_WEIGHT](#) for a replacement

## Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

## Returns

### 16.95.2.4 add\_root()

```
char * add_root (
    const char * structure )
#include <ViennaRNA/RNAstruct.h>
```

Adds a root to an un-rooted tree in any except bracket notation.

## Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

## Returns

**16.95.2.5 expand\_Shapiro()**

```
char * expand_Shapiro (
    const char * coarse )
#include <ViennaRNA/RNAstruct.h>
```

Inserts missing 'S' identifiers in unweighted coarse grained structures as obtained from [b2C\(\)](#).

## Parameters

|               |  |
|---------------|--|
| <i>coarse</i> |  |
|---------------|--|

## Returns

**16.95.2.6 expand\_Full()**

```
char * expand_Full (
    const char * structure )
#include <ViennaRNA/RNAstruct.h>
```

Convert the full structure from bracket notation to the expanded notation including root.

## Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

## Returns

**16.95.2.7 unexpand\_Full()**

```
char * unexpand_Full (
    const char * ffull )
#include <ViennaRNA/RNAstruct.h>
```

Restores the bracket notation from an expanded full or HIT tree, that is any tree using only identifiers 'U' 'P' and 'R'.

## Parameters

|              |  |
|--------------|--|
| <i>ffull</i> |  |
|--------------|--|

## Returns

**16.95.2.8 unweight()**

```
char * unweight (
    const char * wcoarse )
```

```
#include <ViennaRNA/RNAstruct.h>
Strip weights from any weighted tree.
```

#### Parameters

|                |  |
|----------------|--|
| <i>wcoarse</i> |  |
|----------------|--|

#### Returns

### 16.95.2.9 unexpand\_aligned\_F()

```
void unexpand_aligned_F (
    char * align[2] )
```

```
#include <ViennaRNA/RNAstruct.h>
```

Converts two aligned structures in expanded notation.

Takes two aligned structures as produced by [tree\\_edit\\_distance\(\)](#) function back to bracket notation with '\_' as the gap character. The result overwrites the input.

#### Parameters

|              |  |
|--------------|--|
| <i>align</i> |  |
|--------------|--|

### 16.95.2.10 parse\_structure()

```
void parse_structure (
    const char * structure )
```

```
#include <ViennaRNA/RNAstruct.h>
```

Collects a statistic of structure elements of the full structure in bracket notation.

The function writes to the following global variables: [loop\\_size](#), [loop\\_degree](#), [helix\\_size](#), [loops](#), [pairs](#), [unpaired](#)

#### Parameters

|                  |  |
|------------------|--|
| <i>structure</i> |  |
|------------------|--|

### 16.95.2.11 pack\_structure()

```
char * pack_structure (
    const char * struc )
```

```
#include <ViennaRNA/utils/structures.h>
```

Pack secondary secondary structure, 5:1 compression using base 3 encoding.

Returns a binary string encoding of the secondary structure using a 5:1 compression scheme. The string is NULL terminated and can therefore be used with standard string functions such as `strcmp()`. Useful for programs that need to keep many structures in memory.

**Deprecated** Use [vrna\\_db\\_pack\(\)](#) as a replacement

#### Parameters

|              |                                                 |
|--------------|-------------------------------------------------|
| <i>struc</i> | The secondary structure in dot-bracket notation |
|--------------|-------------------------------------------------|



**Returns**

The binary encoded structure

**16.95.2.12 unpack\_structure()**

```
char * unpack_structure (
    const char * packed )
```

```
#include <ViennaRNA/utils/structures.h>
```

Unpack secondary structure previously packed with [pack\\_structure\(\)](#)

Translate a compressed binary string produced by [pack\\_structure\(\)](#) back into the familiar dot-bracket notation.

**Deprecated** Use [vrna\\_db\\_unpack\(\)](#) as a replacement

**Parameters**

|               |                                               |
|---------------|-----------------------------------------------|
| <i>packed</i> | The binary encoded packed secondary structure |
|---------------|-----------------------------------------------|

**Returns**

The unpacked secondary structure in dot-bracket notation

**16.95.2.13 make\_pair\_table()**

```
short * make_pair_table (
    const char * structure )
```

```
#include <ViennaRNA/utils/structures.h>
```

Create a pair table of a secondary structure.

Returns a newly allocated table, such that table[i]=j if (i,j) pair or 0 if i is unpaired, table[0] contains the length of the structure.

**Deprecated** Use [vrna\\_ptable\(\)](#) instead

**Parameters**

|                  |                                                 |
|------------------|-------------------------------------------------|
| <i>structure</i> | The secondary structure in dot-bracket notation |
|------------------|-------------------------------------------------|

**Returns**

A pointer to the created pair\_table

**16.95.2.14 copy\_pair\_table()**

```
short * copy_pair_table (
    const short * pt )
```

```
#include <ViennaRNA/utils/structures.h>
```

Get an exact copy of a pair table.

**Deprecated** Use [vrna\\_ptable\\_copy\(\)](#) instead

## Parameters

|           |                             |
|-----------|-----------------------------|
| <i>pt</i> | The pair table to be copied |
|-----------|-----------------------------|

## Returns

A pointer to the copy of 'pt'

**16.95.2.15 alimake\_pair\_table()**

```
short * alimake_pair_table (
    const char * structure )
#include <ViennaRNA/utils/structures.h>
Pair table for snoop align
```

**Deprecated** Use `vrna_pt.ali_get()` instead!

**16.95.2.16 make\_pair\_table\_snoop()**

```
short * make_pair_table_snoop (
    const char * structure )
#include <ViennaRNA/utils/structures.h>
returns a newly allocated table, such that: table[i]=j if (i,j) pair or 0 if i is unpaired, table[0] contains the length of the
structure. The special pseudoknotted H/ACA-mRNA structure is taken into account.
```

**Deprecated** Use `vrna_pt.snoop_get()` instead!

**16.95.2.17 bp\_distance()**

```
int bp_distance (
    const char * str1,
    const char * str2 )
#include <ViennaRNA/utils/structures.h>
Compute the "base pair" distance between two secondary structures s1 and s2.
The sequences should have the same length. dist = number of base pairs in one structure but not in the other same
as edit distance with open-pair close-pair as move-set
```

**Deprecated** Use `vrna_bp_distance` instead

## Parameters

|             |                                          |
|-------------|------------------------------------------|
| <i>str1</i> | First structure in dot-bracket notation  |
| <i>str2</i> | Second structure in dot-bracket notation |

## Returns

The base pair distance between str1 and str2

**16.95.2.18 make\_referenceBP\_array()**

```
unsigned int * make_referenceBP_array (
```

```

        short * reference_pt,
        unsigned int turn )
#include <ViennaRNA/utils/structures.h>

```

Make a reference base pair count matrix.

Get an upper triangular matrix containing the number of basepairs of a reference structure for each interval [i,j] with i<j. Access it via iindx!!!

**Deprecated** Use `vrna_refBPcnt_matrix()` instead

#### 16.95.2.19 compute\_BPdifferences()

```

unsigned int * compute_BPdifferences (
        short * pt1,
        short * pt2,
        unsigned int turn )
#include <ViennaRNA/utils/structures.h>

```

Make a reference base pair distance matrix.

Get an upper triangular matrix containing the base pair distance of two reference structures for each interval [i,j] with i<j. Access it via iindx!!!

**Deprecated** Use `vrna_refBPdist_matrix()` instead

#### 16.95.2.20 parenthesis\_structure()

```

void parenthesis_structure (
        char * structure,
        vrna_bp_stack_t * bp,
        int length )
#include <ViennaRNA/utils/structures.h>

```

Create a dot-bracket/parenthesis structure from backtracking stack.

**Deprecated** use `vrna_parenthesis_structure()` instead

#### Note

This function is threadsafe

#### 16.95.2.21 parenthesis\_zuker()

```

void parenthesis_zuker (
        char * structure,
        vrna_bp_stack_t * bp,
        int length )
#include <ViennaRNA/utils/structures.h>

```

Create a dot-bracket/parenthesis structure from backtracking stack obtained by zuker suboptimal calculation in cofold.c.

**Deprecated** use `vrna_parenthesis_zuker` instead

#### Note

This function is threadsafe

### 16.95.2.22 `bppm_to_structure()`

```
void bppm_to_structure (
    char * structure,
    FLT_OR_DBL * pr,
    unsigned int length )
#include <ViennaRNA/utils/structures.h>
```

Create a dot-bracket like structure string from base pair probability matrix.

**Deprecated** Use `vrna_db_from_probs()` instead!

### 16.95.2.23 `bppm_symbol()`

```
char bppm_symbol (
    const float * x )
#include <ViennaRNA/utils/structures.h>
```

Get a pseudo dot bracket notation for a given probability information.

**Deprecated** Use `vrna_bpp_symbol()` instead!

## 16.96 Deprecated Interface for Plotting Utilities

### 16.96.1 Detailed Description

Collaboration diagram for Deprecated Interface for Plotting Utilities:

#### Data Structures

- struct [COORDINATE](#)  
*this is a workaround for the SWIG Perl Wrapper RNA plot function that returns an array of type [COORDINATE](#) More...*

#### Functions

- int [PS\\_color\\_aln](#) (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])  
*Produce PostScript sequence alignment color-annotated by consensus structure.*
- int [aliPS\\_color\\_aln](#) (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])  
*PS\_color\_aln for duplexes.*
- int [simple\\_xy\\_coordinates](#) (short \*pair\_table, float \*X, float \*Y)  
*Calculate nucleotide coordinates for secondary structure plot the Simple way*
- int [simple\\_circplot\\_coordinates](#) (short \*pair\_table, float \*x, float \*y)  
*Calculate nucleotide coordinates for Circular Plot*

#### Variables

- int [rna\\_plot\\_type](#)  
*Switch for changing the secondary structure layout algorithm.*

### 16.96.2 Data Structure Documentation

#### 16.96.2.1 struct `COORDINATE`

this is a workaround for the SWIG Perl Wrapper RNA plot function that returns an array of type [COORDINATE](#)

### 16.96.3 Function Documentation

### 16.96.3.1 PS\_color\_aln()

```
int PS_color_aln (
    const char * structure,
    const char * filename,
    const char * seqs[],
    const char * names[] )
#include <ViennaRNA/plotting/alignments.h>
Produce PostScript sequence alignment color-annotated by consensus structure.
```

**Deprecated** Use [vrna\\_file\\_PS\\_aln\(\)](#) instead!

### 16.96.3.2 aliPS\_color\_aln()

```
int aliPS_color_aln (
    const char * structure,
    const char * filename,
    const char * seqs[],
    const char * names[] )
#include <ViennaRNA/plotting/alignments.h>
PS_color_aln for duplexes.
```

**Deprecated** Use [vrna\\_file\\_PS\\_aln\(\)](#) instead!

### 16.96.3.3 simple\_xy\_coordinates()

```
int simple_xy_coordinates (
    short * pair_table,
    float * X,
    float * Y )
#include <ViennaRNA/plotting/layouts.h>
Calculate nucleotide coordinates for secondary structure plot the Simple way
```

See also

[make\\_pair\\_table\(\)](#), [rna\\_plot\\_type](#), [simple\\_circplot\\_coordinates\(\)](#), [naview\\_xy\\_coordinates\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#), [vrna\\_file\\_PS\\_rnaplot](#), [svg\\_rna\\_plot\(\)](#)

**Deprecated** Consider switching to [vrna\\_plot\\_coords\\_simple\\_pt\(\)](#) instead!

#### Parameters

|                   |                                                                             |
|-------------------|-----------------------------------------------------------------------------|
| <i>pair_table</i> | The pair table of the secondary structure                                   |
| <i>X</i>          | a pointer to an array with enough allocated space to hold the x coordinates |
| <i>Y</i>          | a pointer to an array with enough allocated space to hold the y coordinates |

#### Returns

length of sequence on success, 0 otherwise

### 16.96.3.4 simple\_circplot\_coordinates()

```
int simple_circplot_coordinates (
    short * pair_table,
```

```

        float * x,
        float * y )
#include <ViennaRNA/plotting/layouts.h>

```

Calculate nucleotide coordinates for *Circular Plot*

This function calculates the coordinates of nucleotides mapped in equal distances onto a unit circle.

#### Note

In order to draw nice arcs using quadratic bezier curves that connect base pairs one may calculate a second tangential point  $P^t$  in addition to the actual  $R^2$  coordinates. the simplest way to do so may be to compute a radius scaling factor  $rs$  in the interval  $[0, 1]$  that weights the proportion of base pair span to the actual length of the sequence. This scaling factor can then be used to calculate the coordinates for  $P^t$ , i.e.  $P_x^t[i] = X[i] * rs$  and  $P_y^t[i] = Y[i] * rs$ .

#### See also

[make\\_pair\\_table\(\)](#), [rna\\_plot\\_type](#), [simple\\_xy\\_coordinates\(\)](#), [naview\\_xy\\_coordinates\(\)](#), [vrna\\_file\\_PS\\_rnaplot\\_a\(\)](#), [vrna\\_file\\_PS\\_rnaplot](#), [svg\\_rna\\_plot\(\)](#)

**Deprecated** Consider switching to [vrna\\_plot\\_coords\\_circular\\_pt\(\)](#) instead!

#### Parameters

|                   |                                                                             |
|-------------------|-----------------------------------------------------------------------------|
| <i>pair_table</i> | The pair table of the secondary structure                                   |
| <i>x</i>          | a pointer to an array with enough allocated space to hold the x coordinates |
| <i>y</i>          | a pointer to an array with enough allocated space to hold the y coordinates |

#### Returns

length of sequence on success, 0 otherwise

## 16.96.4 Variable Documentation

### 16.96.4.1 rna\_plot\_type

```

int rna_plot_type [extern]
#include <ViennaRNA/plotting/layouts.h>

```

Switch for changing the secondary structure layout algorithm.

Current possibility are 0 for a simple radial drawing or 1 for the modified radial drawing taken from the *naview* program of [5].

#### Note

To provide thread safety please do not rely on this global variable in future implementations but pass a plot type flag directly to the function that decides which layout algorithm it may use!

#### See also

[VRNA\\_PLOT\\_TYPE\\_SIMPLE](#), [VRNA\\_PLOT\\_TYPE\\_NAVIEW](#), [VRNA\\_PLOT\\_TYPE\\_CIRCULAR](#)

## 16.97 Deprecated Interface for (Re-)folding Paths, Saddle Points, and Energy Barriers

### 16.97.1 Detailed Description

Collaboration diagram for Deprecated Interface for (Re-)folding Paths, Saddle Points, and Energy Barriers:

## Typedefs

- typedef struct [vrna\\_path\\_s](#) [path\\_t](#)  
Old typename of [vrna\\_path\\_s](#).

## Functions

- int [find\\_saddle](#) (const char \*seq, const char \*s1, const char \*s2, int width)  
Find energy of a saddle point between 2 structures (search only direct path)
- void [free\\_path](#) ([vrna\\_path\\_t](#) \*path)  
Free memory allocated by [get\\_path\(\)](#) function.
- [vrna\\_path\\_t](#) \* [get\\_path](#) (const char \*seq, const char \*s1, const char \*s2, int width)  
Find refolding path between 2 structures (search only direct path)

## 16.97.2 Typedef Documentation

### 16.97.2.1 path\_t

```
typedef struct vrna\_path\_s path\_t
#include <ViennaRNA/landscape/paths.h>
Old typename of vrna\_path\_s.
```

**Deprecated** Use [vrna\\_path\\_t](#) instead!

## 16.97.3 Function Documentation

### 16.97.3.1 find\_saddle()

```
int find\_saddle (
    const char * seq,
    const char * s1,
    const char * s2,
    int width )
#include <ViennaRNA/landscape/findpath.h>
Find energy of a saddle point between 2 structures (search only direct path)
```

**Deprecated** Use [vrna\\_path\\_findpath\\_saddle\(\)](#) instead!

#### Parameters

|                       |                                                                                                                  |
|-----------------------|------------------------------------------------------------------------------------------------------------------|
| <a href="#">seq</a>   | RNA sequence                                                                                                     |
| <a href="#">s1</a>    | A pointer to the character array where the first secondary structure in dot-bracket notation will be written to  |
| <a href="#">s2</a>    | A pointer to the character array where the second secondary structure in dot-bracket notation will be written to |
| <a href="#">width</a> | integer how many strutures are being kept during the search                                                      |

#### Returns

the saddle energy in 10cal/mol

### 16.97.3.2 free\_path()

```
void free_path (
    vrna_path_t * path )
#include <ViennaRNA/landscape/findpath.h>
Free memory allocated by get_path() function.
```

**Deprecated** Use `vrna_path_free()` instead!

#### Parameters

|             |                               |
|-------------|-------------------------------|
| <i>path</i> | pointer to memory to be freed |
|-------------|-------------------------------|

### 16.97.3.3 get\_path()

```
vrna_path_t * get_path (
    const char * seq,
    const char * s1,
    const char * s2,
    int width )
#include <ViennaRNA/landscape/findpath.h>
Find refolding path between 2 structures (search only direct path)
```

**Deprecated** Use `vrna_path_findpath()` instead!

#### Parameters

|              |                                                                                                                  |
|--------------|------------------------------------------------------------------------------------------------------------------|
| <i>seq</i>   | RNA sequence                                                                                                     |
| <i>s1</i>    | A pointer to the character array where the first secondary structure in dot-bracket notation will be written to  |
| <i>s2</i>    | A pointer to the character array where the second secondary structure in dot-bracket notation will be written to |
| <i>width</i> | integer how many structures are being kept during the search                                                     |

#### Returns

direct refolding path between two structures



## Chapter 17

# Data Structure Documentation

### 17.1 `_struct_en` Struct Reference

Data structure for [energy\\_of\\_move\(\)](#)

#### 17.1.1 Detailed Description

Data structure for [energy\\_of\\_move\(\)](#)

The documentation for this struct was generated from the following file:

- ViennaRNA/move\_set.h

### 17.2 `LIST` Struct Reference

Collaboration diagram for `LIST`:

The documentation for this struct was generated from the following file:

- ViennaRNA/datastructures/lists.h

### 17.3 `LST_BUCKET` Struct Reference

Collaboration diagram for `LST_BUCKET`:

The documentation for this struct was generated from the following file:

- ViennaRNA/datastructures/lists.h

### 17.4 `Postorder_list` Struct Reference

Postorder data structure.

#### 17.4.1 Detailed Description

Postorder data structure.

The documentation for this struct was generated from the following file:

- ViennaRNA/[dist\\_vars.h](#)

### 17.5 `swString` Struct Reference

Some other data structure.

### 17.5.1 Detailed Description

Some other data structure.

The documentation for this struct was generated from the following file:

- [ViennaRNA/dist\\_vars.h](#)

## 17.6 Tree Struct Reference

[Tree](#) data structure.

Collaboration diagram for Tree:

### 17.6.1 Detailed Description

[Tree](#) data structure.

The documentation for this struct was generated from the following file:

- [ViennaRNA/dist\\_vars.h](#)

## 17.7 TwoDpfold\_vars Struct Reference

Variables compound for 2Dfold partition function folding.

Collaboration diagram for TwoDpfold\_vars:

### Data Fields

- char \* **ptype**  
*Precomputed array of pair types.*
- char \* **sequence**  
*The input sequence*
- short \* **S1**  
*The input sequences in numeric form.*
- unsigned int **maxD1**  
*Maximum allowed base pair distance to first reference.*
- unsigned int **maxD2**  
*Maximum allowed base pair distance to second reference.*
- int \* **my\_iindx**  
*Index for moving in quadratic distancy dimensions.*
- int \* **jindx**  
*Index for moving in the triangular matrix qm1.*
- unsigned int \* **referenceBPs1**  
*Matrix containing number of basepairs of reference structure1 in interval [i,j].*
- unsigned int \* **referenceBPs2**  
*Matrix containing number of basepairs of reference structure2 in interval [i,j].*
- unsigned int \* **bpdist**  
*Matrix containing base pair distance of reference structure 1 and 2 on interval [i,j].*
- unsigned int \* **mm1**  
*Maximum matching matrix, reference struct 1 disallowed.*
- unsigned int \* **mm2**  
*Maximum matching matrix, reference struct 2 disallowed.*

### 17.7.1 Detailed Description

Variables compound for 2Dfold partition function folding.

**Deprecated** This data structure will be removed from the library soon! Use [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

The documentation for this struct was generated from the following file:

- [ViennaRNA/2Dpfold.h](#)

## 17.8 vrna\_dimer\_conc\_s Struct Reference

Data structure for concentration dependency computations.

### Data Fields

- double **Ac\_start**  
*start concentration A*
- double **Bc\_start**  
*start concentration B*
- double **ABc**  
*End concentration AB.*

### 17.8.1 Detailed Description

Data structure for concentration dependency computations.

The documentation for this struct was generated from the following file:

- [ViennaRNA/concentrations.h](#)

## 17.9 vrna\_sc\_bp\_storage\_t Struct Reference

A base pair constraint.

### 17.9.1 Detailed Description

A base pair constraint.

The documentation for this struct was generated from the following file:

- [ViennaRNA/constraints/soft.h](#)

## 17.10 vrna\_structured\_domains\_s Struct Reference

The documentation for this struct was generated from the following file:

- [ViennaRNA/structured\\_domains.h](#)

## 17.11 vrna\_subopt\_sol\_s Struct Reference

Solution element from subopt.c.

### Data Fields

- float **energy**  
*Free Energy of structure in kcal/mol.*
- char \* **structure**  
*Structure in dot-bracket notation.*

### 17.11.1 Detailed Description

Solution element from subopt.c.

The documentation for this struct was generated from the following file:

- ViennaRNA/[subopt.h](#)

## 17.12 vrna\_unstructured\_domain\_motif\_s Struct Reference

The documentation for this struct was generated from the following file:

- ViennaRNA/[unstructured\\_domains.h](#)

# Chapter 18

## File Documentation

### 18.1 ViennaRNA/2Dfold.h File Reference

MFE structures for base pair distance classes.

Include dependency graph for 2Dfold.h:

### 18.2 2Dfold.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_TWO_D_FOLD_H
2 #define VIENNA_RNA_PACKAGE_TWO_D_FOLD_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <ViennaRNA/fold_compound.h>
17 #include <ViennaRNA/datastructures/basic.h>
18 #include <ViennaRNA/params/basic.h>
19
20 typedef struct vrna_sol_TwoD_t {
21     int k;
22     int l;
23     float en;
24     char *s;
25 } vrna_sol_TwoD_t;
26
27 vrna_sol_TwoD_t *
28 vrna_mfe_TwoD(vrna_fold_compound_t *vc,
29               int distance1,
30               int distance2);
31
32 char *
33 vrna_backtrack5_TwoD(vrna_fold_compound_t *vc,
34                      int k,
35                      int l,
36                      unsigned int j);
37
38 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
39 #define TwoDfold_solution vrna_sol_TwoD_t /* restore compatibility of struct rename */
40
41 typedef struct TwoDfold_vars {
42     vrna_param_t *P;
43     int do_backtrack;
44     char *ptype;
45     char *sequence;
46     short *S, *S1;
47     unsigned int maxD1;
48     unsigned int maxD2;
49 }
```

```

140 unsigned int      *mm1;
141 unsigned int      *mm2;
143 int               *my_indx;
145 double           temperature;
146
147 unsigned int      *referenceBPs1;
148 unsigned int      *referenceBPs2;
149 unsigned int      *bpdist;
151 short            *reference_pt1;
152 short            *reference_pt2;
153 int              circ;
154 int              dangles;
155 unsigned int      seq_length;
156
157 int              ***E_F5;
158 int              ***E_F3;
159 int              ***E_C;
160 int              ***E_M;
161 int              ***E_M1;
162 int              ***E_M2;
163
164 int              **E_Fc;
165 int              **E_FcH;
166 int              **E_FcI;
167 int              **E_FcM;
168
169 int              *l_min_values;
170 int              *l_max_values;
171 int              *k_min_values;
172 int              *k_max_values;
173
174 int              *l_min_values_m;
175 int              *l_max_values_m;
176 int              *k_min_values_m;
177 int              *k_max_values_m;
178
179 int              *l_min_values_m1;
180 int              *l_max_values_m1;
181 int              *k_min_values_m1;
182 int              *k_max_values_m1;
183
184 int              *l_min_values_f;
185 int              *l_max_values_f;
186 int              *k_min_values_f;
187 int              *k_max_values_f;
188
189 int              *l_min_values_f3;
190 int              *l_max_values_f3;
191 int              *k_min_values_f3;
192 int              *k_max_values_f3;
193
194 int              *l_min_values_m2;
195 int              *l_max_values_m2;
196 int              *k_min_values_m2;
197 int              *k_max_values_m2;
198
199 int              *l_min_values_fc;
200 int              *l_max_values_fc;
201 int              *k_min_values_fc;
202 int              *k_max_values_fc;
203
204 int              *l_min_values_fcH;
205 int              *l_max_values_fcH;
206 int              *k_min_values_fcH;
207 int              *k_max_values_fcH;
208
209 int              *l_min_values_fcI;
210 int              *l_max_values_fcI;
211 int              *k_min_values_fcI;
212 int              *k_max_values_fcI;
213
214 int              *l_min_values_fcM;
215 int              *l_max_values_fcM;
216 int              *k_min_values_fcM;
217 int              *k_max_values_fcM;
218
219 /* auxiliary arrays for remaining set of coarse graining (k,l) > (k_max, l_max) */
220 int              *E_F5_rem;
221 int              *E_F3_rem;
222 int              *E_C_rem;
223 int              *E_M_rem;
224 int              *E_M1_rem;
225 int              *E_M2_rem;
226
227 int              E_Fc_rem;
228 int              E_FcH_rem;
229 int              E_FcI_rem;

```

```

230  int                      E_FcM_rem;
231
232 #ifdef COUNT_STATES
233  unsigned long            ***N_F5;
234  unsigned long            ***N_C;
235  unsigned long            ***N_M;
236  unsigned long            ***N_M1;
237 #endif
238
239  vrna_fold_compound_t     *compatibility;
240 } TwoDfold_vars;
241
242 DEPRECATED(TwoDfold_vars *
243  get_TwoDfold_variables(const char *seq,
244                        const char *structure1,
245                        const char *structure2,
246                        int circ),
247  "Use the new API and corresponding functions vrna_fold_compound_TwoD(), etc. instead");
248
249 DEPRECATED(void
250  destroy_TwoDfold_variables(TwoDfold_vars *our_variables),
251  "Use the new API and vrna_fold_compound_free() instead");
252
253 DEPRECATED(TwoDfold_solution *
254  TwoDfoldList(TwoDfold_vars *vars,
255              int distance1,
256              int distance2),
257  "Use the new API and vrna_mfe_TwoD() instead");
258
259 DEPRECATED(char *TwoDfold_backtrack_f5(unsigned int j,
260                                       int k,
261                                       int l,
262                                       TwoDfold_vars *vars),
263  "Use the new API and vrna_backtrack5_TwoD() instead");
264
265 DEPRECATED(TwoDfold_solution **TwoDfold(TwoDfold_vars *our_variables,
266                                       int distance1,
267                                       int distance2),
268  "Use the new API and vrna_mfe_TwoD() instead");
269
270 #endif
271 #endif

```

## 18.3 ViennaRNA/2Dpfold.h File Reference

Partition function implementations for base pair distance classes.  
Include dependency graph for 2Dpfold.h:

### Data Structures

- struct [vrna\\_sol\\_TwoD\\_pf\\_t](#)  
*Solution element returned from [vrna\\_pf\\_TwoD\(\)](#) [More...](#)*
- struct [TwoDfold\\_vars](#)  
*Variables compound for 2Dfold partition function folding.*

### Typedefs

- typedef struct [vrna\\_sol\\_TwoD\\_pf\\_t](#) [vrna\\_sol\\_TwoD\\_pf\\_t](#)  
*Solution element returned from [vrna\\_pf\\_TwoD\(\)](#)*

### Functions

- [vrna\\_sol\\_TwoD\\_pf\\_t \\* vrna\\_pf\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int maxDistance1, int maxDistance2)  
*Compute the partition function for all distance classes.*
- char \* [vrna\\_pbacktrack\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int d1, int d2)  
*Sample secondary structure representatives from a set of distance classes according to their Boltzmann probability.*
- char \* [vrna\\_pbacktrack5\\_TwoD](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int d1, int d2, unsigned int length)  
*Sample secondary structure representatives with a specified length from a set of distance classes according to their Boltzmann probability.*

- `TwoDpfold_vars * get_TwoDpfold_variables` (const char \*seq, const char \*structure1, char \*structure2, int circ)  
*Get a datastructure containing all necessary attributes and global folding switches.*
- void `destroy_TwoDpfold_variables` (TwoDpfold\_vars \*vars)  
*Free all memory occupied by a `TwoDpfold_vars` datastructure.*
- `vrna_sol_TwoD_pf_t * TwoDpfoldList` (TwoDpfold\_vars \*vars, int maxDistance1, int maxDistance2)  
*Compute the partition function for all distance classes.*
- char \* `TwoDpfold_pbacktrack` (TwoDpfold\_vars \*vars, int d1, int d2)  
*Sample secondary structure representatives from a set of distance classes according to their Boltzmann probability.*
- char \* `TwoDpfold_pbacktrack5` (TwoDpfold\_vars \*vars, int d1, int d2, unsigned int length)  
*Sample secondary structure representatives with a specified length from a set of distance classes according to their Boltzmann probability.*

### 18.3.1 Detailed Description

Partition function implementations for base pair distance classes.

### 18.3.2 Function Documentation

#### 18.3.2.1 get\_TwoDpfold\_variables()

```
TwoDpfold_vars * get_TwoDpfold_variables (
    const char * seq,
    const char * structure1,
    char * structure2,
    int circ )
```

Get a datastructure containing all necessary attributes and global folding switches.

This function prepares all necessary attributes and matrices etc which are needed for a call of `TwoDpfold()`. A snapshot of all current global model switches (dangles, temperature and so on) is done and stored in the returned datastructure. Additionally, all matrices that will hold the partition function values are prepared.

**Deprecated** Use the new API that relies on `vrna_fold_compound_t` and the corresponding functions `vrna_fold_compound_TwoD()`, `vrna_pf_TwoD()`, and `vrna_fold_compound_free()` instead!

#### Parameters

|                   |                                                                            |
|-------------------|----------------------------------------------------------------------------|
| <i>seq</i>        | the RNA sequence in uppercase format with letters from the alphabet {AUCG} |
| <i>structure1</i> | the first reference structure in dot-bracket notation                      |
| <i>structure2</i> | the second reference structure in dot-bracket notation                     |
| <i>circ</i>       | a switch indicating if the sequence is linear (0) or circular (1)          |

#### Returns

the datastructure containing all necessary partition function attributes

#### 18.3.2.2 destroy\_TwoDpfold\_variables()

```
void destroy_TwoDpfold_variables (
    TwoDpfold_vars * vars )
```

Free all memory occupied by a `TwoDpfold_vars` datastructure.

This function free's all memory occupied by a datastructure obtained from `get_TwoDpfold_variables()` or `get_TwoDpfold_variables_from_MFE()`



**Deprecated** Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

See also

[get\\_TwoDpfold\\_variables\(\)](#), [get\\_TwoDpfold\\_variables\\_from\\_MFE\(\)](#)

Parameters

|             |                                |
|-------------|--------------------------------|
| <i>vars</i> | the datastructure to be free'd |
|-------------|--------------------------------|

### 18.3.2.3 TwoDpfoldList()

```
vrna_sol_TwoD_pf_t * TwoDpfoldList (
    TwoDpfold_vars * vars,
    int maxDistance1,
    int maxDistance2 )
```

Compute the partition function for all distance classes.

This function computes the partition functions for all distance classes according the two reference structures specified in the datastructure 'vars'. Similar to [TwoDfold\(\)](#) the arguments `maxDistance1` and `maxDistance2` specify the maximum distance to both reference structures. A value of '-1' in either of them makes the appropriate distance restrictionless, i.e. all basepair distances to the reference are taken into account during computation. In case there is a restriction, the returned solution contains an entry where the attribute `k` is -1 contains the partition function for all structures exceeding the restriction. A values of `INF` in the attribute 'k' of the returned list denotes the end of the list

**Deprecated** Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

See also

[get\\_TwoDpfold\\_variables\(\)](#), [destroy\\_TwoDpfold\\_variables\(\)](#), [vrna\\_sol\\_TwoD\\_pf\\_t](#)

Parameters

|                     |                                                                            |
|---------------------|----------------------------------------------------------------------------|
| <i>vars</i>         | the datastructure containing all necessary folding attributes and matrices |
| <i>maxDistance1</i> | the maximum basepair distance to reference1 (may be -1)                    |
| <i>maxDistance2</i> | the maximum basepair distance to reference2 (may be -1)                    |

Returns

a list of partition funtions for the appropriate distance classes

### 18.3.2.4 TwoDpfold\_pbacktrack()

```
char * TwoDpfold_pbacktrack (
    TwoDpfold_vars * vars,
    int d1,
    int d2 )
```

Sample secondary structure representatives from a set of distance classes according to their Boltzmann probability. If the argument 'd1' is set to '-1', the structure will be backtracked in the distance class where all structures exceeding the maximum basepair distance to either of the references reside.

**Precondition**

The argument 'vars' must contain precalculated partition function matrices, i.e. a call to `TwoDpfold()` preceding this function is mandatory!

**Deprecated** Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), [vrna\\_pbacktrack\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

**See also**

`TwoDpfold()`

**Parameters**

|    |             |                                                                            |
|----|-------------|----------------------------------------------------------------------------|
| in | <i>vars</i> | the datastructure containing all necessary folding attributes and matrices |
| in | <i>d1</i>   | the distance to reference1 (may be -1)                                     |
| in | <i>d2</i>   | the distance to reference2                                                 |

**Returns**

A sampled secondary structure in dot-bracket notation

**18.3.2.5 TwoDpfold\_pbacktrack5()**

```
char * TwoDpfold_pbacktrack5 (
    TwoDpfold_vars * vars,
    int d1,
    int d2,
    unsigned int length )
```

Sample secondary structure representatives with a specified length from a set of distance classes according to their Boltzmann probability.

This function does essentially the same as [TwoDpfold\\_pbacktrack\(\)](#) with the only difference that partial structures, i.e. structures beginning from the 5' end with a specified length of the sequence, are backtracked

**Note**

This function does not work (since it makes no sense) for circular RNA sequences!

**Precondition**

The argument 'vars' must contain precalculated partition function matrices, i.e. a call to `TwoDpfold()` preceding this function is mandatory!

**Deprecated** Use the new API that relies on [vrna\\_fold\\_compound\\_t](#) and the corresponding functions [vrna\\_fold\\_compound\\_TwoD\(\)](#), [vrna\\_pf\\_TwoD\(\)](#), [vrna\\_pbacktrack5\\_TwoD\(\)](#), and [vrna\\_fold\\_compound\\_free\(\)](#) instead!

**See also**

[TwoDpfold\\_pbacktrack\(\)](#), `TwoDpfold()`

**Parameters**

|    |               |                                                                            |
|----|---------------|----------------------------------------------------------------------------|
| in | <i>vars</i>   | the datastructure containing all necessary folding attributes and matrices |
| in | <i>d1</i>     | the distance to reference1 (may be -1)                                     |
| in | <i>d2</i>     | the distance to reference2                                                 |
| in | <i>length</i> | the length of the structure beginning from the 5' end                      |

## Returns

A sampled secondary structure in dot-bracket notation

## 18.4 2Dpfold.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_TWO_D_PF_FOLD_H
2 #define VIENNA_RNA_PACKAGE_TWO_D_PF_FOLD_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(" ", msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <ViennaRNA/fold_compound.h>
17 #include <ViennaRNA/datastructures/basic.h>
18 #include <ViennaRNA/fold_compound.h>
19 #include <ViennaRNA/params/basic.h>
20
21 typedef struct vrna_sol_TwoD_pf_t {
22     int k;
23     int l;
24     FLT_OR_DBL q;
25 } vrna_sol_TwoD_pf_t;
26
27 vrna_sol_TwoD_pf_t *
28 vrna_pf_TwoD(vrna_fold_compound_t *vc,
29             int maxDistance1,
30             int maxDistance2);
31
32 /* End of group kl_neighborhood_pf */
33
34 char *
35 vrna_pbacktrack_TwoD(vrna_fold_compound_t *vc,
36                     int d1,
37                     int d2);
38
39 char *
40 vrna_pbacktrack5_TwoD(vrna_fold_compound_t *vc,
41                      int d1,
42                      int d2,
43                      unsigned int length);
44
45 /* End of group kl_neighborhood_stochbt */
46
47 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
48 #define TwoDpfold_solution vrna_sol_TwoD_pf_t /* restore compatibility of struct rename */
49
50 typedef struct {
51     unsigned int alloc;
52     char *ptype;
53     char *sequence;
54     short *S, *S1;
55     unsigned int maxD1;
56     unsigned int maxD2;
57     double temperature; /* temperature in last call to scale_pf_params */
58     double init_temp; /* temperature in last call to scale_pf_params */
59     FLT_OR_DBL *scale;
60     FLT_OR_DBL pf_scale;
61     vrna_exp_param_t *pf_params; /* holds all [unscaled] pf parameters */
62
63     int *my_iindx;
64     int *jindx;
65     short *reference_pt1;
66     short *reference_pt2;
67
68     unsigned int *referenceBPs1;
69     unsigned int *referenceBPs2;
70     unsigned int *bpdist;
71     unsigned int *mm1;
72     unsigned int *mm2;
73     int circ;
74     int dangles;
75     unsigned int seq_length;
76 }

```

```

185
186 FLT_OR_DBL      ***Q;
187 FLT_OR_DBL      ***Q_B;
188 FLT_OR_DBL      ***Q_M;
189 FLT_OR_DBL      ***Q_M1;
190 FLT_OR_DBL      ***Q_M2;
191
192 FLT_OR_DBL      **Q_c;
193 FLT_OR_DBL      **Q_cH;
194 FLT_OR_DBL      **Q_cI;
195 FLT_OR_DBL      **Q_cM;
196
197 int              *l_min_values;
198 int              *l_max_values;
199 int              *k_min_values;
200 int              *k_max_values;
201
202 int              *l_min_values_b;
203 int              *l_max_values_b;
204 int              *k_min_values_b;
205 int              *k_max_values_b;
206
207 int              *l_min_values_m;
208 int              *l_max_values_m;
209 int              *k_min_values_m;
210 int              *k_max_values_m;
211
212 int              *l_min_values_m1;
213 int              *l_max_values_m1;
214 int              *k_min_values_m1;
215 int              *k_max_values_m1;
216
217 int              *l_min_values_m2;
218 int              *l_max_values_m2;
219 int              *k_min_values_m2;
220 int              *k_max_values_m2;
221
222 int              *l_min_values_qc;
223 int              *l_max_values_qc;
224 int              *k_min_values_qc;
225 int              *k_max_values_qc;
226
227 int              *l_min_values_qcH;
228 int              *l_max_values_qcH;
229 int              *k_min_values_qcH;
230 int              *k_max_values_qcH;
231
232 int              *l_min_values_qcI;
233 int              *l_max_values_qcI;
234 int              *k_min_values_qcI;
235 int              *k_max_values_qcI;
236
237 int              *l_min_values_qcM;
238 int              *l_max_values_qcM;
239 int              *k_min_values_qcM;
240 int              *k_max_values_qcM;
241
242 /* auxiliary arrays for remaining set of coarse graining (k,l) > (k_max, l_max) */
243 FLT_OR_DBL      *Q_rem;
244 FLT_OR_DBL      *Q_B_rem;
245 FLT_OR_DBL      *Q_M_rem;
246 FLT_OR_DBL      *Q_M1_rem;
247 FLT_OR_DBL      *Q_M2_rem;
248
249 FLT_OR_DBL      Q_c_rem;
250 FLT_OR_DBL      Q_cH_rem;
251 FLT_OR_DBL      Q_cI_rem;
252 FLT_OR_DBL      Q_cM_rem;
253
254 vrna_fold_compound_t *compatibility;
255 } TwoDpfold_vars;
256
257 DEPRECATED(TwoDpfold_vars *
258     get_TwoDpfold_variables(const char *seq,
259                             const char *structure1,
260                             char *structure2,
261                             int circ),
262     "Use the new API and vrna_fold_compound_TwoD() instead");
263
264 DEPRECATED(void
265     destroy_TwoDpfold_variables(TwoDpfold_vars *vars),
266     "Use the new API and vrna_fold_compound_free() instead");
267
268 DEPRECATED(TwoDpfold_solution *
269     TwoDpfoldList(TwoDpfold_vars *vars,
270                   int maxDistance1,
271                   int maxDistance2),

```

```

327         "Use the new API and vrna_pf_TwoD() instead");
328
350 DEPRECATED(char *
351             TwoDpfold_pbacktrack(TwoDpfold_vars *vars,
352                                   int d1,
353                                   int d2),
354         "Use the new API and vrna_pbacktrack_TwoD() instead");
355
379 DEPRECATED(char *
380             TwoDpfold_pbacktrack5(TwoDpfold_vars *vars,
381                                   int d1,
382                                   int d2,
383                                   unsigned int length),
384         "Use the new API and vrna_pbacktrack5_TwoD() instead");
385
391 DEPRECATED(FLT_OR_DBL **TwoDpfold(TwoDpfold_vars *our_variables,
392                                   int maxDistance1,
393                                   int maxDistance2),
394         "Use the new API and vrna_pf_TwoD() instead");
395
401 DEPRECATED(FLT_OR_DBL **TwoDpfold_circ(TwoDpfold_vars *our_variables,
402                                   int maxDistance1,
403                                   int maxDistance2),
404         "Use the new API and vrna_pf_TwoD() instead");
405
406 #endif
407
408 #endif

```

## 18.5 ali\_plex.h

```

1 #ifndef VIENNA_RNA_PACKAGE_ALI_PLEX_H
2 #define VIENNA_RNA_PACKAGE_ALI_PLEX_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5
6 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
7
11 duplexT **aliLduplexfold(const char *s1[],
12                          const char *s2[],
13                          const int threshold,
14                          const int extension_cost,
15                          const int alignment_length,
16                          const int delta,
17                          const int fast,
18                          const int il_a,
19                          const int il_b,
20                          const int b_a,
21                          const int b_b);
22
23
27 duplexT **aliLduplexfold_XS(const char *s1[],
28                             const char *s2[],
29                             const int **access_s1,
30                             const int **access_s2,
31                             const int threshold,
32                             const int alignment_length,
33                             const int delta,
34                             const int fast,
35                             const int il_a,
36                             const int il_b,
37                             const int b_a,
38                             const int b_b);
39
40
41 /*
42 * extern duplexT aliduplexfold(const char *s1[], const char *s2[], const int extension_cost);
43 * extern duplexT aliduplexfold_XS(const char *s1[], const char *s2[], const int **access_s1,
44 * const int **access_s2, const int i_pos, const int j_pos, const int threshold);
45 */
46 #endif
47
48 #endif

```

## 18.6 ViennaRNA/alifold.h File Reference

Functions for comparative structure prediction using RNA sequence alignments.

Include dependency graph for alifold.h:

## Functions

- float [energy\\_of\\_alistruct](#) (const char \*\*sequences, const char \*structure, int n\_seq, float \*energy)  
*Calculate the free energy of a consensus structure given a set of aligned sequences.*
- void [update\\_alifold\\_params](#) (void)  
*Update the energy parameters for alifold function.*
- float [alifold](#) (const char \*\*strings, char \*structure)  
*Compute MFE and according consensus structure of an alignment of sequences.*
- float [circularifold](#) (const char \*\*strings, char \*structure)  
*Compute MFE and according structure of an alignment of sequences assuming the sequences are circular instead of linear.*
- void [free\\_alifold\\_arrays](#) (void)  
*Free the memory occupied by MFE alifold functions.*
- float [alipf\\_fold\\_par](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_bppm, int is\_constrained, int is\_circular)
- float [alipf\\_fold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*The partition function version of [alifold\(\)](#) works in analogy to [pf\\_fold\(\)](#). Pair probabilities and information about sequence covariations are returned via the 'pi' variable as a list of [vrna\\_pinfo\\_t](#) structs. The list is terminated by the first entry with pi.i = 0.*
- float [alipf\\_circ\\_fold](#) (const char \*\*sequences, char \*structure, [vrna\\_ep\\_t](#) \*\*pl)
- [FLT\\_OR\\_DBL](#) \* [export\\_alipf\\_bppm](#) (void)  
*Get a pointer to the base pair probability array.*
- void [free\\_alipf\\_arrays](#) (void)  
*Free the memory occupied by folding matrices allocated by [alipf\\_fold](#), [alipf\\_circ\\_fold](#), etc.*
- char \* [alipfbacktrack](#) (double \*prob)  
*Sample a consensus secondary structure from the Boltzmann ensemble according its probability.*
- int [get\\_alipf\\_arrays](#) (short \*\*\*S\_p, short \*\*\*S5\_p, short \*\*\*S3\_p, unsigned short \*\*\*a2s\_p, char \*\*\*Ss↔\_p, [FLT\\_OR\\_DBL](#) \*\*qb\_p, [FLT\\_OR\\_DBL](#) \*\*qm\_p, [FLT\\_OR\\_DBL](#) \*\*q1k\_p, [FLT\\_OR\\_DBL](#) \*\*qln\_p, short \*\*pscore)  
*Get pointers to (almost) all relevant arrays used in alifold's partition function computation.*

## Variables

- double [cv\\_fact](#)  
*This variable controls the weight of the covariance term in the energy function of alignment folding algorithms.*
- double [nc\\_fact](#)  
*This variable controls the magnitude of the penalty for non-compatible sequences in the covariance term of alignment folding algorithms.*

### 18.6.1 Detailed Description

Functions for comparative structure prediction using RNA sequence alignments.

### 18.6.2 Function Documentation

### 18.6.2.1 energy\_of\_alistruct()

```
float energy_of_alistruct (
    const char ** sequences,
    const char * structure,
    int n_seq,
    float * energy )
```

Calculate the free energy of a consensus structure given a set of aligned sequences.

**Deprecated** Usage of this function is discouraged! Use [vrna\\_eval\\_structure\(\)](#), and [vrna\\_eval\\_covar\\_structure\(\)](#) instead!

#### Parameters

|                  |                                                                                                                                                                                  |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>sequences</i> | The NULL terminated array of sequences                                                                                                                                           |
| <i>structure</i> | The consensus structure                                                                                                                                                          |
| <i>n_seq</i>     | The number of sequences in the alignment                                                                                                                                         |
| <i>energy</i>    | A pointer to an array of at least two floats that will hold the free energies (energy[0] will contain the free energy, energy[1] will be filled with the covariance energy term) |

#### Returns

free energy in kcal/mol

### 18.6.2.2 update\_alifold\_params()

```
void update_alifold_params (
    void )
```

Update the energy parameters for alifold function.

Call this to recalculate the pair matrix and energy parameters after a change in folding parameters like [temperature](#)

**Deprecated** Usage of this function is discouraged! The new API uses [vrna\\_fold\\_compound\\_t](#) to lump all folding related necessities together, including the energy parameters. Use [vrna\\_update\\_fold\\_params\(\)](#) to update the energy parameters within a [vrna\\_fold\\_compound\\_t](#).

## 18.6.3 Variable Documentation

### 18.6.3.1 cv\_fact

```
double cv_fact [extern]
```

This variable controls the weight of the covariance term in the energy function of alignment folding algorithms.

**Deprecated** See [vrna\\_md\\_t.cv\\_fact](#), and [vrna\\_mfe\(\)](#) to avoid using global variables

Default is 1.

### 18.6.3.2 nc\_fact

```
double nc_fact [extern]
```

This variable controls the magnitude of the penalty for non-compatible sequences in the covariance term of alignment folding algorithms.

**Deprecated** See [vrna\\_md\\_t.nc\\_fact](#), and [vrna\\_mfe\(\)](#) to avoid using global variables

Default is 1.

## 18.7 alifold.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_ALIFOLD_H
2 #define VIENNA_RNA_PACKAGE_ALIFOLD_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/params/basic.h>
6 #include <ViennaRNA/ribo.h>
7 #include <ViennaRNA/mfe.h>
8 #include <ViennaRNA/part_func.h>
9 #include <ViennaRNA/utils/alignments.h>
10 #include <ViennaRNA/utils/structures.h>
11 #include <ViennaRNA/boltzmann_sampling.h>
12
13 #ifdef VRNA_WARN_DEPRECATED
14 # if defined(__clang__)
15 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
16 # elif defined(__GNUC__)
17 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
18 # else
19 #   define DEPRECATED(func, msg) func
20 # endif
21 #else
22 # define DEPRECATED(func, msg) func
23 #endif
24
25 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
26 /*
27  * DEPRECATED FUNCTIONS
28  */
29
30 DEPRECATED(float alifold(const char **strings, char *structure),
31             "Use vrna_alifold() or vrna_mfe() instead");
32
33 DEPRECATED(float circalifold(const char **strings, char *structure),
34             "Use vrna_alicircfold() or vrna_mfe() instead");
35
36 DEPRECATED(void free_alifold_arrays(void),
37             "This function is obsolete");
38
39 /* End group mfe_global_deprecated */
40 DEPRECATED(float energy_of_alistruct(const char **sequences, const char *structure, int n_seq, float
41                                     *energy),
42             "Use vrna_eval_structure() and vrna_eval_covar_structure() instead");
43
44 DEPRECATED(float energy_of_ali_gquad_structure(const char **sequences, const char *structure, int n_seq,
45  float *energy),
46             "Use vrna_eval_structure() and vrna_eval_covar_structure() instead");
47
48 DEPRECATED(extern double cv_fact,
49             "Use the cv_fact attribute of the vrna_md_t datastructure instead");
50 DEPRECATED(extern double nc_fact,
51             "Use the nc_fact attribute of the vrna_md_t datastructure instead");
52
53 DEPRECATED(float alipf_fold_par(const char **sequences,
54                                char *structure,
55                                vrna_ep_t **pl,
56                                vrna_exp_param_t *parameters,
57                                int calculate_bppm,
58                                int is_constrained,
59                                int is_circular),
60             "Use vrna_pf_alifold() or vrna_pf() instead");
61
62 DEPRECATED(float alipf_fold(const char **sequences, char *structure, vrna_ep_t **pl),
63             "Use vrna_pf_alifold() or vrna_pf() instead");
64
65 DEPRECATED(float alipf_circ_fold(const char **sequences, char *structure, vrna_ep_t **pl),
66             "Use vrna_pf_circalifold() or vrna_pf() instead");
67
68 DEPRECATED(FLT_OR_DBL *export_ali_bppm(void),
69             "Use the new API with vrna_fold_compound_t datastructure instead");
70
71 DEPRECATED(void free_alipf_arrays(void),
72             "This function is obsolete");
73
74 DEPRECATED(char *alipbacktrack(double *prob),
75             "Use the new API and vrna_pbacktrack() instead");
76
77 DEPRECATED(int get_alipf_arrays(short ***S_p,
78                                short ***S5_p,
79                                short ***S3_p,
```



```

274         unsigned short ***a2s_p,
275         char ***Ss_p,
276         FLT_OR_DBL **qb_p,
277         FLT_OR_DBL **qm_p,
278         FLT_OR_DBL **qlk_p,
279         FLT_OR_DBL **qln_p,
280         short **pscore),
281     "Use the new API with vrna_fold_compound_t datastructure instead");
282
283
284 /* End group part_func_global_deprecated */
298 DEPRECATED(void update_alifold_params(void),
299     "Use the new API with vrna_fold_compound_t datastructure instead");
300
301 #endif
302
303
304 #endif

```

## 18.8 ViennaRNA/aln\_util.h File Reference

Use [ViennaRNA/utls/alignments.h](#) instead.

Include dependency graph for aln\_util.h:

### 18.8.1 Detailed Description

Use [ViennaRNA/utls/alignments.h](#) instead.

**Deprecated** Use [ViennaRNA/utls/alignments.h](#) instead

## 18.9 aln\_util.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_ALN_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_ALN_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/aln_util.h>! Use <ViennaRNA/utls/alignments.h>
    instead!"
13 # endif
14 #include <ViennaRNA/utls/alignments.h>
15 #endif
16
17 #endif

```

## 18.10 ViennaRNA/alphabet.h File Reference

Functions to process, convert, and generally handle different nucleotide and/or base pair alphabets.

Include dependency graph for alphabet.h: This graph shows which files directly or indirectly include this file:

### Functions

- char \* [vrna\\_ptypes](#) (const short \*S, [vrna\\_md\\_t](#) \*md)  
*Get an array of the numerical encoding for each possible base pair (i,j)*
- short \* [vrna\\_seq\\_encode](#) (const char \*sequence, [vrna\\_md\\_t](#) \*md)  
*Get a numerical representation of the nucleotide sequence.*
- short \* [vrna\\_seq\\_encode\\_simple](#) (const char \*sequence, [vrna\\_md\\_t](#) \*md)  
*Get a numerical representation of the nucleotide sequence (simple version)*
- int [vrna\\_nucleotide\\_encode](#) (char c, [vrna\\_md\\_t](#) \*md)  
*Encode a nucleotide character to numerical value.*
- char [vrna\\_nucleotide\\_decode](#) (int enc, [vrna\\_md\\_t](#) \*md)  
*Decode a numerical representation of a nucleotide back into nucleotide alphabet.*

## 18.10.1 Detailed Description

Functions to process, convert, and generally handle different nucleotide and/or base pair alphabets.

,

## 18.11 alphabet.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_ALPHABET_H
2 #define VIENNA_RNA_PACKAGE_ALPHABET_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <ViennaRNA/fold_compound.h>
17 #include <ViennaRNA/model.h>
18
19 unsigned int
20 vrna_sequence_length_max(unsigned int options);
21
22 int
23 vrna_nucleotide_IUPAC_identity(char a,
24                                char b);
25
26 void
27 vrna_ptypes_prepare(vrna_fold_compound_t *fc,
28                    unsigned int options);
29
30 char *
31 vrna_ptypes(const short *S,
32             vrna_md_t *md);
33
34 short *
35 vrna_seq_encode(const char *sequence,
36                vrna_md_t *md);
37
38 short *
39 vrna_seq_encode_simple(const char *sequence,
40                       vrna_md_t *md);
41
42 int
43 vrna_nucleotide_encode(char c,
44                       vrna_md_t *md);
45
46 char
47 vrna_nucleotide_decode(int enc,
48                       vrna_md_t *md);
49
50 void
51 vrna_aln_encode(const char *sequence,
52                short **S_p,
53                short **s5_p,
54                short **s3_p,
55                char **ss_p,
56                unsigned int **as_p,
57                vrna_md_t *md);
58
59 unsigned int
60 vrna_get_ptype_md(int i,
61                  int j,
62                  vrna_md_t *md);
63
64 unsigned int
65 vrna_get_ptype(int ij,
```

```

131         char *ptype);
132
133
134 unsigned int
135 vrna_get_ptype_window(int    i,
136                      int    j,
137                      char   **ptype);
138
139
140 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
141
142 DEPRECATED(char *get_ptypes(const short *S,
143                             vrna_md_t  *md,
144                             unsigned int idx_type),
145            "Use vrna_pytypes() instead");
146
147 #endif
148
149 #endif

```

## 18.12 ViennaRNA/boltzmann\_sampling.h File Reference

Boltzmann Sampling of secondary structures from the ensemble.

Include dependency graph for boltzmann\_sampling.h: This graph shows which files directly or indirectly include this file:

### Macros

- #define [VRNA\\_PBACKTRACK\\_DEFAULT](#) 0  
*Boltzmann sampling flag indicating default backtracing mode.*
- #define [VRNA\\_PBACKTRACK\\_NON\\_REDUNDANT](#) 1  
*Boltzmann sampling flag indicating non-redundant backtracing mode.*

### Typedefs

- typedef void() [vrna\\_boltzmann\\_sampling\\_callback](#)(const char \*structure, void \*data)  
*Callback for Boltzmann sampling.*
- typedef struct vrna\_pbacktrack\_memory\_s \* [vrna\\_pbacktrack\\_mem\\_t](#)  
*Boltzmann sampling memory data structure.*

### Functions

- char \* [vrna\\_pbacktrack5](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int length)  
*Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.*
- char \*\* [vrna\\_pbacktrack5\\_num](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int length, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack5\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int length, [vrna\\_boltzmann\\_sampling\\_callback](#) \*cb, void \*data, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- char \*\* [vrna\\_pbacktrack5\\_resume](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, unsigned int num\_samples, unsigned int length, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack5\\_resume\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int length, [vrna\\_boltzmann\\_sampling\\_callback](#) \*cb, void \*data, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*

- char \* [vrna\\_pbacktrack](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)  
*Sample a secondary structure from the Boltzmann ensemble according its probability.*
- char \*\* [vrna\\_pbacktrack\\_num](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int options)  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, [vrna\\_boltzmann\\_sampling\\_callback](#) \*cb, void \*data, unsigned int options)  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- char \*\* [vrna\\_pbacktrack\\_resume](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack\\_resume\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, [vrna\\_boltzmann\\_sampling\\_callback](#) \*cb, void \*data, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples from the Boltzmann ensemble according their probability.*
- char \* [vrna\\_pbacktrack\\_sub](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int start, unsigned int end)  
*Sample a secondary structure of a subsequence from the Boltzmann ensemble according its probability.*
- char \*\* [vrna\\_pbacktrack\\_sub\\_num](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int start, unsigned int end, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack\\_sub\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int start, unsigned int end, [vrna\\_boltzmann\\_sampling\\_callback](#) \*cb, void \*data, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- char \*\* [vrna\\_pbacktrack\\_sub\\_resume](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, unsigned int num\_samples, unsigned int start, unsigned int end, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- unsigned int [vrna\\_pbacktrack\\_sub\\_resume\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, unsigned int num\_samples, unsigned int start, unsigned int end, [vrna\\_boltzmann\\_sampling\\_callback](#) \*bs\_cb, void \*data, [vrna\\_pbacktrack\\_mem\\_t](#) \*nr\_mem, unsigned int options)  
*Obtain a set of secondary structure samples for a subsequence from the Boltzmann ensemble according their probability.*
- void [vrna\\_pbacktrack\\_mem\\_free](#) ([vrna\\_pbacktrack\\_mem\\_t](#) s)  
*Release memory occupied by a Boltzmann sampling memory data structure.*

### 18.12.1 Detailed Description

Boltzmann Sampling of secondary structures from the ensemble.

A.k.a. Stochastic backtracking

## 18.13 [boltzmann\\_sampling.h](#)

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_BOLTZMANN_SAMPLING_H
2 #define VIENNA_RNA_PACKAGE_BOLTZMANN_SAMPLING_H
3
4 #define VRNA_PBACKTRACK_DEFAULT      0
5
6 #define VRNA_PBACKTRACK_NON_REDUNDANT 1
7
8 typedef void (vrna_boltzmann_sampling_callback) (const char *structure,
9 void *data);
10
11 typedef struct vrna_pbacktrack_memory_s *vrna_pbacktrack_mem_t;
12
13 #include <ViennaRNA/fold_compound.h>
14
15 char *
16 vrna_pbacktrack5(vrna_fold_compound_t *fc,
```

```

110             unsigned int      length);
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157 char **
158 vrna_pbacktrack5_num(vrna_fold_compound_t *fc,
159                     unsigned int      num_samples,
160                     unsigned int      length,
161                     unsigned int      options);
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181 unsigned int
182 vrna_pbacktrack5_cb(vrna_fold_compound_t      *fc,
183                    unsigned int      num_samples,
184                    unsigned int      length,
185                    vrna_boltzmann_sampling_callback *cb,
186                    void      *data,
187                    unsigned int      options);
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296 char **
297 vrna_pbacktrack5_resume(vrna_fold_compound_t *vc,
298                        unsigned int      num_samples,
299                        unsigned int      length,
300                        vrna_pbacktrack_mem_t *nr_mem,
301                        unsigned int      options);
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418 char *
419 vrna_pbacktrack(vrna_fold_compound_t *fc);
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465 vrna_pbacktrack_num(vrna_fold_compound_t *fc,
466                    unsigned int      num_samples,
467                    unsigned int      options);
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517 unsigned int
518 vrna_pbacktrack_cb(vrna_fold_compound_t      *fc,
519                   unsigned int      num_samples,
520                   vrna_boltzmann_sampling_callback *cb,
521                   void      *data,
522                   unsigned int      options);
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675 unsigned int
676 vrna_pbacktrack_resume_cb(vrna_fold_compound_t      *fc,
677                          unsigned int      num_samples,
678                          vrna_boltzmann_sampling_callback *cb,
679                          void      *data,
680                          vrna_pbacktrack_mem_t      *nr_mem,
681                          unsigned int      options);
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722 char *
723 vrna_pbacktrack_sub(vrna_fold_compound_t *fc,
724                   unsigned int      start,
725                   unsigned int      end);
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```

```

777             unsigned int      end,
778             unsigned int      options);
779
780
831 unsigned int
832 vrna_pbacktrack_sub_cb(vrna_fold_compound_t      *fc,
833             unsigned int      num_samples,
834             unsigned int      start,
835             unsigned int      end,
836             vrna_boltzmann_sampling_callback *cb,
837             void               *data,
838             unsigned int      options);
839
840
916 char **
917 vrna_pbacktrack_sub_resume(vrna_fold_compound_t *vc,
918             unsigned int      num_samples,
919             unsigned int      start,
920             unsigned int      end,
921             vrna_pbacktrack_mem_t *nr_mem,
922             unsigned int      options);
923
924
1003 unsigned int
1004 vrna_pbacktrack_sub_resume_cb(vrna_fold_compound_t      *fc,
1005             unsigned int      num_samples,
1006             unsigned int      start,
1007             unsigned int      end,
1008             vrna_boltzmann_sampling_callback *bs_cb,
1009             void               *data,
1010             vrna_pbacktrack_mem_t *nr_mem,
1011             unsigned int      options);
1012
1013
1022 void
1023 vrna_pbacktrack_mem_free(vrna_pbacktrack_mem_t s);
1024
1025
1029 #endif

```

## 18.14 ViennaRNA/centroid.h File Reference

Centroid structure computation.

Include dependency graph for centroid.h: This graph shows which files directly or indirectly include this file:

### Functions

- char \* [vrna\\_centroid](#) (vrna\_fold\_compound\_t \*vc, double \*dist)  
*Get the centroid structure of the ensemble.*
- char \* [vrna\\_centroid\\_from\\_plist](#) (int length, double \*dist, vrna\_ep\_t \*pl)  
*Get the centroid structure of the ensemble.*
- char \* [vrna\\_centroid\\_from\\_probs](#) (int length, double \*dist, FLT\_OR\_DBL \*probs)  
*Get the centroid structure of the ensemble.*
- char \* [get\\_centroid\\_struct\\_pl](#) (int length, double \*dist, vrna\_ep\_t \*pl)  
*Get the centroid structure of the ensemble.*
- char \* [get\\_centroid\\_struct\\_pr](#) (int length, double \*dist, FLT\_OR\_DBL \*pr)  
*Get the centroid structure of the ensemble.*

### 18.14.1 Detailed Description

Centroid structure computation.

### 18.14.2 Function Documentation

**18.14.2.1 get\_centroid\_struct\_pl()**

```
char * get_centroid_struct_pl (
    int length,
    double * dist,
    vrna_ep_t * pl )
```

Get the centroid structure of the ensemble.

**Deprecated** This function was renamed to `vrna_centroid_from_plist()`

**18.14.2.2 get\_centroid\_struct\_pr()**

```
char * get_centroid_struct_pr (
    int length,
    double * dist,
    FLT_OR_DBL * pr )
```

Get the centroid structure of the ensemble.

**Deprecated** This function was renamed to `vrna_centroid_from_probs()`

**18.15 centroid.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CENTROID_H
2 #define VIENNA_RNA_PACKAGE_CENTROID_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/fold_compound.h>
6 #include <ViennaRNA/utils/structures.h>
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(__clang__)
10 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
11 # elif defined(__GNUC__)
12 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
13 # else
14 #  define DEPRECATED(func, msg) func
15 # endif
16 #else
17 # define DEPRECATED(func, msg) func
18 #endif
19
20 char *
21 vrna_centroid(vrna_fold_compound_t *vc,
22              double *dist);
23
24 char *
25 vrna_centroid_from_plist(int length,
26                          double *dist,
27                          vrna_ep_t *pl);
28
29 char *
30 vrna_centroid_from_probs(int length,
31                          double *dist,
32                          FLT_OR_DBL *probs);
33
34 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
35
36 DEPRECATED(char *get_centroid_struct_pl(int length,
37   double *dist,
38   vrna_ep_t *pl),
39            "Use vrna_centroid_from_plist() instead");
40
41 DEPRECATED(char *get_centroid_struct_pr(int length,
42   double *dist,
43   FLT_OR_DBL *pr),
44            "Use vrna_centroid_from_probs() instead");
45
46 #endif
47 #endif
```

## 18.16 ViennaRNA/char\_stream.h File Reference

Use [ViennaRNA/datastructures/char\\_stream.h](#) instead.

Include dependency graph for char\_stream.h:

### 18.16.1 Detailed Description

Use [ViennaRNA/datastructures/char\\_stream.h](#) instead.

**Deprecated** Use [ViennaRNA/datastructures/char\\_stream.h](#) instead

## 18.17 char\_stream.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_DATA_STRUCTURES_CHAR_STREAM_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_DATA_STRUCTURES_CHAR_STREAM_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/char_stream.h>! Use
    <ViennaRNA/datastructures/char_stream.h> instead!"
13 # endif
14 #include <ViennaRNA/datastructures/char_stream.h>
15 #endif
16
17 #endif
```

## 18.18 ViennaRNA/datastructures/char\_stream.h File Reference

Implementation of a dynamic, buffered character stream.

Include dependency graph for char\_stream.h: This graph shows which files directly or indirectly include this file:

### Functions

- `vrna_cstr_t vrna_cstr` (size\_t size, FILE \*output)  
*Create a dynamic char \* stream data structure.*
- `void vrna_cstr_discard` (struct vrna\_cstr\_s \*buf)  
*Discard the current content of the dynamic char \* stream data structure.*
- `void vrna_cstr_free` (vrna\_cstr\_t buf)  
*Free the memory occupied by a dynamic char \* stream data structure.*
- `void vrna_cstr_close` (vrna\_cstr\_t buf)  
*Free the memory occupied by a dynamic char \* stream and close the output stream.*
- `void vrna_cstr_fflush` (struct vrna\_cstr\_s \*buf)  
*Flush the dynamic char \* output stream.*

### 18.18.1 Detailed Description

Implementation of a dynamic, buffered character stream.

,

## 18.19 char\_stream.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CHAR_STREAM_H
2 #define VIENNA_RNA_PACKAGE_CHAR_STREAM_H
3
16 #include <stdarg.h>
17 #include <stdio.h>
18
19 /* below is our own implementation of a dynamic char * stream */
20 typedef struct vrna_cstr_s *vrna_cstr_t;
21
```



```
30 vrna_cstr_t
31 vrna_cstr(size_t size,
32           FILE *output);
33
34
42 void
43 vrna_cstr_discard(struct vrna_cstr_s *buf);
44
45
56 void
57 vrna_cstr_free(vrna_cstr_t buf);
58
59
71 void
72 vrna_cstr_close(vrna_cstr_t buf);
73
74
88 void
89 vrna_cstr_fflush(struct vrna_cstr_s *buf);
90
91
92 const char *
93 vrna_cstr_string(vrna_cstr_t buf);
94
95
96 int
97 vrna_cstr_vprintf(vrna_cstr_t buf,
98                  const char *format,
99                  va_list args);
100
101
102 int
103 vrna_cstr_printf(vrna_cstr_t buf,
104                  const char *format,
105                  ...);
106
107
108 void
109 vrna_cstr_message_info(vrna_cstr_t buf,
110                        const char *format,
111                        ...);
112
113
114 void
115 vrna_cstr_message_vinfo(vrna_cstr_t buf,
116                          const char *format,
117                          va_list args);
118
119
120 void
121 vrna_cstr_message_warning(struct vrna_cstr_s *buf,
122                           const char *format,
123                           ...);
124
125
126 void
127 vrna_cstr_message_vwarning(struct vrna_cstr_s *buf,
128                             const char *format,
129                             va_list args);
130
131
132 void
133 vrna_cstr_print_fasta_header(vrna_cstr_t buf,
134                               const char *head);
135
136
137 void
138 vrna_cstr_printf_structure(struct vrna_cstr_s *buf,
139                            const char *structure,
140                            const char *format,
141                            ...);
142
143
144 void
145 vrna_cstr_vprintf_structure(struct vrna_cstr_s *buf,
146                             const char *structure,
147                             const char *format,
148                             va_list args);
149
150
151 void
152 vrna_cstr_printf_comment(struct vrna_cstr_s *buf,
153                           const char *format,
154                           ...);
155
156
157 void
```

```
158 vrna_cstr_vprintf_comment(struct vrna_cstr_s *buf,
159                          const char *format,
160                          va_list args);
161
162
163 void
164 vrna_cstr_printf_thead(struct vrna_cstr_s *buf,
165                      const char *format,
166                      ...);
167
168
169 void
170 vrna_cstr_vprintf_thead(struct vrna_cstr_s *buf,
171                       const char *format,
172                       va_list args);
173
174
175 void
176 vrna_cstr_printf_tbody(struct vrna_cstr_s *buf,
177                      const char *format,
178                      ...);
179
180
181 void
182 vrna_cstr_vprintf_tbody(struct vrna_cstr_s *buf,
183                       const char *format,
184                       va_list args);
185
186
187 void
188 vrna_cstr_print_eval_sd_corr(struct vrna_cstr_s *buf);
189
190
191 void
192 vrna_cstr_print_eval_ext_loop(struct vrna_cstr_s *buf,
193                             int energy);
194
195
196 void
197 vrna_cstr_print_eval_hp_loop(struct vrna_cstr_s *buf,
198                             int i,
199                             int j,
200                             char si,
201                             char sj,
202                             int energy);
203
204
205 void
206 vrna_cstr_print_eval_hp_loop_revert(struct vrna_cstr_s *buf,
207                                    int i,
208                                    int j,
209                                    char si,
210                                    char sj,
211                                    int energy);
212
213
214 void
215 vrna_cstr_print_eval_int_loop(struct vrna_cstr_s *buf,
216                              int i,
217                              int j,
218                              char si,
219                              char sj,
220                              int k,
221                              int l,
222                              char sk,
223                              char sl,
224                              int energy);
225
226
227 void
228 vrna_cstr_print_eval_int_loop_revert(struct vrna_cstr_s *buf,
229                                     int i,
230                                     int j,
231                                     char si,
232                                     char sj,
233                                     int k,
234                                     int l,
235                                     char sk,
236                                     char sl,
237                                     int energy);
238
239
240 void
241 vrna_cstr_print_eval_mb_loop(struct vrna_cstr_s *buf,
242                             int i,
243                             int j,
244                             char si,
```

```

245             char          sj,
246             int           energy);
247
248
249 void
250 vrna_cstr_print_eval_mb_loop_revert(struct vrna_cstr_s *buf,
251                                     int           i,
252                                     int           j,
253                                     char          si,
254                                     char          sj,
255                                     int           energy);
256
257
258 void
259 vrna_cstr_print_eval_gquad(struct vrna_cstr_s *buf,
260                           int           i,
261                           int           L,
262                           int           l[3],
263                           int           energy);
264
265
266 #endif

```

## 18.20 ViennaRNA/cofold.h File Reference

MFE implementations for RNA-RNA interaction.

Include dependency graph for cofold.h:

### Functions

- float [cofold](#) (const char \*sequence, char \*structure)  
*Compute the minimum free energy of two interacting RNA molecules.*
- float [cofold\\_par](#) (const char \*string, char \*structure, [vrna\\_param\\_t](#) \*parameters, int is\_constrained)  
*Compute the minimum free energy of two interacting RNA molecules.*
- void [free\\_co\\_arrays](#) (void)  
*Free memory occupied by [cofold\(\)](#)*
- void [update\\_cofold\\_params](#) (void)  
*Recalculate parameters.*
- void [update\\_cofold\\_params\\_par](#) ([vrna\\_param\\_t](#) \*parameters)  
*Recalculate parameters.*
- void [export\\_cofold\\_arrays\\_gq](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*ggg\_p, int \*\*indx\_p, char \*\*ptype\_p)  
*Export the arrays of partition function cofold (with gquadruplex support)*
- void [export\\_cofold\\_arrays](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*fc\_p, int \*\*indx\_p, char \*\*ptype\_p)  
*Export the arrays of partition function cofold.*
- void [initialize\\_cofold](#) (int length)

### 18.20.1 Detailed Description

MFE implementations for RNA-RNA interaction.

## 18.21 cofold.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_COFOLD_H
2 #define VIENNA_RNA_PACKAGE_COFOLD_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/params/basic.h>
6 #include <ViennaRNA/mfe.h>
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(__clang__)
10 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))

```

```

11 # elif defined(__GNUC__)
12 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
13 # else
14 #   define DEPRECATED(func, msg) func
15 # endif
16 #else
17 # define DEPRECATED(func, msg) func
18 #endif
19
26 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
27
42 DEPRECATED(float
43     cofold(const char *sequence,
44            char *structure),
45     "Use vrna_cofold() instead");
46
54 DEPRECATED(float
55     cofold_par(const char *string,
56                char *structure,
57                vrna_param_t *parameters,
58                int is_constrained),
59     "Use the new API and vrna_mfe_dimer() instead");
60
72 DEPRECATED(void
73     free_co_arrays(void),
74     "This function is obsolete");
75
82 DEPRECATED(void
83     update_cofold_params(void),
84     "This function is obsolete");
85
92 DEPRECATED(void
93     update_cofold_params_par(vrna_param_t *parameters),
94     "Use the new API with vrna_fold_compound_t instead");
95
96
118 DEPRECATED(void
119     export_cofold_arrays_gq(int **f5_p,
120                             int **c_p,
121                             int **fML_p,
122                             int **fMl_p,
123                             int **fc_p,
124                             int **ggg_p,
125                             int **indx_p,
126                             char **ptype_p),
127     "Use the new API with vrna_fold_compound_t instead");
128
149 DEPRECATED(void
150     export_cofold_arrays(int **f5_p,
151                          int **c_p,
152                          int **fML_p,
153                          int **fMl_p,
154                          int **fc_p,
155                          int **indx_p,
156                          char **ptype_p),
157     "Use the new API with vrna_fold_compound_t instead");
158
159
166 DEPRECATED(void
167     initialize_cofold(int length),
168     "This function is obsolete");
169
170 #endif
171
172 #endif

```

## 18.22 ViennaRNA/combinatorics.h File Reference

Various implementations that deal with combinatorial aspects of objects.

Include dependency graph for combinatorics.h:

### Functions

- unsigned int [vrna\\_enumerate\\_necklaces](#) (const unsigned int \*type\_counts)  
*Enumerate all necklaces with fixed content.*
- unsigned int [vrna\\_rotational\\_symmetry\\_num](#) (const unsigned int \*string, size\_t string\_length)  
*Determine the order of rotational symmetry for a string of objects represented by natural numbers.*
- unsigned int [vrna\\_rotational\\_symmetry\\_pos\\_num](#) (const unsigned int \*string, size\_t string\_length, unsigned int \*\*positions)

- Determine the order of rotational symmetry for a string of objects represented by natural numbers.*
- unsigned int `vrna_rotational_symmetry` (const char \*string)
- Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.*
- unsigned int `vrna_rotational_symmetry_pos` (const char \*string, unsigned int \*\*positions)
- Determine the order of rotational symmetry for a NULL-terminated string of ASCII characters.*
- unsigned int `vrna_rotational_symmetry_db` (vrna\_fold\_compound\_t \*fc, const char \*structure)
- Determine the order of rotational symmetry for a dot-bracket structure.*
- unsigned int `vrna_rotational_symmetry_db_pos` (vrna\_fold\_compound\_t \*fc, const char \*structure, unsigned int \*\*positions)
- Determine the order of rotational symmetry for a dot-bracket structure.*
- unsigned int \*\* `vrna_n_multichoose_k` (size\_t n, size\_t k)
- Obtain a list of k-combinations with repetition (n multichoose k)*
- unsigned int \* `vrna_boustrophedon` (size\_t start, size\_t end)
- Generate a sequence of Boustrophedon distributed numbers.*
- unsigned int `vrna_boustrophedon_pos` (size\_t start, size\_t end, size\_t pos)
- Obtain the i-th element in a Boustrophedon distributed interval of natural numbers.*

### 18.22.1 Detailed Description

Various implementations that deal with combinatorial aspects of objects.

## 18.23 combinatorics.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_COMBINATORICS_H
2 #define VIENNA_RNA_PACKAGE_COMBINATORICS_H
3
10 #include <ViennaRNA/fold_compound.h>
11
33 unsigned int **
34 vrna_enumerate_necklaces(const unsigned int *type_counts);
35
36
56 unsigned int
57 vrna_rotational_symmetry_num(const unsigned int *string,
58                             size_t string_length);
59
60
87 unsigned int
88 vrna_rotational_symmetry_pos_num(const unsigned int *string,
89                                 size_t string_length,
90                                 unsigned int **positions);
91
92
110 unsigned int
111 vrna_rotational_symmetry(const char *string);
112
113
138 unsigned int
139 vrna_rotational_symmetry_pos(const char *string,
140                             unsigned int **positions);
141
142
165 unsigned int
166 vrna_rotational_symmetry_db(vrna_fold_compound_t *fc,
167                             const char *structure);
168
169
200 unsigned int
201 vrna_rotational_symmetry_db_pos(vrna_fold_compound_t *fc,
202                                 const char *structure,
203                                 unsigned int **positions);
204
205
218 unsigned int **
219 vrna_n_multichoose_k(size_t n,
220                     size_t k);
221
222
245 unsigned int *
```

```

246 vrna_boustrophedon(size_t start,
247                     size_t end);
248
249 unsigned int
262 vrna_boustrophedon_pos(size_t start,
263                         size_t end,
264                         size_t pos);
265
266
270 #endif

```

## 18.24 ViennaRNA/commands.h File Reference

Parse and apply different commands that alter the behavior of secondary structure prediction and evaluation. Include dependency graph for commands.h:

### Macros

- `#define VRNA_CMD_PARSE_HC 1U`  
*Command parse/apply flag indicating hard constraints.*
- `#define VRNA_CMD_PARSE_SC 2U`  
*Command parse/apply flag indicating soft constraints.*
- `#define VRNA_CMD_PARSE_UD 4U`  
*Command parse/apply flag indicating unstructured domains.*
- `#define VRNA_CMD_PARSE_SD 8U`  
*Command parse/apply flag indicating structured domains.*
- `#define VRNA_CMD_PARSE_DEFAULTS`  
*Command parse/apply flag indicating default set of commands.*

### Typedefs

- `typedef struct vrna_command_s * vrna_cmd_t`  
*A data structure that contains commands.*

### Functions

- `vrna_cmd_t vrna_file_commands_read` (const char \*filename, unsigned int options)  
*Extract a list of commands from a command file.*
- `int vrna_file_commands_apply` (vrna\_fold\_compound\_t \*vc, const char \*filename, unsigned int options)  
*Apply a list of commands from a command file.*
- `int vrna_commands_apply` (vrna\_fold\_compound\_t \*vc, vrna\_cmd\_t commands, unsigned int options)  
*Apply a list of commands to a vrna\_fold\_compound\_t.*
- `void vrna_commands_free` (vrna\_cmd\_t commands)  
*Free memory occupied by a list of commands.*

#### 18.24.1 Detailed Description

Parse and apply different commands that alter the behavior of secondary structure prediction and evaluation.

, ,

## 18.25 commands.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_COMMANDS_H
2 #define VIENNA_RNA_PACKAGE_COMMANDS_H
3
18 typedef struct vrna_command_s *vrna_cmd_t;
19

```

```

20
21 #include <ViennaRNA/fold_compound.h>
22
27 #define VRNA_CMD_PARSE_HC      1U
32 #define VRNA_CMD_PARSE_SC      2U
37 #define VRNA_CMD_PARSE_UD      4U
42 #define VRNA_CMD_PARSE_SD      8U
47 #define VRNA_CMD_PARSE_DEFAULTS (VRNA_CMD_PARSE_HC \
48                                   | VRNA_CMD_PARSE_SC \
49                                   | VRNA_CMD_PARSE_UD \
50                                   | VRNA_CMD_PARSE_SD \
51                                   )
52
53 #define VRNA_CMD_PARSE_SILENT  16U
54
68 vrna_cmd_t
69 vrna_file_commands_read(const char    *filename,
70                        unsigned int  options);
71
72
86 int
87 vrna_file_commands_apply(vrna_fold_compound_t *vc,
88                        const char    *filename,
89                        unsigned int  options);
90
91
100 int
101 vrna_commands_apply(vrna_fold_compound_t *vc,
102                   vrna_cmd_t            commands,
103                   unsigned int          options);
104
105
112 void
113 vrna_commands_free(vrna_cmd_t commands);
114
115
120 #endif

```

## 18.26 ViennaRNA/concentrations.h File Reference

Concentration computations for RNA-RNA interactions.

Include dependency graph for concentrations.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_dimer\\_conc\\_s](#)  
*Data structure for concentration dependency computations.*

### Functions

- [vrna\\_dimer\\_conc\\_t](#) \* [get\\_concentrations](#) (double FEAB, double FEAA, double FEBB, double FEA, double FEB, double \*startconc)  
*Given two start monomer concentrations a and b, compute the concentrations in thermodynamic equilibrium of all dimers and the monomers.*
- typedef struct [vrna\\_dimer\\_conc\\_s](#) [vrna\\_dimer\\_conc\\_t](#)  
*Typename for the data structure that stores the dimer concentrations, [vrna\\_dimer\\_conc\\_s](#), as required by [vrna\\_pf\\_dimer\\_concentration\(\)](#)*
- typedef struct [vrna\\_dimer\\_conc\\_s](#) [ConcEnt](#)  
*Backward compatibility typedef for [vrna\\_dimer\\_conc\\_s](#).*
- [vrna\\_dimer\\_conc\\_t](#) \* [vrna\\_pf\\_dimer\\_concentrations](#) (double FcAB, double FcAA, double FcBB, double FEA, double FEB, const double \*startconc, const [vrna\\_exp\\_param\\_t](#) \*exp\_params)  
*Given two start monomer concentrations a and b, compute the concentrations in thermodynamic equilibrium of all dimers and the monomers.*

### 18.26.1 Detailed Description

Concentration computations for RNA-RNA interactions.

## 18.26.2 Function Documentation

### 18.26.2.1 `get_concentrations()`

```
vrna_dimer_conc_t * get_concentrations (
    double FEAB,
    double FEAA,
    double FEBB,
    double FEA,
    double FEB,
    double * startconc )
```

Given two start monomer concentrations a and b, compute the concentrations in thermodynamic equilibrium of all dimers and the monomers.

This function takes an array 'startconc' of input concentrations with alternating entries for the initial concentrations of molecules A and B (terminated by two zeroes), then computes the resulting equilibrium concentrations from the free energies for the dimers. Dimer free energies should be the dimer-only free energies, i.e. the FcAB entries from the `vrna_dimer_pf_t` struct.

**Deprecated** { Use `vrna_pf_dimer_concentrations()` instead!}

#### Parameters

|                  |                                                                        |
|------------------|------------------------------------------------------------------------|
| <i>FEAB</i>      | Free energy of AB dimer (FcAB entry)                                   |
| <i>FEAA</i>      | Free energy of AA dimer (FcAB entry)                                   |
| <i>FEBB</i>      | Free energy of BB dimer (FcAB entry)                                   |
| <i>FEA</i>       | Free energy of monomer A                                               |
| <i>FEB</i>       | Free energy of monomer B                                               |
| <i>startconc</i> | List of start concentrations [a0],[b0],[a1],[b1],...,[an],[bn],[0],[0] |

#### Returns

`vrna_dimer_conc_t` array containing the equilibrium energies and start concentrations

## 18.27 `concentrations.h`

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CONCENTRATIONS_H
2 #define VIENNA_RNA_PACKAGE_CONCENTRATIONS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
28 typedef struct vrna_dimer_conc_s vrna_dimer_conc_t;
29
30
31 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
32
36 typedef struct vrna_dimer_conc_s ConcEnt;
37
38 #endif
39
40 #include <ViennaRNA/params/basic.h>
41
45 struct vrna_dimer_conc_s {
46     double Ac_start;
```



```

47  double  Bc_start;
48  double  ABc;
49  double  AAc;
50  double  BBc;
51  double  Ac;
52  double  Bc;
53  };
54
55
75  vrna_dimer_conc_t *vrna_pf_dimer_concentrations(double          FcAB,
76  double          FcAA,
77  double          FcBB,
78  double          FEA,
79  double          FEB,
80  const double      *startconc,
81  const vrna_exp_param_t *exp_params);
82
83 double *
84 vrna_equilibrium_constants(const double      *dG_complexes,
85                           const double      *dG_strands,
86                           const unsigned int **A,
87                           double          kT,
88                           size_t          strands,
89                           size_t          complexes);
90
91 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
92 /*
93 #####
94 # DEPRECATED FUNCTIONS                                #
95 #####
96 */
97
123 DEPRECATED(vrna_dimer_conc_t *get_concentrations(double FEAB,
124  double FEAA,
125  double FEBB,
126  double FEA,
127  double FEB,
128  double *startconc),
129           "Use vrna_pf_dimer_concentrations() instead");
130
131 #endif
132
133 #endif

```

## 18.28 ViennaRNA/constraints.h File Reference

Use [ViennaRNA/constraints/basic.h](#) instead.

Include dependency graph for constraints.h:

### 18.28.1 Detailed Description

Use [ViennaRNA/constraints/basic.h](#) instead.

**Deprecated** Use [ViennaRNA/constraints/basic.h](#) instead

## 18.29 constraints.h

[Go to the documentation of this file.](#)

```

1  #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_DEPRECATED_H
2  #define VIENNA_RNA_PACKAGE_CONSTRAINTS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/constraints.h>! Use <ViennaRNA/constraints/basic.h>
    instead!"
13 #  endif
14 #include <ViennaRNA/constraints/basic.h>
15 #include <ViennaRNA/constraints/hard.h>
16 #include <ViennaRNA/constraints/soft.h>
17 #include <ViennaRNA/constraints/SHAPE.h>
18 #include <ViennaRNA/constraints/ligand.h>
19 #endif
20
21 #endif

```

## 18.30 ViennaRNA/constraints/hard.h File Reference

Functions and data structures for handling of secondary structure hard constraints.

Include dependency graph for hard.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_hc\\_s](#)  
The hard constraints data structure. [More...](#)
- struct [vrna\\_hc\\_up\\_s](#)  
A single hard constraint for a single nucleotide. [More...](#)

### Macros

- `#define VRNA_CONSTRAINT_NO_HEADER 0`  
do not print the header information line
- `#define VRNA_CONSTRAINT_DB 16384U`  
Flag for [vrna\\_constraints\\_add\(\)](#) to indicate that constraint is passed in pseudo dot-bracket notation.
- `#define VRNA_CONSTRAINT_DB_ENFORCE_BP 32768U`  
Switch for dot-bracket structure constraint to enforce base pairs.
- `#define VRNA_CONSTRAINT_DB_PIPE 65536U`  
Flag that is used to indicate the pipe '|' sign in pseudo dot-bracket notation of hard constraints.
- `#define VRNA_CONSTRAINT_DB_DOT 131072U`  
dot '.' switch for structure constraints (no constraint at all)
- `#define VRNA_CONSTRAINT_DB_X 262144U`  
'x' switch for structure constraint (base must not pair)
- `#define VRNA_CONSTRAINT_DB_ANG_BRACK 524288U`  
angle brackets '<', '>' switch for structure constraint (paired downstream/upstream)
- `#define VRNA_CONSTRAINT_DB_RND_BRACK 1048576U`  
round brackets '(', ')' switch for structure constraint (base i pairs base j)
- `#define VRNA_CONSTRAINT_DB_INTRAMOL 2097152U`  
Flag that is used to indicate the character 'I' in pseudo dot-bracket notation of hard constraints.
- `#define VRNA_CONSTRAINT_DB_INTERMOL 4194304U`  
Flag that is used to indicate the character 'e' in pseudo dot-bracket notation of hard constraints.
- `#define VRNA_CONSTRAINT_DB_GQUAD 8388608U`  
'+' switch for structure constraint (base is involved in a gquad)
- `#define VRNA_CONSTRAINT_DB_WUSS 33554432U`  
Flag to indicate Washington University Secondary Structure (WUSS) notation of the hard constraint string.
- `#define VRNA_CONSTRAINT_DB_DEFAULT`  
Switch for dot-bracket structure constraint with default symbols.
- `#define VRNA_CONSTRAINT_CONTEXT_EXT_LOOP (unsigned char)0x01`  
Hard constraints flag, base pair in the exterior loop.
- `#define VRNA_CONSTRAINT_CONTEXT_HP_LOOP (unsigned char)0x02`  
Hard constraints flag, base pair encloses hairpin loop.
- `#define VRNA_CONSTRAINT_CONTEXT_INT_LOOP (unsigned char)0x04`  
Hard constraints flag, base pair encloses an interior loop.
- `#define VRNA_CONSTRAINT_CONTEXT_INT_LOOP_ENC (unsigned char)0x08`  
Hard constraints flag, base pair encloses a multi branch loop.
- `#define VRNA_CONSTRAINT_CONTEXT_MB_LOOP (unsigned char)0x10`  
Hard constraints flag, base pair is enclosed in an interior loop.
- `#define VRNA_CONSTRAINT_CONTEXT_MB_LOOP_ENC (unsigned char)0x20`  
Hard constraints flag, base pair is enclosed in a multi branch loop.

- `#define VRNA_CONSTRAINT_CONTEXT_ENFORCE` (unsigned char)0x40  
*Hard constraint flag to indicate enforcement of constraints.*
- `#define VRNA_CONSTRAINT_CONTEXT_NO_REMOVE` (unsigned char)0x80  
*Hard constraint flag to indicate not to remove base pairs that conflict with a given constraint.*
- `#define VRNA_CONSTRAINT_CONTEXT_NONE` (unsigned char)0  
*Constraint context flag that forbids any loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_CLOSING_LOOPS`  
*Constraint context flag indicating base pairs that close any loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_ENCLOSED_LOOPS`  
*Constraint context flag indicating base pairs enclosed by any loop.*
- `#define VRNA_CONSTRAINT_CONTEXT_ALL_LOOPS`  
*Constraint context flag indicating any loop context.*

## Typedefs

- typedef struct `vrna_hc_s` `vrna_hc_t`  
*Typename for the hard constraints data structure `vrna_hc_s`.*
- typedef struct `vrna_hc_up_s` `vrna_hc_up_t`  
*Typename for the single nucleotide hard constraint data structure `vrna_hc_up_s`.*
- typedef unsigned char() `vrna_callback_hc_evaluate`(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to evaluate whether or not a particular decomposition step is contributing to the solution space.*

## Enumerations

- enum `vrna_hc_type_e` { `VRNA_HC_DEFAULT` , `VRNA_HC_WINDOW` }  
*The hard constraints type.*

## Functions

- void `vrna_message_constraint_options` (unsigned int option)  
*Print a help message for pseudo dot-bracket structure constraint characters to stdout. (constraint support is specified by option parameter)*
- void `vrna_message_constraint_options_all` (void)  
*Print structure constraint characters to stdout (full constraint support)*
- void `vrna_hc_init` (`vrna_fold_compound_t` \*vc)  
*Initialize/Reset hard constraints to default values.*
- void `vrna_hc_add_up` (`vrna_fold_compound_t` \*vc, int i, unsigned char option)  
*Make a certain nucleotide unpaired.*
- int `vrna_hc_add_up_batch` (`vrna_fold_compound_t` \*vc, `vrna_hc_up_t` \*constraints)  
*Apply a list of hard constraints for single nucleotides.*
- int `vrna_hc_add_bp` (`vrna_fold_compound_t` \*vc, int i, int j, unsigned char option)  
*Favorize/Enforce a certain base pair (i,j)*
- void `vrna_hc_add_bp_nonspecific` (`vrna_fold_compound_t` \*vc, int i, int d, unsigned char option)  
*Enforce a nucleotide to be paired (upstream/downstream)*
- void `vrna_hc_free` (`vrna_hc_t` \*hc)  
*Free the memory allocated by a `vrna_hc_t` data structure.*
- void `vrna_hc_add_f` (`vrna_fold_compound_t` \*vc, `vrna_callback_hc_evaluate` \*f)  
*Add a function pointer pointer for the generic hard constraint feature.*
- void `vrna_hc_add_data` (`vrna_fold_compound_t` \*vc, void \*data, `vrna_callback_free_auxdata` \*f)  
*Add an auxiliary data structure for the generic hard constraints callback function.*
- int `vrna_hc_add_from_db` (`vrna_fold_compound_t` \*vc, const char \*constraint, unsigned int options)  
*Add hard constraints from pseudo dot-bracket notation.*

- void [print\\_tty\\_constraint](#) (unsigned int option)  
*Print structure constraint characters to stdout. (constraint support is specified by option parameter)*
- void [print\\_tty\\_constraint\\_full](#) (void)  
*Print structure constraint characters to stdout (full constraint support)*
- void [constrain\\_ptypes](#) (const char \*constraint, unsigned int length, char \*ptype, int \*BP, int min\_loop\_size, unsigned int idx\_type)  
*Insert constraining pair types according to constraint structure string.*

### 18.30.1 Detailed Description

Functions and data structures for handling of secondary structure hard constraints.

### 18.30.2 Macro Definition Documentation

#### 18.30.2.1 VRNA\_CONSTRAINT\_NO\_HEADER

```
#define VRNA_CONSTRAINT_NO_HEADER 0
```

do not print the header information line

**Deprecated** This mode is not supported anymore!

#### 18.30.2.2 VRNA\_CONSTRAINT\_DB\_ANG\_BRACK

```
#define VRNA_CONSTRAINT_DB_ANG_BRACK 524288U
```

angle brackets '<', '>' switch for structure constraint (paired downstream/upstream)

See also

[vrna\\_hc\\_add\\_from\\_db\(\)](#), [vrna\\_constraints\\_add\(\)](#), [vrna\\_message\\_constraint\\_options\(\)](#), [vrna\\_message\\_constraint\\_options\\_all\(\)](#)

### 18.30.3 Enumeration Type Documentation

#### 18.30.3.1 vrna\_hc\_type\_e

```
enum vrna_hc_type_e
```

The hard constraints type.

Global and local structure prediction methods use a slightly different way to handle hard constraints internally. This enum is used to distinguish both types.

Enumerator

|                 |                                                                                                                                                                                                                  |
|-----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| VRNA_HC_DEFAULT | Default Hard Constraints.                                                                                                                                                                                        |
| VRNA_HC_WINDOW  | Hard Constraints suitable for local structure prediction using window approach.<br><br>See also<br><br><a href="#">vrna_mfe_window()</a> , <a href="#">vrna_mfe_window_zscore()</a> , <a href="#">pfl_fold()</a> |

### 18.30.4 Function Documentation

**18.30.4.1 vrna\_hc\_add\_data()**

```
void vrna_hc_add_data (
    vrna_fold_compound_t * vc,
    void * data,
    vrna_callback_free_auxdata * f )
```

Add an auxiliary data structure for the generic hard constraints callback function.

See also

[vrna\\_hc\\_add\\_f\(\)](#)

**Parameters**

|             |                                                                                                   |
|-------------|---------------------------------------------------------------------------------------------------|
| <i>vc</i>   | The fold compound the generic hard constraint function should be bound to                         |
| <i>data</i> | A pointer to the data structure that holds required data for function 'f'                         |
| <i>f</i>    | A pointer to a function that free's the memory occupied by <i>data</i> (Maybe <code>NULL</code> ) |

**18.30.4.2 print\_tty\_constraint()**

```
void print_tty_constraint (
    unsigned int option )
```

Print structure constraint characters to stdout. (constraint support is specified by option parameter)

**Deprecated** Use [vrna\\_message\\_constraints\(\)](#) instead!

**Parameters**

|               |                                                                |
|---------------|----------------------------------------------------------------|
| <i>option</i> | Option switch that tells which constraint help will be printed |
|---------------|----------------------------------------------------------------|

**18.30.4.3 print\_tty\_constraint\_full()**

```
void print_tty_constraint_full (
    void )
```

Print structure constraint characters to stdout (full constraint support)

**Deprecated** Use [vrna\\_message\\_constraint\\_options\\_all\(\)](#) instead!

**18.30.4.4 constrain\_ptypes()**

```
void constrain_ptypes (
    const char * constraint,
    unsigned int length,
    char * ptype,
    int * BP,
    int min_loop_size,
    unsigned int idx_type )
```

Insert constraining pair types according to constraint structure string.

**Deprecated** Do not use this function anymore! Structure constraints are now handled through [vrna\\_hc\\_t](#) and related functions.

## Parameters

|                         |                                                                       |
|-------------------------|-----------------------------------------------------------------------|
| <i>constraint</i>       | The structure constraint string                                       |
| <i>length</i>           | The actual length of the sequence (constraint may be shorter)         |
| <i>p<sub>type</sub></i> | A pointer to the basepair type array                                  |
| <i>BP</i>               | (not used anymore)                                                    |
| <i>min_loop_size</i>    | The minimal loop size (usually <a href="#">TURN</a> )                 |
| <i>idx_type</i>         | Define the access type for base pair type array (0 = indx, 1 = iindx) |

## 18.31 hard.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_HARD_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_HARD_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(" ", msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16
34 typedef struct vrna_hc_s vrna_hc_t;
35
40 typedef struct vrna_hc_up_s vrna_hc_up_t;
41
42 typedef struct vrna_hc_depot_s vrna_hc_depot_t;
43
44 #include <ViennaRNA/fold_compound.h>
45 #include <ViennaRNA/constraints/basic.h>
46
78 typedef unsigned char (vrna_callback_hc_evaluate)(int i,
79 int j,
80 int k,
81 int l,
82 unsigned char d,
83 void *data);
84
90 #define VRNA_CONSTRAINT_NO_HEADER 0
91
100 #define VRNA_CONSTRAINT_DB 16384U
101
113 #define VRNA_CONSTRAINT_DB_ENFORCE_BP 32768U
114
126 #define VRNA_CONSTRAINT_DB_PIPE 65536U
127
136 #define VRNA_CONSTRAINT_DB_DOT 131072U
145 #define VRNA_CONSTRAINT_DB_X 262144U
152 #define VRNA_CONSTRAINT_DB_ANG_BRACK 524288U
161 #define VRNA_CONSTRAINT_DB_RND_BRACK 1048576U
162
174 #define VRNA_CONSTRAINT_DB_INTRAMOL 2097152U
175
187 #define VRNA_CONSTRAINT_DB_INTERMOL 4194304U
188
199 #define VRNA_CONSTRAINT_DB_GQUAD 8388608U
200
201 #define VRNA_CONSTRAINT_DB_CANONICAL_BP 16777216U
202
211 #define VRNA_CONSTRAINT_DB_WUSS 33554432U
212
213
225 #define VRNA_CONSTRAINT_DB_DEFAULT \
226 (VRNA_CONSTRAINT_DB \
227 | VRNA_CONSTRAINT_DB_PIPE \
228 | VRNA_CONSTRAINT_DB_DOT \
229 | VRNA_CONSTRAINT_DB_X \
230 | VRNA_CONSTRAINT_DB_ANG_BRACK \
231 | VRNA_CONSTRAINT_DB_RND_BRACK \
232 | VRNA_CONSTRAINT_DB_INTRAMOL \
233 | VRNA_CONSTRAINT_DB_INTERMOL \

```

```

234 | VRNA_CONSTRAINT_DB_GQUAD \
235 )
236
243 #define VRNA_CONSTRAINT_CONTEXT_EXT_LOOP      (unsigned char)0x01
244
251 #define VRNA_CONSTRAINT_CONTEXT_HP_LOOP      (unsigned char)0x02
252
259 #define VRNA_CONSTRAINT_CONTEXT_INT_LOOP      (unsigned char)0x04
260
267 #define VRNA_CONSTRAINT_CONTEXT_INT_LOOP_ENC  (unsigned char)0x08
268
275 #define VRNA_CONSTRAINT_CONTEXT_MB_LOOP      (unsigned char)0x10
276
283 #define VRNA_CONSTRAINT_CONTEXT_MB_LOOP_ENC  (unsigned char)0x20
284
288 #define VRNA_CONSTRAINT_CONTEXT_ENFORCE      (unsigned char)0x40
289
293 #define VRNA_CONSTRAINT_CONTEXT_NO_REMOVE    (unsigned char)0x80
294
295
299 #define VRNA_CONSTRAINT_CONTEXT_NONE         (unsigned char)0
300
304 #define VRNA_CONSTRAINT_CONTEXT_CLOSING_LOOPS (unsigned char)(VRNA_CONSTRAINT_CONTEXT_EXT_LOOP | \
305  VRNA_CONSTRAINT_CONTEXT_HP_LOOP | \
306  VRNA_CONSTRAINT_CONTEXT_INT_LOOP | \
307  VRNA_CONSTRAINT_CONTEXT_MB_LOOP)
308
312 #define VRNA_CONSTRAINT_CONTEXT_ENCLOSED_LOOPS (unsigned char)(VRNA_CONSTRAINT_CONTEXT_INT_LOOP_ENC | \
313  VRNA_CONSTRAINT_CONTEXT_MB_LOOP_ENC)
314
321 #define VRNA_CONSTRAINT_CONTEXT_ALL_LOOPS     (unsigned char)(VRNA_CONSTRAINT_CONTEXT_CLOSING_LOOPS | \
322  VRNA_CONSTRAINT_CONTEXT_ENCLOSED_LOOPS)
323
324
325 #define VRNA_CONSTRAINT_WINDOW_UPDATE_5       1U
326
327 #define VRNA_CONSTRAINT_WINDOW_UPDATE_3       2U
328
335 typedef enum {
336     VRNA_HC_DEFAULT,
337     VRNA_HC_WINDOW
341 } vrna_hc_type_e;
342
343
368 struct vrna_hc_s {
369     vrna_hc_type_e  type;
370     unsigned int     n;
371
372     unsigned char    state;
373
374 #ifndef VRNA_DISABLE_C11_FEATURES
375     /* C11 support for unnamed unions/structs */
376     union {
377         struct {
378 #endif
379             unsigned char *mx;
380 #ifndef VRNA_DISABLE_C11_FEATURES
381         };
382         struct {
383 #endif
384             unsigned char **matrix_local;
385 #ifndef VRNA_DISABLE_C11_FEATURES
386         };
387     };
388 #endif
389
390     int          *up_ext;
391     int          *up_hp;
392     int          *up_int;
393     int          *up_ml;
394     vrna_callback_hc_evaluate *f;
395     void         *data;
396     vrna_callback_free_auxdata *free_data;
397     vrna_hc_depot_t *depot;
398 };
399
401 struct vrna_hc_up_s {
402     int position;
403     int strand;
404     unsigned char options;
405 };
406
407 void vrna_message_constraint_options(unsigned int option);
408
409 void vrna_message_constraint_options_all(void);
410

```

```

474
489 void vrna_hc_init(vrna_fold_compound_t *vc);
490
491
492 void vrna_hc_init_window(vrna_fold_compound_t *vc);
493
494
495 int
496 vrna_hc_prepare(vrna_fold_compound_t *fc,
497                unsigned int          options);
498
499 void
500 vrna_hc_update(vrna_fold_compound_t *fc,
501               unsigned int          i,
502               unsigned int          options);
503
504
519 void vrna_hc_add_up(vrna_fold_compound_t *vc,
520                    int                    i,
521                    unsigned char         option);
522
523
524 int
525 vrna_hc_add_up_strand(vrna_fold_compound_t *fc,
526                     unsigned int          i,
527                     unsigned int          strand,
528                     unsigned char         option);
529
530 int
540 vrna_hc_add_up_batch(vrna_fold_compound_t *vc,
541                     vrna_hc_up_t         *constraints);
542
543 int
544 vrna_hc_add_up_strand_batch(vrna_fold_compound_t *fc,
545                             vrna_hc_up_t         *constraints);
546
563 int vrna_hc_add_bp(vrna_fold_compound_t *vc,
564                    int                    i,
565                    int                    j,
566                    unsigned char         option);
567
568
569 int
570 vrna_hc_add_bp_strand(vrna_fold_compound_t *fc,
571                      unsigned int          i,
572                      unsigned int          strand_i,
573                      unsigned int          j,
574                      unsigned int          strand_j,
575                      unsigned char         option);
576
594 void vrna_hc_add_bp_nonspecific(vrna_fold_compound_t *vc,
595                                int                    i,
596                                int                    d,
597                                unsigned char         option);
598
599
611 void vrna_hc_free(vrna_hc_t *hc);
612
613
618 void vrna_hc_add_f(vrna_fold_compound_t *vc,
619                   vrna_callback_hc_evaluate *f);
620
621
633 void vrna_hc_add_data(vrna_fold_compound_t *vc,
634                      void                  *data,
635                      vrna_callback_free_auxdata *f);
636
637
656 int
657 vrna_hc_add_from_db(vrna_fold_compound_t *vc,
658                   const char             *constraint,
659                   unsigned int           options);
660
661
662 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
663
671 DEPRECATED(void print_tty_constraint(unsigned int option),
672            "Use vrna_message_constraint_options() instead");
673
680 DEPRECATED(void print_tty_constraint_full(void),
681            "Use vrna_message_constraint_options_all() instead");
682
695 DEPRECATED(void constrain_ptypes(const char *constraint,
696                                unsigned int length,
697                                char *ptype,
698                                int *BP,
699                                int min_loop_size,

```



```

700                                     unsigned int idx_type),
701     "Use the new API and the hard constraint framework instead");
702
703 #endif
704
705 #endif

```

## 18.32 ViennaRNA/constraints/ligand.h File Reference

Functions for incorporation of ligands binding to hairpin and interior loop motifs using the soft constraints framework. Include dependency graph for ligand.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_sc\\_motif\\_s](#)

### Typedefs

- typedef struct [vrna\\_sc\\_motif\\_s](#) [vrna\\_sc\\_motif\\_t](#)

*Type definition for soft constraint motif.*

### Functions

- int [vrna\\_sc\\_add\\_hi\\_motif](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*seq, const char \*structure, [FLT\\_OR\\_DBL](#) energy, unsigned int options)

*Add soft constraints for hairpin or interior loop binding motif.*

#### 18.32.1 Detailed Description

Functions for incorporation of ligands binding to hairpin and interior loop motifs using the soft constraints framework.

## 18.33 ligand.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LIGAND_H
2 #define VIENNA_RNA_PACKAGE_LIGAND_H
3
19 typedef struct vrna_sc_motif_s vrna_sc_motif_t;
20
21 #include <ViennaRNA/datastructures/basic.h>
22 #include <ViennaRNA/fold_compound.h>
23
24 struct vrna_sc_motif_s {
25     int i;
26     int j;
27     int k;
28     int l;
29     int number;
30 };
31
32
59 int
60 vrna_sc_add_hi_motif(vrna_fold_compound_t *fc,
61                     const char *seq,
62                     const char *structure,
63                     FLT_OR_DBL energy,
64                     unsigned int options);
65
66
67 vrna_sc_motif_t *
68 vrna_sc_ligand_detect_motifs(vrna_fold_compound_t *fc,
69                             const char *structure);
70
71
72 vrna_sc_motif_t *
73 vrna_sc_ligand_get_all_motifs(vrna_fold_compound_t *fc);
74
75 #endif

```

## 18.34 ViennaRNA/constraints/SHAPE.h File Reference

This module provides function to incorporate SHAPE reactivity data into the folding recursions by means of soft constraints.

Include dependency graph for SHAPE.h: This graph shows which files directly or indirectly include this file:

### Functions

- int [vrna\\_sc\\_add\\_SHAPE\\_deigan](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const double \*reactivities, double m, double b, unsigned int options)  
*Add SHAPE reactivity data as soft constraints (Deigan et al. method)*
- int [vrna\\_sc\\_add\\_SHAPE\\_deigan\\_al](#)i ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*\*shape\_files, const int \*shape\_file\_association, double m, double b, unsigned int options)  
*Add SHAPE reactivity data from files as soft constraints for consensus structure prediction (Deigan et al. method)*
- int [vrna\\_sc\\_add\\_SHAPE\\_zarringhalam](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const double \*reactivities, double b, double default\_value, const char \*shape\_conversion, unsigned int options)  
*Add SHAPE reactivity data as soft constraints (Zarringhalam et al. method)*
- int [vrna\\_sc\\_SHAPE\\_parse\\_method](#) (const char \*method\_string, char \*method, float \*param\_1, float \*param\_2)  
*Parse a character string and extract the encoded SHAPE reactivity conversion method and possibly the parameters for conversion into pseudo free energies.*
- int [vrna\\_sc\\_SHAPE\\_to\\_pr](#) (const char \*shape\_conversion, double \*values, int length, double default\_value)  
*Convert SHAPE reactivity values to probabilities for being unpaired.*

### 18.34.1 Detailed Description

This module provides function to incorporate SHAPE reactivity data into the folding recursions by means of soft constraints.

### 18.34.2 Function Documentation

#### 18.34.2.1 vrna\_sc\_SHAPE\_parse\_method()

```
int vrna_sc_SHAPE_parse_method (
    const char * method_string,
    char * method,
    float * param_1,
    float * param_2 )
```

Parse a character string and extract the encoded SHAPE reactivity conversion method and possibly the parameters for conversion into pseudo free energies.

#### Parameters

|                      |                                                                                                        |
|----------------------|--------------------------------------------------------------------------------------------------------|
| <i>method_string</i> | The string that contains the encoded SHAPE reactivity conversion method                                |
| <i>method</i>        | A pointer to the memory location where the method character will be stored                             |
| <i>param_1</i>       | A pointer to the memory location where the first parameter of the corresponding method will be stored  |
| <i>param_2</i>       | A pointer to the memory location where the second parameter of the corresponding method will be stored |

## Returns

1 on successful extraction of the method, 0 on errors

## 18.35 SHAPE.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_SHAPE_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_SHAPE_H
3
4 #include <ViennaRNA/fold_compound.h>
5
23 void vrna_constraints_add_SHAPE(vrna_fold_compound_t *vc,
24                               const char *shape_file,
25                               const char *shape_method,
26                               const char *shape_conversion,
27                               int verbose,
28                               unsigned int constraint_type);
29
30 void vrna_constraints_add_SHAPE_alic(vrna_fold_compound_t *vc,
31                                     const char *shape_method,
32                                     const char **shape_files,
33                                     const int *shape_file_association,
34                                     int verbose,
35                                     unsigned int constraint_type);
61 int vrna_sc_add_SHAPE_deigan(vrna_fold_compound_t *vc,
62                              const double *reactivities,
63                              double m,
64                              double b,
65                              unsigned int options);
66
79 int vrna_sc_add_SHAPE_deigan_alic(vrna_fold_compound_t *vc,
80                                   const char **shape_files,
81                                   const int *shape_file_association,
82                                   double m,
83                                   double b,
84                                   unsigned int options);
85
108 int vrna_sc_add_SHAPE_zarringhalam(vrna_fold_compound_t *vc,
109                                    const double *reactivities,
110                                    double b,
111                                    double default_value,
112                                    const char *shape_conversion,
113                                    unsigned int options);
114
127 int vrna_sc_SHAPE_parse_method(const char *method_string,
128                                 char *method,
129                                 float *param_1,
130                                 float *param_2);
131
146 int vrna_sc_SHAPE_to_pr(const char *shape_conversion,
147                          double *values,
148                          int length,
149                          double default_value);
150
151 #endif

```

## 18.36 ViennaRNA/constraints/soft.h File Reference

Functions and data structures for secondary structure soft constraints.

Include dependency graph for soft.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_sc\\_bp\\_storage\\_t](#)  
*A base pair constraint.*
- struct [vrna\\_sc\\_s](#)  
*The soft constraints data structure. [More...](#)*

### Typedefs

- typedef struct [vrna\\_sc\\_s](#) [vrna\\_sc\\_t](#)  
*Typename for the soft constraints data structure [vrna\\_sc\\_s](#).*

- typedef int() [vrna\\_callback\\_sc\\_energy](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve pseudo energy contribution for soft constraint feature.*
- typedef FLT\_OR\_DBL() [vrna\\_callback\\_sc\\_exp\\_energy](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve pseudo energy contribution as Boltzmann Factors for soft constraint feature.*
- typedef [vrna\\_basepair\\_t](#) \*() [vrna\\_callback\\_sc\\_backtrack](#)(int i, int j, int k, int l, unsigned char d, void \*data)  
*Callback to retrieve auxiliary base pairs for soft constraint feature.*

## Enumerations

- enum [vrna\\_sc\\_type\\_e](#) { [VRNA\\_SC\\_DEFAULT](#) , [VRNA\\_SC\\_WINDOW](#) }  
*The type of a soft constraint.*

## Functions

- void [vrna\\_sc\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Initialize an empty soft constraints data structure within a [vrna\\_fold\\_compound\\_t](#).*
- int [vrna\\_sc\\_set\\_bp](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const FLT\_OR\_DBL \*\*constraints, unsigned int options)  
*Set soft constraints for paired nucleotides.*
- int [vrna\\_sc\\_add\\_bp](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, FLT\_OR\_DBL energy, unsigned int options)  
*Add soft constraints for paired nucleotides.*
- int [vrna\\_sc\\_set\\_up](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const FLT\_OR\_DBL \*constraints, unsigned int options)  
*Set soft constraints for unpaired nucleotides.*
- int [vrna\\_sc\\_add\\_up](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, FLT\_OR\_DBL energy, unsigned int options)  
*Add soft constraints for unpaired nucleotides.*
- void [vrna\\_sc\\_remove](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Remove soft constraints from [vrna\\_fold\\_compound\\_t](#).*
- void [vrna\\_sc\\_free](#) ([vrna\\_sc\\_t](#) \*sc)  
*Free memory occupied by a [vrna\\_sc\\_t](#) data structure.*
- int [vrna\\_sc\\_add\\_data](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, void \*data, [vrna\\_callback\\_free\\_auxdata](#) \*free\_data)  
*Add an auxiliary data structure for the generic soft constraints callback function.*
- int [vrna\\_sc\\_add\\_f](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_energy](#) \*f)  
*Bind a function pointer for generic soft constraint feature (MFE version)*
- int [vrna\\_sc\\_add\\_bt](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_backtrack](#) \*f)  
*Bind a backtracking function pointer for generic soft constraint feature.*
- int [vrna\\_sc\\_add\\_exp\\_f](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_sc\\_exp\\_energy](#) \*exp\_f)  
*Bind a function pointer for generic soft constraint feature (PF version)*

### 18.36.1 Detailed Description

Functions and data structures for secondary structure soft constraints.

### 18.36.2 Enumeration Type Documentation

#### 18.36.2.1 [vrna\\_sc\\_type\\_e](#)

enum [vrna\\_sc\\_type\\_e](#)

The type of a soft constraint.

#### Enumerator

|                                 |                           |
|---------------------------------|---------------------------|
| <a href="#">VRNA_SC_DEFAULT</a> | Default Soft Constraints. |
|---------------------------------|---------------------------|

## Enumerator

|                |                                                                                                                                       |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------|
| VRNA_SC_WINDOW | Soft Constraints suitable for local structure prediction using window approach.                                                       |
|                | <p><b>See also</b></p> <p><a href="#">vrna_mfe_window()</a>, <a href="#">vrna_mfe_window_zscore()</a>, <a href="#">pfl_fold()</a></p> |

## 18.37 soft.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_SOFT_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_SOFT_H
3
26 typedef struct vrna_sc_s vrna_sc_t;
27
28 #include <ViennaRNA/datastructures/basic.h>
29 #include <ViennaRNA/fold_compound.h>
30 #include <ViennaRNA/constraints/basic.h>
31
64 typedef int (vrna_callback_sc_energy) (int i,
65   int j,
66   int k,
67   int l,
68   unsigned char d,
69   void *data);
70
103 typedef FLT_OR_DBL (vrna_callback_sc_exp_energy) (int i,
104  int j,
105  int k,
106  int l,
107  unsigned char d,
108  void *data);
109
136 typedef vrna_basepair_t * (vrna_callback_sc_backtrack) (int i,
137   int j,
138   int k,
139   int l,
140   unsigned char d,
141   void *data);
142
143
147 typedef enum {
148     VRNA_SC_DEFAULT,
149     VRNA_SC_WINDOW
153 } vrna_sc_type_e;
154
155
159 typedef struct {
160     unsigned int interval_start;
161     unsigned int interval_end;
162     int e;
163 } vrna_sc_bp_storage_t;
164
165
171 struct vrna_sc_s {
172     const vrna_sc_type_e type;
173     unsigned int n;
174
175     unsigned char state;
176
177     int **energy_up;
178     FLT_OR_DBL **exp_energy_up;
179     int *up_storage;
180     vrna_sc_bp_storage_t **bp_storage;
181
183 #ifndef VRNA_DISABLE_C11_FEATURES
184     /* C11 support for unnamed unions/structs */
185     union {
186         struct {
187 #endif
188         int *energy_bp;
189         FLT_OR_DBL *exp_energy_bp;
190 #ifndef VRNA_DISABLE_C11_FEATURES
191     /* C11 support for unnamed unions/structs */
192     };
193     struct {
194 #endif
195         int **energy_bp_local;
196         FLT_OR_DBL **exp_energy_bp_local;
197 #ifndef VRNA_DISABLE_C11_FEATURES

```

```

198  /* C11 support for unnamed unions/structs */
199  };
200  };
201  #endif
202
203  int                *energy_stack;
204  FLT_OR_DBL        *exp_energy_stack;
205  /* generic soft constraints below */
206  vrna_callback_sc_energy *f;
207  vrna_callback_sc_backtrack *bt;
208  vrna_callback_sc_exp_energy *exp_f;
209  void                *data;
210  vrna_callback_free_auxdata *free_data;
211  };
212
213  void vrna_sc_init(vrna_fold_compound_t *vc);
214
215  void
216  vrna_sc_prepare(vrna_fold_compound_t *vc,
217                 unsigned int          options);
218
219  int
220  vrna_sc_update(vrna_fold_compound_t *vc,
221                unsigned int          i,
222                unsigned int          options);
223
224  int
225  vrna_sc_set_bp(vrna_fold_compound_t *vc,
226                const FLT_OR_DBL      **constraints,
227                unsigned int          options);
228
229  int
230  vrna_sc_add_bp(vrna_fold_compound_t *vc,
231                int                    i,
232                int                    j,
233                FLT_OR_DBL            energy,
234                unsigned int          options);
235
236  int
237  vrna_sc_set_up(vrna_fold_compound_t *vc,
238                const FLT_OR_DBL      **constraints,
239                unsigned int          options);
240
241  int
242  vrna_sc_add_up(vrna_fold_compound_t *vc,
243                int                    i,
244                FLT_OR_DBL            energy,
245                unsigned int          options);
246
247  int
248  vrna_sc_set_stack(vrna_fold_compound_t *vc,
249                  const FLT_OR_DBL      **constraints,
250                  unsigned int          options);
251
252  int
253  vrna_sc_set_stack_comparative(vrna_fold_compound_t *fc,
254                               const FLT_OR_DBL      **constraints,
255                               unsigned int          options);
256
257  int
258  vrna_sc_add_stack(vrna_fold_compound_t *vc,
259                  int                    i,
260                  FLT_OR_DBL            energy,
261                  unsigned int          options);
262
263  int
264  vrna_sc_add_stack_comparative(vrna_fold_compound_t *fc,
265                               int                    i,
266                               const FLT_OR_DBL      **energies,
267                               unsigned int          options);
268
269  void
270  vrna_sc_remove(vrna_fold_compound_t *vc);
271
272  void

```

```

392 vrna_sc_free(vrna_sc_t *sc);
393
394
407 int
408 vrna_sc_add_data(vrna_fold_compound_t      *vc,
409                 void                      *data,
410                 vrna_callback_free_auxdata *free_data);
411
412
413 int
414 vrna_sc_add_data_comparative(vrna_fold_compound_t      *vc,
415                              void                      **data,
416                              vrna_callback_free_auxdata **free_data);
417
418
435 int
436 vrna_sc_add_f(vrna_fold_compound_t      *vc,
437               vrna_callback_sc_energy *f);
438
439
440 int
441 vrna_sc_add_f_comparative(vrna_fold_compound_t      *vc,
442                           vrna_callback_sc_energy **f);
443
444
463 int
464 vrna_sc_add_bt(vrna_fold_compound_t      *vc,
465               vrna_callback_sc_backtrack *f);
466
467
485 int
486 vrna_sc_add_exp_f(vrna_fold_compound_t      *vc,
487                  vrna_callback_sc_exp_energy *exp_f);
488
489
490 int
491 vrna_sc_add_exp_f_comparative(vrna_fold_compound_t      *vc,
492                               vrna_callback_sc_exp_energy **exp_f);
493
494
495 #endif

```

## 18.38 ViennaRNA/constraints\_hard.h File Reference

Use [ViennaRNA/constraints/hard.h](#) instead.

Include dependency graph for constraints\_hard.h:

### 18.38.1 Detailed Description

Use [ViennaRNA/constraints/hard.h](#) instead.

**Deprecated** Use [ViennaRNA/constraints/hard.h](#) instead

## 18.39 constraints\_hard.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_HARD_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_HARD_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/constraints_hard.h>! Use
    <ViennaRNA/constraints/hard.h> instead!"
13 #  endif
14 #include <ViennaRNA/constraints/hard.h>
15 #endif
16
17 #endif

```

## 18.40 ViennaRNA/constraints\_ligand.h File Reference

Use [ViennaRNA/constraints/ligand.h](#) instead.

Include dependency graph for constraints\_ligand.h:

### 18.40.1 Detailed Description

Use [ViennaRNA/constraints/ligand.h](#) instead.

**Deprecated** Use [ViennaRNA/constraints/ligand.h](#) instead

## 18.41 constraints\_ligand.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_LIGAND_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_LIGAND_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/constraints_ligand.h>! Use
    <ViennaRNA/constraints/ligand.h> instead!"
13 # endif
14 #include <ViennaRNA/constraints/ligand.h>
15 #endif
16
17 #endif
```

## 18.42 ViennaRNA/constraints\_SHAPE.h File Reference

Use [ViennaRNA/constraints/SHAPE.h](#) instead.

Include dependency graph for constraints\_SHAPE.h:

### 18.42.1 Detailed Description

Use [ViennaRNA/constraints/SHAPE.h](#) instead.

**Deprecated** Use [ViennaRNA/constraints/SHAPE.h](#) instead

## 18.43 constraints\_SHAPE.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_SHAPE_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_SHAPE_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/constraints_SHAPE.h>! Use
    <ViennaRNA/constraints/SHAPE.h> instead!"
13 # endif
14 #include <ViennaRNA/constraints/SHAPE.h>
15 #endif
16
17 #endif
```

## 18.44 ViennaRNA/constraints\_soft.h File Reference

Use [ViennaRNA/constraints/soft.h](#) instead.

Include dependency graph for constraints\_soft.h:

### 18.44.1 Detailed Description

Use [ViennaRNA/constraints/soft.h](#) instead.

**Deprecated** Use [ViennaRNA/constraints/soft.h](#) instead

## 18.45 constraints\_soft.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_SOFT_DEPRECATED_H
```



```
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_SOFT_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/constraints_soft.h>! Use
    <ViennaRNA/constraints/soft.h> instead!"
13 # endif
14 #include <ViennaRNA/constraints/soft.h>
15 #endif
16
17 #endif
```

## 18.46 ViennaRNA/convert\_epars.h File Reference

Use [ViennaRNA/params/convert.h](#) instead.

Include dependency graph for convert\_epars.h:

### 18.46.1 Detailed Description

Use [ViennaRNA/params/convert.h](#) instead.

**Deprecated** Use [ViennaRNA/params/convert.h](#) instead

## 18.47 convert\_epars.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_CONVERT_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_CONVERT_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/convert_epars.h>! Use <ViennaRNA/params/convert.h>
    instead!"
13 # endif
14 #include <ViennaRNA/params/convert.h>
15 #endif
16
17 #endif
```

## 18.48 ViennaRNA/data\_structures.h File Reference

Use [ViennaRNA/datastructures/basic.h](#) instead.

Include dependency graph for data\_structures.h:

### 18.48.1 Detailed Description

Use [ViennaRNA/datastructures/basic.h](#) instead.

**Deprecated** Use [ViennaRNA/datastructures/basic.h](#) instead

## 18.49 data\_structures.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_DATA_STRUCTURES_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_DATA_STRUCTURES_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/data_structures.h>! Use
    <ViennaRNA/datastructures/basic.h> instead!"
13 # endif
14 #include <ViennaRNA/datastructures/basic.h>
15 #endif
16
17 #endif
```

## 18.50 ViennaRNA/datastructures/hash\_tables.h File Reference

Implementations of hash table functions.

### Data Structures

- struct [vrna\\_ht\\_entry\\_db\\_t](#)  
Default hash table entry. [More...](#)

### Functions

#### Dot-Bracket / Free Energy entries

- int [vrna\\_ht\\_db\\_comp](#) (void \*x, void \*y)  
Default hash table entry comparison.
- unsigned int [vrna\\_ht\\_db\\_hash\\_func](#) (void \*x, unsigned long hashtable\_size)  
Default hash function.
- int [vrna\\_ht\\_db\\_free\\_entry](#) (void \*hash\_entry)  
Default function to free memory occupied by a hash entry.

### Abstract interface

- typedef struct vrna\_hash\_table\_s \* [vrna\\_hash\\_table\\_t](#)  
A hash table object.
- typedef int() [vrna\\_callback\\_ht\\_compare\\_entries](#)(void \*x, void \*y)  
Callback function to compare two hash table entries.
- typedef unsigned int() [vrna\\_callback\\_ht\\_hash\\_function](#)(void \*x, unsigned long hashtable\_size)  
Callback function to generate a hash key, i.e. hash function.
- typedef int() [vrna\\_callback\\_ht\\_free\\_entry](#)(void \*x)  
Callback function to free a hash table entry.
- [vrna\\_hash\\_table\\_t](#) [vrna\\_ht\\_init](#) (unsigned int b, [vrna\\_callback\\_ht\\_compare\\_entries](#) \*compare\_function, [vrna\\_callback\\_ht\\_hash\\_function](#) \*hash\_function, [vrna\\_callback\\_ht\\_free\\_entry](#) \*free\_hash\_entry)  
Get an initialized hash table.
- unsigned long [vrna\\_ht\\_size](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Get the size of the hash table.
- unsigned long [vrna\\_ht\\_collisions](#) (struct vrna\_hash\_table\_s \*ht)  
Get the number of collisions in the hash table.
- void \* [vrna\\_ht\\_get](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Get an element from the hash table.
- int [vrna\\_ht\\_insert](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Insert an object into a hash table.
- void [vrna\\_ht\\_remove](#) ([vrna\\_hash\\_table\\_t](#) ht, void \*x)  
Remove an object from the hash table.
- void [vrna\\_ht\\_clear](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Clear the hash table.
- void [vrna\\_ht\\_free](#) ([vrna\\_hash\\_table\\_t](#) ht)  
Free all memory occupied by the hash table.

### 18.50.1 Detailed Description

Implementations of hash table functions.

## 18.51 hash\_tables.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_HASH_UTIL_H
2 #define VIENNA_RNA_PACKAGE_HASH_UTIL_H
3
4 /* Taken from the barriers tool and modified by GE. */
5
6 typedef struct vrna_hash_table_s *vrna_hash_table_t;
7
8 typedef int (vrna_callback_ht_compare_entries)(void *x,
9 void *y);
10
11 typedef unsigned int (vrna_callback_ht_hash_function)(void *x,
12 unsigned long hashtable_size);
13
14 typedef int (vrna_callback_ht_free_entry)(void *x);
15
16 vrna_hash_table_t
17 vrna_ht_init(unsigned int b,
18 vrna_callback_ht_compare_entries *compare_function,
19 vrna_callback_ht_hash_function *hash_function,
20 vrna_callback_ht_free_entry *free_hash_entry);
21
22 unsigned long
23 vrna_ht_size(vrna_hash_table_t ht);
24
25 unsigned long
26 vrna_ht_collisions(struct vrna_hash_table_s *ht);
27
28 void *
29 vrna_ht_get(vrna_hash_table_t ht,
30 void *x);
31
32 int
33 vrna_ht_insert(vrna_hash_table_t ht,
34 void *x);
35
36 void
37 vrna_ht_remove(vrna_hash_table_t ht,
38 void *x);
39
40 void
41 vrna_ht_clear(vrna_hash_table_t ht);
42
43 void
44 vrna_ht_free(vrna_hash_table_t ht);
45
46 /* End of abstract interface */
47 typedef struct {
48 char *structure;
49 float energy;
50 } vrna_ht_entry_db_t;
51
52 int
53 vrna_ht_db_comp(void *x,
54 void *y);
55
56 unsigned int
57 vrna_ht_db_hash_func(void *x,
58 unsigned long hashtable_size);
59
60 int vrna_ht_db_free_entry(void *hash_entry);
61
62 /* End of dot-bracket interface */
63 #endif

```

## 18.52 ViennaRNA/datastructures/heap.h File Reference

Implementation of an abstract heap data structure.

### Typedefs

- typedef struct vrna\_heap\_s \* [vrna\\_heap\\_t](#)  
*An abstract heap data structure.*
- typedef int([vrna\\_callback\\_heap\\_cmp](#))(const void \*a, const void \*b, void \*data)  
*Heap compare function prototype.*
- typedef size\_t([vrna\\_callback\\_heap\\_get\\_pos](#))(const void \*a, void \*data)  
*Retrieve the position of a particular heap entry within the heap.*
- typedef void([vrna\\_callback\\_heap\\_set\\_pos](#))(const void \*a, size\_t pos, void \*data)  
*Store the position of a particular heap entry within the heap.*

### Functions

- [vrna\\_heap\\_t vrna\\_heap\\_init](#) (size\_t n, [vrna\\_callback\\_heap\\_cmp](#) \*cmp, [vrna\\_callback\\_heap\\_get\\_pos](#) \*get↔  
\_entry\_pos, [vrna\\_callback\\_heap\\_set\\_pos](#) \*set\_entry\_pos, void \*data)  
*Initialize a heap data structure.*
- void [vrna\\_heap\\_free](#) ([vrna\\_heap\\_t](#) h)  
*Free memory occupied by a heap data structure.*
- size\_t [vrna\\_heap\\_size](#) (struct vrna\_heap\_s \*h)  
*Get the size of a heap data structure, i.e. the number of stored elements.*
- void [vrna\\_heap\\_insert](#) ([vrna\\_heap\\_t](#) h, void \*v)  
*Insert an element into the heap.*
- void \* [vrna\\_heap\\_pop](#) ([vrna\\_heap\\_t](#) h)  
*Pop (remove and return) the object at the root of the heap.*
- const void \* [vrna\\_heap\\_top](#) ([vrna\\_heap\\_t](#) h)  
*Get the object at the root of the heap.*
- void \* [vrna\\_heap\\_remove](#) ([vrna\\_heap\\_t](#) h, const void \*v)  
*Remove an arbitrary element within the heap.*
- void \* [vrna\\_heap\\_update](#) ([vrna\\_heap\\_t](#) h, void \*v)  
*Update an arbitrary element within the heap.*

### 18.52.1 Detailed Description

Implementation of an abstract heap data structure.

## 18.53 heap.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_HEAP_H
2 #define VIENNA_RNA_PACKAGE_HEAP_H
3
25 typedef struct vrna_heap_s *vrna_heap_t;
26
27
44 typedef int (vrna_callback_heap_cmp) (const void *a,
45                                     const void *b,
46                                     void *data);
47
48
56 typedef size_t (vrna_callback_heap_get_pos) (const void *a,
57  void *data);
58
59
67 typedef void (vrna_callback_heap_set_pos) (const void *a,
68   size_t pos,
69   void *data);

```

```

70
71
105 vrna_heap_t
106 vrna_heap_init(size_t          n,
107                vrna_callback_heap_cmp *cmp,
108                vrna_callback_heap_get_pos *get_entry_pos,
109                vrna_callback_heap_set_pos *set_entry_pos,
110                void                  *data);
111
112
120 void
121 vrna_heap_free(vrna_heap_t h);
122
123
130 size_t
131 vrna_heap_size(struct vrna_heap_s *h);
132
133
143 void
144 vrna_heap_insert(vrna_heap_t h,
145                 void        *v);
146
147
159 void *
160 vrna_heap_pop(vrna_heap_t h);
161
162
172 const void *
173 vrna_heap_top(vrna_heap_t h);
174
175
189 void *
190 vrna_heap_remove(vrna_heap_t h,
191                 const void  *v);
192
193
210 void *
211 vrna_heap_update(vrna_heap_t h,
212                 void        *v);
213
214
219 #endif

```

## 18.54 lists.h

```

1 /*
2  $Log: lists.h,v $
3  Revision 1.2  2000/10/10 08:50:01  ivo
4  some annotation for lclint
5
6  Revision 1.1  1997/08/04 21:05:32  walter
7  Initial revision
8
9 */
10
11 #ifndef __LIST_H
12 #define __LIST_H
13
14 /*----- Macros and type definitions -----*/
15
16 typedef struct LST_BUCKET {
17     struct LST_BUCKET *next;
18 }
19 LST_BUCKET;
20
21 typedef struct {
22     int count; /* Number of elements currently in list */
23     LST_BUCKET *head; /* Pointer to head element of list */
24     LST_BUCKET *z; /* Pointer to last node of list */
25     LST_BUCKET hz[2]; /* Space for head and z nodes */
26 }
27 LIST;
28
29 /* Return a pointer to the user space given the address of the header of
30 * a node.
31 */
32
33 #define LST_USERSPACE(h) ((void*)((LST_BUCKET*)(h) + 1))
34
35 /* Return a pointer to the header of a node, given the address of the
36 * user space.
37 */
38
39 #define LST_HEADER(n) ((LST_BUCKET*)(n) - 1)
40

```

```

41 /* Return a pointer to the user space of the list's head node. This user
42 * space does not actually exist, but it is useful to be able to address
43 * it to enable insertion at the start of the list.
44 */
45
46 #define LST_HEAD(l)    LST_USERSPACE((l)->head)
47
48 /* Determine if a list is empty
49 */
50
51 #define LST_EMPTY(l)    ((l)->count == 0)
52
53 /*----- Function Prototypes -----*/
54
55 /*@only@*//*@out@*/ void *lst_newnode (int size);
56 void lst_freemnode (/*@only@*/ void *node);
57 /*@only@*//*@out@*/ LIST *lst_init (void);
58 void lst_kill (LIST * l, void (*freeNode) ());
59 void lst_insertafter (LIST * l, /*@keep@*/ void *node, void *after);
60 void *lst_deletenext (/*@only@*/ LIST * l, void *node);
61 /*@dependent@*/ void *lst_first (LIST * l);
62 /*@dependent@*/ void *lst_next (void *prev);
63 void lst_mergesort (LIST * l, int (*cmp_func) ());
64
65 #endif

```

## 18.55 ViennaRNA/dist\_vars.h File Reference

Global variables for Distance-Package.

This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [Postorder\\_list](#)  
*Postorder data structure.*
- struct [Tree](#)  
*Tree data structure.*
- struct [swString](#)  
*Some other data structure.*

### Variables

- int [edit\\_backtrack](#)  
*Produce an alignment of the two structures being compared by tracing the editing path giving the minimum distance.*
- char \* [aligned\\_line](#) [4]  
*Contains the two aligned structures after a call to one of the distance functions with [edit\\_backtrack](#) set to 1.*
- int [cost\\_matrix](#)  
*Specify the cost matrix to be used for distance calculations.*

### 18.55.1 Detailed Description

Global variables for Distance-Package.

### 18.55.2 Variable Documentation

#### 18.55.2.1 edit\_backtrack

int [edit\\_backtrack](#) [extern]

Produce an alignment of the two structures being compared by tracing the editing path giving the minimum distance.  
set to 1 if you want backtracking

### 18.55.2.2 cost\_matrix

```
int cost_matrix [extern]
```

Specify the cost matrix to be used for distance calculations.

if 0, use the default cost matrix (upper matrix in example), otherwise use Shapiro's costs (lower matrix).

## 18.56 dist\_vars.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_DIST_VARS_H
2 #define VIENNA_RNA_PACKAGE_DIST_VARS_H
3
9 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
10
17 extern int    edit_backtrack;
18
23 extern char *aligned_line[4];
24
31 extern int    cost_matrix;
32
33 /* Global type defs for Distance-Package */
34
38 typedef struct {
39     int    type;
40     int    weight;
41     int    father;
42     int    sons;
43     int    leftmostleaf;
44 } Postorder_list;
45
49 typedef struct {
50     Postorder_list *postorder_list;
51     int             *keyroots;
52 } Tree;
53
57 typedef struct {
58     int    type;
59     int    sign;
60     float  weight;
61 } swString;
62 #endif
63
64 #endif
```

## 18.57 ViennaRNA/dp\_matrices.h File Reference

Functions to deal with standard dynamic programming (DP) matrices.

Include dependency graph for dp\_matrices.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_mx\\_mfe\\_s](#)  
Minimum Free Energy (MFE) Dynamic Programming (DP) matrices data structure required within the [vrna\\_fold\\_compound\\_t](#). [More...](#)
- struct [vrna\\_mx\\_pf\\_s](#)  
Partition function (PF) Dynamic Programming (DP) matrices data structure required within the [vrna\\_fold\\_compound\\_t](#). [More...](#)

### Typedefs

- typedef struct [vrna\\_mx\\_mfe\\_s](#) [vrna\\_mx\\_mfe\\_t](#)  
Typename for the Minimum Free Energy (MFE) DP matrices data structure [vrna\\_mx\\_mfe\\_s](#).
- typedef struct [vrna\\_mx\\_pf\\_s](#) [vrna\\_mx\\_pf\\_t](#)  
Typename for the Partition Function (PF) DP matrices data structure [vrna\\_mx\\_pf\\_s](#).

## Enumerations

- enum `vrna_mx_type_e` { `VRNA_MX_DEFAULT` , `VRNA_MX_WINDOW` , `VRNA_MX_2DFOLD` }  
*An enumerator that is used to specify the type of a polymorphic Dynamic Programming (DP) matrix data structure.*

## Functions

- int `vrna_mx_add` (`vrna_fold_compound_t` \*vc, `vrna_mx_type_e` type, unsigned int options)  
*Add Dynamic Programming (DP) matrices (allocate memory)*
- void `vrna_mx_mfe_free` (`vrna_fold_compound_t` \*vc)  
*Free memory occupied by the Minimum Free Energy (MFE) Dynamic Programming (DP) matrices.*
- void `vrna_mx_pf_free` (`vrna_fold_compound_t` \*vc)  
*Free memory occupied by the Partition Function (PF) Dynamic Programming (DP) matrices.*

### 18.57.1 Detailed Description

Functions to deal with standard dynamic programming (DP) matrices.

## 18.58 dp\_matrices.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_DP_MATRICES_H
2 #define VIENNA_RNA_PACKAGE_DP_MATRICES_H
3
4 typedef struct vrna_mx_mfe_s vrna_mx_mfe_t;
5 typedef struct vrna_mx_pf_s vrna_mx_pf_t;
6
7 #include <ViennaRNA/datastructures/basic.h>
8 #include <ViennaRNA/fold_compound.h>
9
10 typedef enum {
11     VRNA_MX_DEFAULT,
12     VRNA_MX_WINDOW,
13     VRNA_MX_2DFOLD
14 } vrna_mx_type_e;
15
16 struct vrna_mx_mfe_s {
17     const vrna_mx_type_e type;
18     unsigned int length;
19     unsigned int strands;
20 #ifndef VRNA_DISABLE_C11_FEATURES
21     /* C11 support for unnamed unions/structs */
22     union {
23         struct {
24 #endif
25             int *c;
26             int *f5;
27             int *f3;
28             int **fms5;
29             int **fms3;
30             int *fML;
31             int *fM1;
32             int *fM2;
33             int *ggg;
34             int Fc;
35             int FcH;
36             int FcI;
37             int FcM;
38 #ifndef VRNA_DISABLE_C11_FEATURES
39             /* C11 support for unnamed unions/structs */
40         };
41     } struct {
42 #endif
43         int **c_local;
44         int *f3_local;
45         int **fML_local;
46         int **ggg_local;
47 #ifndef VRNA_DISABLE_C11_FEATURES
48         /* C11 support for unnamed unions/structs */
49     };
50     struct {
51 #endif
52         int ***E_F5;
53         int **l_min_F5;
54     };
55 };
```



```

114  int          **l_max_F5;
115  int          *k_min_F5;
116  int          *k_max_F5;
117
118  int          ***E_F3;
119  int          **l_min_F3;
120  int          **l_max_F3;
121  int          *k_min_F3;
122  int          *k_max_F3;
123
124  int          ***E_C;
125  int          **l_min_C;
126  int          **l_max_C;
127  int          *k_min_C;
128  int          *k_max_C;
129
130  int          ***E_M;
131  int          **l_min_M;
132  int          **l_max_M;
133  int          *k_min_M;
134  int          *k_max_M;
135
136  int          ***E_M1;
137  int          **l_min_M1;
138  int          **l_max_M1;
139  int          *k_min_M1;
140  int          *k_max_M1;
141
142  int          ***E_M2;
143  int          **l_min_M2;
144  int          **l_max_M2;
145  int          *k_min_M2;
146  int          *k_max_M2;
147
148  int          **E_Fc;
149  int          *l_min_Fc;
150  int          *l_max_Fc;
151  int          k_min_Fc;
152  int          k_max_Fc;
153
154  int          **E_FcH;
155  int          *l_min_FcH;
156  int          *l_max_FcH;
157  int          k_min_FcH;
158  int          k_max_FcH;
159
160  int          **E_FcI;
161  int          *l_min_FcI;
162  int          *l_max_FcI;
163  int          k_min_FcI;
164  int          k_max_FcI;
165
166  int          **E_FcM;
167  int          *l_min_FcM;
168  int          *l_max_FcM;
169  int          k_min_FcM;
170  int          k_max_FcM;
171
172  /* auxiliary arrays for remaining set of coarse graining (k,l) > (k_max, l_max) */
173  int          *E_F5_rem;
174  int          *E_F3_rem;
175  int          *E_C_rem;
176  int          *E_M_rem;
177  int          *E_M1_rem;
178  int          *E_M2_rem;
179
180  int          E_Fc_rem;
181  int          E_FcH_rem;
182  int          E_FcI_rem;
183  int          E_FcM_rem;
184
185  #ifdef COUNT_STATES
186  unsigned long ***N_F5;
187  unsigned long ***N_C;
188  unsigned long ***N_M;
189  unsigned long ***N_M1;
190  #endif
191
192  #ifndef VRNA_DISABLE_C11_FEATURES
193  /* C11 support for unnamed unions/structs */
194  };
195  };
196  #endif
197
206  struct vrna_mx_pf_s {
207      const vrna_mx_type_e type;

```

```

211 unsigned int          length;
212 FLT_OR_DBL            *scale;
213 FLT_OR_DBL            *expMLbase;
219 #ifndef VRNA_DISABLE_C11_FEATURES
220 /* C11 support for unnamed unions/structs */
221 union {
222     struct {
223 #endif
224
225     FLT_OR_DBL *q;
226     FLT_OR_DBL *qb;
227     FLT_OR_DBL *qm;
228     FLT_OR_DBL *qml;
229     FLT_OR_DBL *probs;
230     FLT_OR_DBL *qlk;
231     FLT_OR_DBL *qln;
232     FLT_OR_DBL *G;
233
234     FLT_OR_DBL qo;
235     FLT_OR_DBL qm2;
236     FLT_OR_DBL qho;
237     FLT_OR_DBL qio;
238     FLT_OR_DBL qmo;
239
240 #ifndef VRNA_DISABLE_C11_FEATURES
241 /* C11 support for unnamed unions/structs */
242 };
243 struct {
244 #endif
245
246     FLT_OR_DBL **q_local;
247     FLT_OR_DBL **qb_local;
248     FLT_OR_DBL **qm_local;
249     FLT_OR_DBL **pR;
250     FLT_OR_DBL **qm2_local;
251     FLT_OR_DBL **QI5;
252     FLT_OR_DBL **q2l;
253     FLT_OR_DBL **qmb;
254     FLT_OR_DBL **G_local;
255 #ifndef VRNA_DISABLE_C11_FEATURES
256 /* C11 support for unnamed unions/structs */
257 };
258 struct {
259 #endif
260
261     FLT_OR_DBL ***Q;
262     int **l_min_Q;
263     int **l_max_Q;
264     int *k_min_Q;
265     int *k_max_Q;
266
267     FLT_OR_DBL ***Q_B;
268     int **l_min_Q_B;
269     int **l_max_Q_B;
270     int *k_min_Q_B;
271     int *k_max_Q_B;
272
273     FLT_OR_DBL ***Q_M;
274     int **l_min_Q_M;
275     int **l_max_Q_M;
276     int *k_min_Q_M;
277     int *k_max_Q_M;
278
279     FLT_OR_DBL ***Q_M1;
280     int **l_min_Q_M1;
281     int **l_max_Q_M1;
282     int *k_min_Q_M1;
283     int *k_max_Q_M1;
284
285     FLT_OR_DBL ***Q_M2;
286     int **l_min_Q_M2;
287     int **l_max_Q_M2;
288     int *k_min_Q_M2;
289     int *k_max_Q_M2;
290
291     FLT_OR_DBL **Q_c;
292     int *l_min_Q_c;
293     int *l_max_Q_c;
294     int k_min_Q_c;
295     int k_max_Q_c;
296
297     FLT_OR_DBL **Q_cH;
298     int *l_min_Q_cH;
299     int *l_max_Q_cH;
300     int k_min_Q_cH;
301     int k_max_Q_cH;
302

```

```

326
327     FLT_OR_DBL **Q_cI;
328     int *l_min_Q_cI;
329     int *l_max_Q_cI;
330     int k_min_Q_cI;
331     int k_max_Q_cI;
332
333     FLT_OR_DBL **Q_cM;
334     int *l_min_Q_cM;
335     int *l_max_Q_cM;
336     int k_min_Q_cM;
337     int k_max_Q_cM;
338
339     /* auxiliary arrays for remaining set of coarse graining (k,l) > (k_max, l_max) */
340     FLT_OR_DBL *Q_rem;
341     FLT_OR_DBL *Q_B_rem;
342     FLT_OR_DBL *Q_M_rem;
343     FLT_OR_DBL *Q_M1_rem;
344     FLT_OR_DBL *Q_M2_rem;
345
346     FLT_OR_DBL Q_c_rem;
347     FLT_OR_DBL Q_cH_rem;
348     FLT_OR_DBL Q_cI_rem;
349     FLT_OR_DBL Q_cM_rem;
350 #ifndef VRNA_DISABLE_C11_FEATURES
351     /* C11 support for unnamed unions/structs */
352 };
353 #endif
354 };
355
356 int
357 vrna_mx_add(vrna_fold_compound_t *vc,
358             vrna_mx_type_e type,
359             unsigned int options);
360
361 int
362 vrna_mx_mfe_add(vrna_fold_compound_t *vc,
363                 vrna_mx_type_e mx_type,
364                 unsigned int options);
365
366 int
367 vrna_mx_pf_add(vrna_fold_compound_t *vc,
368                vrna_mx_type_e mx_type,
369                unsigned int options);
370
371 int
372 vrna_mx_prepare(vrna_fold_compound_t *vc,
373                 unsigned int options);
374
375 void
376 vrna_mx_mfe_free(vrna_fold_compound_t *vc);
377
378 void
379 vrna_mx_pf_free(vrna_fold_compound_t *vc);
380 #endif

```

## 18.59 ViennaRNA/duplex.h File Reference

Functions for simple RNA-RNA duplex interactions.  
Include dependency graph for duplex.h:

### 18.59.1 Detailed Description

Functions for simple RNA-RNA duplex interactions.

## 18.60 duplex.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_DUPLEX_H
2 #define VIENNA_RNA_PACKAGE_DUPLEX_H

```

```

3
4 #include <ViennaRNA/datastructures/basic.h>
5
6 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
7
15 duplexT duplexfold(const char *s1,
16                     const char *s2);
17
18
19 duplexT *duplex_subopt(const char *s1,
20                       const char *s2,
21                       int delta,
22                       int w);
23
24
25 duplexT aliduplexfold(const char *s1[],
26                      const char *s2[]);
27
28
29 duplexT *aliduplex_subopt(const char *s1[],
30                          const char *s2[],
31                          int delta,
32                          int w);
33
34
35 #endif
36
37 #endif

```

## 18.61 ViennaRNA/edit\_cost.h File Reference

global variables for Edit Costs included by treedist.c and stringdist.c

### 18.61.1 Detailed Description

global variables for Edit Costs included by treedist.c and stringdist.c

## 18.62 edit\_cost.h

[Go to the documentation of this file.](#)

```

1
6 #define PRIVATE static
7
8 PRIVATE char sep = ':';
9 PRIVATE char *coding = "Null:U:P:H:B:I:M:S:E:R";
10
11 #define DIST_INF 10000 /* infinity */
12
13 typedef int CostMatrix[10][10];
14
15 PRIVATE CostMatrix *EditCost; /* will point to UsualCost or ShapiroCost */
16
17 PRIVATE CostMatrix UsualCost =
18 {
19
20 /* Null, U, P, H, B, I, M, S, E, R
21 */
22 { 0, 1, 2, 2, 2, 2, 2, 1, 1, DIST_INF},
23 /* Null replaced */
24 { 1, 0, 1, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF},
25 /* U replaced */
26 { 2, 1, 0, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF},
27 /* P replaced */
28 { 2, DIST_INF, DIST_INF, 0, 2, 2, 2, DIST_INF, DIST_INF, DIST_INF},
29 /* H replaced */
30 { 2, DIST_INF, DIST_INF, 2, 0, 1, 2, DIST_INF, DIST_INF, DIST_INF},
31 /* B replaced */
32 { 2, DIST_INF, DIST_INF, 2, 1, 0, 2, DIST_INF, DIST_INF, DIST_INF},
33 /* I replaced */
34 { 2, DIST_INF, DIST_INF, 2, 2, 2, 0, DIST_INF, DIST_INF, DIST_INF},
35 /* M replaced */
36 { 1, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, 0, DIST_INF, DIST_INF},
37 /* S replaced */
38 { 1, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, 0, DIST_INF},
39 /* E replaced */
40 { DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, 0},
41 /* R replaced */
42

```

```

33 };
34
35
36 PRIVATE CostMatrix ShapiroCost =
37 {
38
39 /*      Null,      U,      P,      H,      B,      I,      M,      S,      E,      R
40      */
41 {      0,      1,      2,      100,      5,      5,      75,      5,      5, DIST_INF},
42 /* Null replaced */
43 {      1,      0,      1, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF},
44 /* U replaced */
45 {      2,      1,      0, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF},
46 /* P replaced */
47 { 100, DIST_INF, DIST_INF,      0,      8,      8,      8, DIST_INF, DIST_INF, DIST_INF},
48 /* H replaced */
49 {      5, DIST_INF, DIST_INF,      8,      0,      3,      8, DIST_INF, DIST_INF, DIST_INF},
50 /* B replaced */
51 {      5, DIST_INF, DIST_INF,      8,      3,      0,      8, DIST_INF, DIST_INF, DIST_INF},
52 /* I replaced */
53 { 75, DIST_INF, DIST_INF,      8,      8,      8,      0, DIST_INF, DIST_INF, DIST_INF},
54 /* M replaced */
55 {      5, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF,      0, DIST_INF, DIST_INF},
56 /* S replaced */
57 {      5, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF,      0, DIST_INF},
58 /* E replaced */
59 { DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF, DIST_INF,      0},
60 /* R replaced */
61
62 };
63

```

## 18.63 ViennaRNA/energy\_const.h File Reference

Use [ViennaRNA/params/constants.h](#) instead.

Include dependency graph for energy\_const.h:

### 18.63.1 Detailed Description

Use [ViennaRNA/params/constants.h](#) instead.

**Deprecated** Use [ViennaRNA/params/constants.h](#) instead

## 18.64 energy\_const.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_CONSTANTS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_CONSTANTS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/energy_const.h>! Use <ViennaRNA/params/constants.h>
13 #   instead!"
14 #   endif
15 #include <ViennaRNA/params/constants.h>
16 #endif
17 #endif

```

## 18.65 ViennaRNA/energy\_par.h File Reference

Use [ViennaRNA/params/default.h](#) instead.

Include dependency graph for energy\_par.h:

### 18.65.1 Detailed Description

Use [ViennaRNA/params/default.h](#) instead.

**Deprecated** Use [ViennaRNA/params/default.h](#) instead

## 18.66 energy\_par.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_DEFAULT_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_DEFAULT_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/energy_par.h>! Use <ViennaRNA/params/default.h>
    instead!"
13 #   endif
14 #include <ViennaRNA/params/default.h>
15 #endif
16
17 #endif
```

## 18.67 ViennaRNA/equilibrium\_probs.h File Reference

Equilibrium Probability implementations.

Include dependency graph for equilibrium\_probs.h: This graph shows which files directly or indirectly include this file:

### Functions

#### Base pair probabilities and derived computations

- int [vrna\\_pairing\\_probs](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)
- double [vrna\\_mean\\_bp\\_distance\\_pr](#) (int length, [FLT\\_OR\\_DBL](#) \*pr)  
*Get the mean base pair distance in the thermodynamic ensemble from a probability matrix.*
- double [vrna\\_mean\\_bp\\_distance](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Get the mean base pair distance in the thermodynamic ensemble.*
- double [vrna\\_ensemble\\_defect\\_pt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const short \*pt)  
*Compute the Ensemble Defect for a given target structure provided as a **vrna\_ptable**.*
- double [vrna\\_ensemble\\_defect](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Compute the Ensemble Defect for a given target structure.*
- double \* [vrna\\_positional\\_entropy](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)  
*Compute a vector of positional entropies.*
- [vrna\\_ep\\_t](#) \* [vrna\\_stack\\_prob](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double cutoff)  
*Compute stacking probabilities.*

#### Multimer probabilities computations

- void [vrna\\_pf\\_dimer\\_probs](#) (double FAB, double FA, double FB, [vrna\\_ep\\_t](#) \*prAB, const [vrna\\_ep\\_t](#) \*prA, const [vrna\\_ep\\_t](#) \*prB, int Alength, const [vrna\\_exp\\_param\\_t](#) \*exp\_params)  
*Compute Boltzmann probabilities of dimerization without homodimers.*

#### Structure probability computations

- double [vrna\\_pr\\_structure](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Compute the equilibrium probability of a particular secondary structure.*
- double [vrna\\_pr\\_energy](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double e)

### 18.67.1 Detailed Description

Equilibrium Probability implementations.

This file includes various implementations for equilibrium probability computations based on the partition function of an RNA sequence, two concatenated sequences, or a sequence alignment.

## 18.68 equilibrium\_probs.h

[Go to the documentation of this file.](#)

```

1  #ifndef VIENNA_RNA_PACKAGE_EQUILIBRIUM_PROBS_H
2  #define VIENNA_RNA_PACKAGE_EQUILIBRIUM_PROBS_H
3
4  #include <ViennaRNA/datastructures/basic.h>
5  #include <ViennaRNA/fold_compound.h>
6  #include <ViennaRNA/utils/structures.h>
7  #include <ViennaRNA/params/basic.h>
8
20 /*
21 #####
22 # BASE PAIR PROBABILITY RELATED FUNCTIONS #
23 #####
24 */
25
62 int
63 vrna_pairing_probs(vrna_fold_compound_t *vc,
64                   char *structure);
65
66
82 double
83 vrna_mean_bp_distance_pr(int length,
84                          FLT_OR_DBL *pr);
85
86
101 double
102 vrna_mean_bp_distance(vrna_fold_compound_t *vc);
103
104
127 double
128 vrna_ensemble_defect_pt(vrna_fold_compound_t *fc,
129                         const short *pt);
130
131
155 double
156 vrna_ensemble_defect(vrna_fold_compound_t *fc,
157                     const char *structure);
158
159
182 double *
183 vrna_positional_entropy(vrna_fold_compound_t *fc);
184
185
196 vrna_ep_t *
197 vrna_stack_prob(vrna_fold_compound_t *vc,
198                double cutoff);
199
200
201 /* End base pair related functions */
202 void
203 vrna_pf_dimer_probs(double FAB,
204                    double FA,
205                    double FB,
206                    vrna_ep_t *prAB,
207                    const vrna_ep_t *prA,
208                    const vrna_ep_t *prB,
209                    int Alength,
210                    const vrna_exp_param_t *exp_params);
211
212
238 /* End multimer probability related functions */
239 double
240 vrna_pr_structure(vrna_fold_compound_t *fc,
241                  const char *structure);
242
243 double
244 vrna_pr_energy(vrna_fold_compound_t *vc,
245               double e);
246
247
278 /* End structure probability related functions */
281 /* End thermodynamics */
284 #endif

```

## 18.69 ViennaRNA/eval.h File Reference

Functions and variables related to energy evaluation of sequence/structure pairs.

Include dependency graph for eval.h: This graph shows which files directly or indirectly include this file:

## Macros

- `#define VRNA_VERBOSITY_QUIET -1`  
*Quiet level verbosity setting.*
- `#define VRNA_VERBOSITY_DEFAULT 1`  
*Default level verbosity setting.*

## Functions

- `int vrna_eval_loop_pt (vrna_fold_compound_t *fc, int i, const short *pt)`  
*Calculate energy of a loop.*
- `int vrna_eval_loop_pt_v (vrna_fold_compound_t *fc, int i, const short *pt, int verbosity_level)`  
*Calculate energy of a loop.*
- `float vrna_eval_move (vrna_fold_compound_t *fc, const char *structure, int m1, int m2)`  
*Calculate energy of a move (closing or opening of a base pair)*
- `int vrna_eval_move_pt (vrna_fold_compound_t *fc, short *pt, int m1, int m2)`  
*Calculate energy of a move (closing or opening of a base pair)*
- `float energy_of_structure (const char *string, const char *structure, int verbosity_level)`  
*Calculate the free energy of an already folded RNA using global model detail settings.*
- `float energy_of_struct_par (const char *string, const char *structure, vrna_param_t *parameters, int verbosity_level)`  
*Calculate the free energy of an already folded RNA.*
- `float energy_of_circ_structure (const char *string, const char *structure, int verbosity_level)`  
*Calculate the free energy of an already folded circular RNA.*
- `float energy_of_circ_struct_par (const char *string, const char *structure, vrna_param_t *parameters, int verbosity_level)`  
*Calculate the free energy of an already folded circular RNA.*
- `int energy_of_structure_pt (const char *string, short *ptable, short *s, short *s1, int verbosity_level)`  
*Calculate the free energy of an already folded RNA.*
- `int energy_of_struct_pt_par (const char *string, short *ptable, short *s, short *s1, vrna_param_t *parameters, int verbosity_level)`  
*Calculate the free energy of an already folded RNA.*
- `float energy_of_move (const char *string, const char *structure, int m1, int m2)`  
*Calculate energy of a move (closing or opening of a base pair)*
- `int energy_of_move_pt (short *pt, short *s, short *s1, int m1, int m2)`  
*Calculate energy of a move (closing or opening of a base pair)*
- `int loop_energy (short *ptable, short *s, short *s1, int i)`  
*Calculate energy of a loop.*
- `float energy_of_struct (const char *string, const char *structure)`
- `int energy_of_struct_pt (const char *string, short *ptable, short *s, short *s1)`
- `float energy_of_circ_struct (const char *string, const char *structure)`

## Basic Energy Evaluation Interface with Dot-Bracket Structure String

- `float vrna_eval_structure (vrna_fold_compound_t *fc, const char *structure)`  
*Calculate the free energy of an already folded RNA.*
- `float vrna_eval_covar_structure (vrna_fold_compound_t *fc, const char *structure)`  
*Calculate the pseudo energy derived by the covariance scores of a set of aligned sequences.*
- `float vrna_eval_structure_verbose (vrna_fold_compound_t *fc, const char *structure, FILE *file)`  
*Calculate the free energy of an already folded RNA and print contributions on a per-loop base.*
- `float vrna_eval_structure_v (vrna_fold_compound_t *fc, const char *structure, int verbosity_level, FILE *file)`  
*Calculate the free energy of an already folded RNA and print contributions on a per-loop base.*
- `float vrna_eval_structure_cstr (vrna_fold_compound_t *fc, const char *structure, int verbosity_level, vrna_cstr_t output_stream)`



### Basic Energy Evaluation Interface with Structure Pair Table

- int [vrna\\_eval\\_structure\\_pt](#) (vrna\_fold\_compound\_t \*fc, const short \*pt)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_verbose](#) (vrna\_fold\_compound\_t \*fc, const short \*pt, FILE \*file)  
*Calculate the free energy of an already folded RNA.*
- int [vrna\\_eval\\_structure\\_pt\\_v](#) (vrna\_fold\_compound\_t \*fc, const short \*pt, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA.*

### Simplified Energy Evaluation with Sequence and Dot-Bracket Strings

- float [vrna\\_eval\\_structure\\_simple](#) (const char \*string, const char \*structure)  
*Calculate the free energy of an already folded RNA.*
- float [vrna\\_eval\\_circ\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the sequence is circular.*
- float [vrna\\_eval\\_gquad\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_circ\\_gquad\\_structure](#) (const char \*string, const char \*structure)  
*Evaluate the free energy of a sequence/structure pair where the sequence is circular and the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_structure\\_simple\\_verbose](#) (const char \*string, const char \*structure, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions per loop.*
- float [vrna\\_eval\\_structure\\_simple\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate free energy of a sequence/structure pair, assume sequence to be circular and print contributions per loop.*
- float [vrna\\_eval\\_gquad\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate free energy of a sequence/structure pair, allow for G-Quadruplexes in the structure and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_gquad\\_structure\\_v](#) (const char \*string, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate free energy of a sequence/structure pair, assume sequence to be circular, allow for G-Quadruplexes in the structure, and print contributions per loop.*

### Simplified Energy Evaluation with Sequence Alignments and Consensus Structure Dot-Bracket String

- float [vrna\\_eval\\_consensus\\_structure\\_simple](#) (const char \*\*alignment, const char \*structure)  
*Calculate the free energy of an already folded RNA sequence alignment.*
- float [vrna\\_eval\\_circ\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequences are circular.*
- float [vrna\\_eval\\_gquad\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_circ\\_gquad\\_consensus\\_structure](#) (const char \*\*alignment, const char \*structure)  
*Evaluate the free energy of a multiple sequence alignment/consensus structure pair where the sequence is circular and the structure may contain G-Quadruplexes.*
- float [vrna\\_eval\\_consensus\\_structure\\_simple\\_verbose](#) (const char \*\*alignment, const char \*structure, FILE \*file)  
*Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop.*
- float [vrna\\_eval\\_consensus\\_structure\\_simple\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)  
*Evaluate the free energy of a consensus structure for an RNA sequence alignment and print contributions per loop.*
- float [vrna\\_eval\\_circ\\_consensus\\_structure\\_v](#) (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)

*Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences and print contributions per loop.*

- float `vrna_eval_gquad_consensus_structure_v` (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)

*Evaluate the free energy of a consensus structure for an RNA sequence alignment, allow for annotated G↔Quadruplexes in the structure and print contributions per loop.*

- float `vrna_eval_circ_gquad_consensus_structure_v` (const char \*\*alignment, const char \*structure, int verbosity\_level, FILE \*file)

*Evaluate the free energy of a consensus structure for an alignment of circular RNA sequences, allow for annotated G-Quadruplexes in the structure and print contributions per loop.*

### Simplified Energy Evaluation with Sequence String and Structure Pair Table

- int `vrna_eval_structure_pt_simple` (const char \*string, const short \*pt)  
*Calculate the free energy of an already folded RNA.*
- int `vrna_eval_structure_pt_simple_verbose` (const char \*string, const short \*pt, FILE \*file)  
*Calculate the free energy of an already folded RNA.*
- int `vrna_eval_structure_pt_simple_v` (const char \*string, const short \*pt, int verbosity\_level, FILE \*file)  
*Calculate the free energy of an already folded RNA.*

### Simplified Energy Evaluation with Sequence Alignment and Consensus Structure Pair Table

- int `vrna_eval_consensus_structure_pt_simple` (const char \*\*alignment, const short \*pt)  
*Evaluate the Free Energy of a Consensus Secondary Structure given a Sequence Alignment.*
- int `vrna_eval_consensus_structure_pt_simple_verbose` (const char \*\*alignment, const short \*pt, FILE \*file)
- int `vrna_eval_consensus_structure_pt_simple_v` (const char \*\*alignment, const short \*pt, int verbosity\_level, FILE \*file)

## Variables

- int `cut_point`  
*first pos of second seq for cofolding*
- int `eos_debug`  
*verbose info from energy\_of\_struct*

## 18.69.1 Detailed Description

Functions and variables related to energy evaluation of sequence/structure pairs.

## 18.70 eval.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_EVAL_H
2 #define VIENNA_RNA_PACKAGE_EVAL_H
3
4 #include <stdio.h>
5 #include <ViennaRNA/datastructures/basic.h>
6 #include <ViennaRNA/fold_compound.h>
7 #include <ViennaRNA/datastructures/char_stream.h>
8 #include <ViennaRNA/landscape/move.h>
9 #include <ViennaRNA/params/basic.h> /* for deprecated functions */
10
11 #ifdef VRNA_WARN_DEPRECATED
12 # if defined(__clang__)
13 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
14 # elif defined(__GNUC__)
15 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
16 # else
17 #  define DEPRECATED(func, msg) func
18 # endif
19 #else
20 # define DEPRECATED(func, msg) func
21 #endif
22
23
```

```

58 #define VRNA_VERBOSITY_QUIET      -1
59
60
64 #define VRNA_VERBOSITY_DEFAULT    1
65
66
93 float
94 vrna_eval_structure(vrna_fold_compound_t *fc,
95                    const char *structure);
96
97
118 float
119 vrna_eval_covar_structure(vrna_fold_compound_t *fc,
120                          const char *structure);
121
122
136 float
137 vrna_eval_structure_verbose(vrna_fold_compound_t *fc,
138                            const char *structure,
139                            FILE *file);
140
141
167 float
168 vrna_eval_structure_v(vrna_fold_compound_t *fc,
169                      const char *structure,
170                      int verbosity_level,
171                      FILE *file);
172
173
174 float
175 vrna_eval_structure_cstr(vrna_fold_compound_t *fc,
176                        const char *structure,
177                        int verbosity_level,
178                        vrna_cstr_t output_stream);
179
180
181 /* End basic eval interface */
208 int
209 vrna_eval_structure_pt(vrna_fold_compound_t *fc,
210                      const short *pt);
211
212
226 int
227 vrna_eval_structure_pt_verbose(vrna_fold_compound_t *fc,
228                               const short *pt,
229                               FILE *file);
230
231
257 int
258 vrna_eval_structure_pt_v(vrna_fold_compound_t *fc,
259                         const short *pt,
260                         int verbosity_level,
261                         FILE *file);
262
263
264 /* End basic eval interface with pair table */
288 float
289 vrna_eval_structure_simple(const char *string,
290                          const char *structure);
291
292
303 float
304 vrna_eval_circ_structure(const char *string,
305                        const char *structure);
306
307
325 float
326 vrna_eval_gquad_structure(const char *string,
327                          const char *structure);
328
329
348 float
349 vrna_eval_circ_gquad_structure(const char *string,
350                              const char *structure);
351
352
367 float
368 vrna_eval_structure_simple_verbose(const char *string,
369                                   const char *structure,
370                                   FILE *file);
371
372
396 float
397 vrna_eval_structure_simple_v(const char *string,
398                             const char *structure,
399                             int verbosity_level,
400                             FILE *file);

```

```
401
402
418 float
419 vrna_eval_circ_structure_v(const char *string,
420                           const char *structure,
421                           int         verbosity_level,
422                           FILE        *file);
423
424
447 float
448 vrna_eval_gquad_structure_v(const char *string,
449                             const char *structure,
450                             int         verbosity_level,
451                             FILE        *file);
452
453
474 float
475 vrna_eval_circ_gquad_structure_v(const char *string,
476                                 const char *structure,
477                                 int         verbosity_level,
478                                 FILE        *file);
479
480
481 /* End simplified eval interface */
511 float
512 vrna_eval_consensus_structure_simple(const char **alignment,
513                                     const char *structure);
514
515
531 float
532 vrna_eval_circ_consensus_structure(const char **alignment,
533                                   const char *structure);
534
535
558 float
559 vrna_eval_gquad_consensus_structure(const char **alignment,
560                                    const char *structure);
561
562
585 float
586 vrna_eval_circ_gquad_consensus_structure(const char **alignment,
587  const char *structure);
588
589
609 float
610 vrna_eval_consensus_structure_simple_verbose(const char **alignment,
611  const char *structure,
612  FILE        *file);
613
614
639 float
640 vrna_eval_consensus_structure_simple_v(const char **alignment,
641                                       const char *structure,
642                                       int         verbosity_level,
643                                       FILE        *file);
644
645
665 float
666 vrna_eval_circ_consensus_structure_v(const char **alignment,
667                                       const char *structure,
668                                       int         verbosity_level,
669                                       FILE        *file);
670
671
698 float
699 vrna_eval_gquad_consensus_structure_v(const char **alignment,
700                                       const char *structure,
701                                       int         verbosity_level,
702                                       FILE        *file);
703
704
731 float
732 vrna_eval_circ_gquad_consensus_structure_v(const char **alignment,
733   const char *structure,
734   int         verbosity_level,
735   FILE        *file);
736
737
738 /* End simplified comparative eval interface */
761 int
762 vrna_eval_structure_pt_simple(const char *string,
763                              const short *pt);
764
765
779 int
780 vrna_eval_structure_pt_simple_verbose(const char *string,
781                                       const short *pt,
```

```

782                                     FILE          *file);
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808
809 int
810 vrna_eval_structure_pt_simple_v(const char *string,
811                                const short *pt,
812                                int          verbosity_level,
813                                FILE        *file);
814
815
816 /* End simplified eval interface with pair table */
817
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832
833 vrna_eval_consensus_structure_pt_simple(const char **alignment,
834   const short *pt);
835
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838
839
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841
842
843 int
844 vrna_eval_consensus_structure_pt_simple_verbose(const char **alignment,
845  const short *pt,
846  FILE        *file);
847
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855
856 /* End simplified eval interface with pair table */
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887
888 vrna_eval_loop_pt(vrna_fold_compound_t *fc,
889                  int                    i,
890                  const short            *pt);
891
892
893
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895
896
897
898
899
900
901
902 int
903 vrna_eval_loop_pt_v(vrna_fold_compound_t *fc,
904                    int                    i,
905                    const short            *pt,
906                    int                    verbosity_level);
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942
943 float
944 vrna_eval_move(vrna_fold_compound_t *fc,
945               const char             *structure,
946               int                    m1,
947               int                    m2);
948
949
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961
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963
964 int
965 vrna_eval_move_pt(vrna_fold_compound_t *fc,
966                  short                  *pt,
967                  int                    m1,
968                  int                    m2);
969
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1002
1003 extern int cut_point;
1004
1005
1006
1007
1008 extern int eos_debug;
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1028 DEPRECATED(float energy_of_structure(const char *string,
1029                                     const char *structure,
1030                                     int          verbosity_level),
1031             "Use vrna_eval_structure_simple() and vrna_eval_structure() instead");
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1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000

```

```

1072 DEPRECATED(float energy_of_circ_structure(const char *string,
1073   const char *structure,
1074   int verbosity_level),
1075             "Use vrna_eval_circ_structure_simple() and vrna_eval_structure() instead");
1076
1092 DEPRECATED(float energy_of_circ_struct_par(const char *string,
1093   const char *structure,
1094   vrna_param_t *parameters,
1095   int verbosity_level),
1096             "Use vrna_eval_structure() instead");
1097
1098
1099 DEPRECATED(float energy_of_gquad_structure(const char *string,
1100   const char *structure,
1101   int verbosity_level),
1102             "Use vrna_eval_structure_simple() instead");
1103
1104 DEPRECATED(float energy_of_gquad_struct_par(const char *string,
1105   const char *structure,
1106   vrna_param_t *parameters,
1107   int verbosity_level),
1108             "Use vrna_eval_structure() instead");
1109
1110
1131 DEPRECATED(int energy_of_structure_pt(const char *string,
1132                                     short *ptable,
1133                                     short *s,
1134                                     short *sl,
1135                                     int verbosity_level),
1136             "Use vrna_eval_structure_pt_simple() and vrna_eval_structure_pt() instead");
1137
1155 DEPRECATED(int energy_of_struct_pt_par(const char *string,
1156                                     short *ptable,
1157                                     short *s,
1158                                     short *sl,
1159                                     vrna_param_t *parameters,
1160                                     int verbosity_level),
1161             "Use vrna_eval_structure_pt() instead");
1162
1163
1180 DEPRECATED(float energy_of_move(const char *string,
1181                                 const char *structure,
1182                                 int m1,
1183                                 int m2),
1184             "Use vrna_eval_move() instead");
1185
1186
1205 DEPRECATED(int energy_of_move_pt(short *pt,
1206                                 short *s,
1207                                 short *sl,
1208                                 int m1,
1209                                 int m2),
1210             "Use vrna_eval_move_pt_simple() and vrna_eval_move_pt() instead");
1211
1225 DEPRECATED(int loop_energy(short *ptable,
1226                             short *s,
1227                             short *sl,
1228                             int i),
1229             "Use vrna_eval_loop_pt() instead");
1230
1245 DEPRECATED(float energy_of_struct(const char *string,
1246                                   const char *structure),
1247             "Use vrna_eval_structure_simple() instead");
1248
1265 DEPRECATED(int energy_of_struct_pt(const char *string,
1266                                   short *ptable,
1267                                   short *s,
1268                                   short *sl),
1269             "Use vrna_eval_structure_pt_simple() instead");
1270
1285 DEPRECATED(float energy_of_circ_struct(const char *string,
1286                                       const char *structure),
1287             "Use vrna_eval_circ_structure_simple() and vrna_eval_structure() instead");
1288
1289 #endif
1290
1295 #endif

```

## 18.71 ViennaRNA/exterior\_loops.h File Reference

Use [ViennaRNA/loops/external.h](#) instead.

Include dependency graph for exterior\_loops.h:

### 18.71.1 Detailed Description

Use [ViennaRNA/loops/external.h](#) instead.

**Deprecated** Use [ViennaRNA/loops/external.h](#) instead

## 18.72 exterior\_loops.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_EXTERNAL_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_EXTERNAL_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/exterior_loops.h>! Use <ViennaRNA/loops/external.h>
    instead!"
13 # endif
14 #include <ViennaRNA/loops/external.h>
15 #endif
16
17 #endif
```

## 18.73 ViennaRNA/file\_formats.h File Reference

Use [ViennaRNA/io/file\\_formats.h](#) instead.

Include dependency graph for file\_formats.h:

### 18.73.1 Detailed Description

Use [ViennaRNA/io/file\\_formats.h](#) instead.

**Deprecated** Use [ViennaRNA/io/file\\_formats.h](#) instead

## 18.74 file\_formats.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_FILE_FORMATS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_FILE_FORMATS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/file_formats.h>! Use <ViennaRNA/io/file_formats.h>
    instead!"
13 # endif
14 #include <ViennaRNA/io/file_formats.h>
15 #include <ViennaRNA/io/file_formats_msa.h>
16 #endif
17
18 #endif
```

## 18.75 ViennaRNA/io/file\_formats.h File Reference

Read and write different file formats for RNA sequences, structures.

Include dependency graph for file\_formats.h: This graph shows which files directly or indirectly include this file:

### Macros

- `#define VRNA_OPTION_MULTILINE 32U`  
Tell a function that an input is assumed to span several lines.
- `#define VRNA_CONSTRAINT_MULTILINE 32U`  
parse multiline constraint

## Functions

- void [vrna\\_file\\_helixlist](#) (const char \*seq, const char \*db, float energy, FILE \*file)  
*Print a secondary structure as helix list.*
- void [vrna\\_file\\_connect](#) (const char \*seq, const char \*db, float energy, const char \*identifier, FILE \*file)  
*Print a secondary structure as connect table.*
- void [vrna\\_file\\_bpseq](#) (const char \*seq, const char \*db, FILE \*file)  
*Print a secondary structure in bpseq format.*
- void [vrna\\_file\\_json](#) (const char \*seq, const char \*db, double energy, const char \*identifier, FILE \*file)  
*Print a secondary structure in jsonformat.*
- unsigned int [vrna\\_file\\_fasta\\_read\\_record](#) (char \*\*header, char \*\*sequence, char \*\*\*rest, FILE \*file, unsigned int options)
- char \* [vrna\\_extract\\_record\\_rest\\_structure](#) (const char \*\*lines, unsigned int length, unsigned int option)  
*Extract a dot-bracket structure string from (multiline)character array.*
- int [vrna\\_file\\_SHAPE\\_read](#) (const char \*file\_name, int length, double default\_value, char \*sequence, double \*values)  
*Read data from a given SHAPE reactivity input file.*
- void [vrna\\_extract\\_record\\_rest\\_constraint](#) (char \*\*cstruc, const char \*\*lines, unsigned int option)  
*Extract a hard constraint encoded as pseudo dot-bracket string.*
- unsigned int [read\\_record](#) (char \*\*header, char \*\*sequence, char \*\*\*rest, unsigned int options)  
*Get a data record from stdin.*

### 18.75.1 Detailed Description

Read and write different file formats for RNA sequences, structures.

## 18.76 file\_formats.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_FILE_FORMATS_H
2 #define VIENNA_RNA_PACKAGE_FILE_FORMATS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
28 #include <stdio.h>
29
30 #include <ViennaRNA/datastructures/basic.h>
31
40 void
41 vrna_file_helixlist(const char *seq,
42                   const char *db,
43                   float energy,
44                   FILE *file);
45
46
47 void
48 vrna_file_connect(const char *seq,
49                 const char *db,
50                 float energy,
51                 const char *identifier,
52                 FILE *file);
53
54
55 void
56 vrna_file_bpseq(const char *seq,
57                const char *db,
58                FILE *file);

```



```

89
90
91 #if VRNA_WITH_JSON_SUPPORT
92
93 void
94 vrna_file_json(const char *seq,
95               const char *db,
96               double energy,
97               const char *identifier,
98               FILE *file);
99
100 #endif
101
102 #define VRNA_OPTION_MULTILINE 32U
103 #define VRNA_CONSTRAINT_MULTILINE 32U
104
105 unsigned int
106 vrna_file_fasta_read_record(char **header,
107                             char **sequence,
108                             char ***rest,
109                             FILE *file,
110                             unsigned int options);
111
112 char *
113 vrna_extract_record_rest_structure(const char **lines,
114                                   unsigned int length,
115                                   unsigned int option);
116
117 int
118 vrna_file_SHAPE_read(const char *file_name,
119                     int length,
120                     double default_value,
121                     char *sequence,
122                     double *values);
123
124 #define VRNA_INPUT_VERBOSE 16384U
125
126 int
127 vrna_file_connect_read_record(FILE *fp,
128                               char **id,
129                               char **sequence,
130                               char **structure,
131                               char **remainder,
132                               unsigned int options);
133
134 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
135
136 DEPRECATED(void vrna_extract_record_rest_constraint(char **cstruc,
137   const char **lines,
138   unsigned int option),
139            "This function is obsolete");
140
141 DEPRECATED(char *extract_record_rest_structure(const char **lines,
142   unsigned int length,
143   unsigned int option),
144            "Use vrna_extract_record_rest_structure() instead");
145
146 DEPRECATED(unsigned int read_record(char **header,
147                                     char **sequence,
148                                     char ***rest,
149                                     unsigned int options),
150            "Use vrna_file_fasta_read_record() instead");
151
152 DEPRECATED(unsigned int get_multi_input_line(char **string,
153  unsigned int options),
154            "This function is obsolete");
155
156 #endif
157 #endif

```

## 18.77 ViennaRNA/file\_formats\_msa.h File Reference

Use [ViennaRNA/io/file\\_formats\\_msa.h](#) instead.

Include dependency graph for file\_formats\_msa.h:

### 18.77.1 Detailed Description

Use [ViennaRNA/io/file\\_formats\\_msa.h](#) instead.

**Deprecated** Use [ViennaRNA/io/file\\_formats\\_msa.h](#) instead

## 18.78 file\_formats\_msa.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_FILE_FORMATS_MSA_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_FILE_FORMATS_MSA_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/file_formats_msa.h>! Use
    <ViennaRNA/io/file_formats_msa.h> instead!"
13 # endif
14 #include <ViennaRNA/io/file_formats_msa.h>
15 #endif
16
17 #endif
```

## 18.79 ViennaRNA/io/file\_formats\_msa.h File Reference

Functions dealing with file formats for Multiple Sequence Alignments (MSA)

Include dependency graph for file\_formats\_msa.h: This graph shows which files directly or indirectly include this file:

### Macros

- `#define VRNA_FILE_FORMAT_MSA_CLUSTAL 1U`  
Option flag indicating ClustalW formatted files.
- `#define VRNA_FILE_FORMAT_MSA_STOCKHOLM 2U`  
Option flag indicating Stockholm 1.0 formatted files.
- `#define VRNA_FILE_FORMAT_MSA_FASTA 4U`  
Option flag indicating FASTA (Pearson) formatted files.
- `#define VRNA_FILE_FORMAT_MSA_MAF 8U`  
Option flag indicating MAF formatted files.
- `#define VRNA_FILE_FORMAT_MSA_MIS 16U`  
Option flag indicating most informative sequence (MIS) output.
- `#define VRNA_FILE_FORMAT_MSA_DEFAULT`  
Option flag indicating the set of default file formats.
- `#define VRNA_FILE_FORMAT_MSA_NOCHECK 4096U`  
Option flag to disable validation of the alignment.
- `#define VRNA_FILE_FORMAT_MSA_UNKNOWN 8192U`  
Return flag of `vrna_file_msa_detect_format()` to indicate unknown or malformed alignment.
- `#define VRNA_FILE_FORMAT_MSA_APPEND 16384U`  
Option flag indicating to append data to a multiple sequence alignment file rather than overwriting it.
- `#define VRNA_FILE_FORMAT_MSA_QUIET 32768U`  
Option flag to suppress unnecessary spam messages on `stderr`
- `#define VRNA_FILE_FORMAT_MSA_SILENT 65536U`  
Option flag to completely silence any warnings on `stderr`

## Functions

- `int vrna_file_msa_read` (const char \*filename, char \*\*\*names, char \*\*\*aln, char \*\*id, char \*\*structure, unsigned int options)  
*Read a multiple sequence alignment from file.*
- `int vrna_file_msa_read_record` (FILE \*fp, char \*\*\*names, char \*\*\*aln, char \*\*id, char \*\*structure, unsigned int options)  
*Read a multiple sequence alignment from file handle.*
- `unsigned int vrna_file_msa_detect_format` (const char \*filename, unsigned int options)  
*Detect the format of a multiple sequence alignment file.*
- `int vrna_file_msa_write` (const char \*filename, const char \*\*names, const char \*\*aln, const char \*id, const char \*structure, const char \*source, unsigned int options)  
*Write multiple sequence alignment file.*

### 18.79.1 Detailed Description

Functions dealing with file formats for Multiple Sequence Alignments (MSA)

, ,

## 18.80 file\_formats\_msa.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_FILE_FORMATS_MSA_H
2 #define VIENNA_RNA_PACKAGE_FILE_FORMATS_MSA_H
3
10 #include <stdio.h>
11
22 #define VRNA_FILE_FORMAT_MSA_CLUSTAL      1U
23
28 #define VRNA_FILE_FORMAT_MSA_STOCKHOLM   2U
29
34 #define VRNA_FILE_FORMAT_MSA_FASTA       4U
35
40 #define VRNA_FILE_FORMAT_MSA_MAF         8U
41
50 #define VRNA_FILE_FORMAT_MSA_MIS         16U
51
56 #define VRNA_FILE_FORMAT_MSA_DEFAULT     ( \
57     VRNA_FILE_FORMAT_MSA_CLUSTAL \
58     | VRNA_FILE_FORMAT_MSA_STOCKHOLM \
59     | VRNA_FILE_FORMAT_MSA_FASTA \
60     | VRNA_FILE_FORMAT_MSA_MAF \
61     )
62
67 #define VRNA_FILE_FORMAT_MSA_NOCHECK      4096U
68
73 #define VRNA_FILE_FORMAT_MSA_UNKNOWN      8192U
74
79 #define VRNA_FILE_FORMAT_MSA_APPEND       16384U
80
85 #define VRNA_FILE_FORMAT_MSA_QUIET       32768U
86
91 #define VRNA_FILE_FORMAT_MSA_SILENT       65536U
92
145 int
146 vrna_file_msa_read(const char    *filename,
147                    char          ***names,
148                    char          ***aln,
149                    char          **id,
150                    char          **structure,
151                    unsigned int  options);
152
153
210 int
211 vrna_file_msa_read_record(FILE      *fp,
212                           char      ***names,
213                           char      ***aln,
214                           char      **id,
215                           char      **structure,
216                           unsigned int  options);
217
218
244 unsigned int
245 vrna_file_msa_detect_format(const char    *filename,
```

```

246             unsigned int  options);
247
248
266 int
267 vrna_file_msa_write(const char    *filename,
268                   const char    **names,
269                   const char    **aln,
270                   const char    *id,
271                   const char    *structure,
272                   const char    *source,
273                   unsigned int  options);
274
275
280 #endif

```

## 18.81 ViennaRNA/file\_utils.h File Reference

Use [ViennaRNA/io/utlis.h](#) instead.

Include dependency graph for file\_utils.h:

### 18.81.1 Detailed Description

Use [ViennaRNA/io/utlis.h](#) instead.

**Deprecated** Use [ViennaRNA/io/utlis.h](#) instead

## 18.82 file\_utils.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_FILE_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_FILE_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/file_utils.h>! Use <ViennaRNA/io/utlis.h> instead!"
13 #  endif
14 #include <ViennaRNA/io/utlis.h>
15 #endif
16
17 #endif

```

## 18.83 ViennaRNA/findpath.h File Reference

Use [ViennaRNA/landscape/findpath.h](#) instead.

Include dependency graph for findpath.h:

### 18.83.1 Detailed Description

Use [ViennaRNA/landscape/findpath.h](#) instead.

**Deprecated** Use [ViennaRNA/landscape/findpath.h](#) instead

## 18.84 findpath.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_FINDPATH_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_FINDPATH_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/findpath.h>! Use <ViennaRNA/landscape/findpath.h> instead!"
13 #  endif
14 #include <ViennaRNA/landscape/findpath.h>
15 #endif
16
17 #endif

```

## 18.85 ViennaRNA/landscape/findpath.h File Reference

A breadth-first search heuristic for optimal direct folding paths.

Include dependency graph for findpath.h: This graph shows which files directly or indirectly include this file:

### Functions

- `int vrna_path_findpath_saddle (vrna_fold_compound_t *fc, const char *s1, const char *s2, int width)`  
*Find energy of a saddle point between 2 structures (search only direct path)*
- `int vrna_path_findpath_saddle_ub (vrna_fold_compound_t *fc, const char *s1, const char *s2, int width, int maxE)`  
*Find energy of a saddle point between 2 structures (search only direct path)*
- `vrna_path_t * vrna_path_findpath (vrna_fold_compound_t *fc, const char *s1, const char *s2, int width)`  
*Find refolding path between 2 structures (search only direct path)*
- `vrna_path_t * vrna_path_findpath_ub (vrna_fold_compound_t *fc, const char *s1, const char *s2, int width, int maxE)`  
*Find refolding path between 2 structures (search only direct path)*
- `int find_saddle (const char *seq, const char *s1, const char *s2, int width)`  
*Find energy of a saddle point between 2 structures (search only direct path)*
- `void free_path (vrna_path_t *path)`  
*Free memory allocated by `get_path()` function.*
- `vrna_path_t * get_path (const char *seq, const char *s1, const char *s2, int width)`  
*Find refolding path between 2 structures (search only direct path)*

### 18.85.1 Detailed Description

A breadth-first search heuristic for optimal direct folding paths.

## 18.86 findpath.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_FIND_PATH_H
2 #define VIENNA_RNA_PACKAGE_FIND_PATH_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
30 #include <ViennaRNA/fold_compound.h>
31 #include <ViennaRNA/landscape/paths.h>
32
54 int
55 vrna_path_findpath_saddle(vrna_fold_compound_t *fc,
56                          const char *s1,
57                          const char *s2,
58                          int width);
59
60
87 int
88 vrna_path_findpath_saddle_ub(vrna_fold_compound_t *fc,
89                              const char *s1,
90                              const char *s2,
91                              int width,
92                              int maxE);
93
94
116 vrna_path_t *
117 vrna_path_findpath(vrna_fold_compound_t *fc,
118                   const char *s1,
119                   const char *s2,
```

```

120             int                width);
121
122
123
150 vrna_path_t *
151 vrna_path_findpath_ub(vrna_fold_compound_t *fc,
152                      const char *s1,
153                      const char *s2,
154                      int width,
155                      int maxE);
156
157
158 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
159
160 DEPRECATED(int
161            find_saddle(const char *seq,
162                      const char *s1,
163                      const char *s2,
164                      int width),
165            "Use vrna_path_findpath_saddle() instead!");
166
167
168 DEPRECATED(void
169            free_path(vrna_path_t *path),
170            "Use vrna_path_free() instead!");
171
172
173 DEPRECATED(vrna_path_t *
174            get_path(const char *seq,
175                   const char *s1,
176                   const char *s2,
177                   int width),
178            "Use vrna_path_findpath() instead!");
179
180
181 #endif
182 #endif
183 #endif

```

## 18.87 ViennaRNA/fold.h File Reference

MFE calculations for single RNA sequences.

Include dependency graph for fold.h:

### Functions

- float [fold\\_par](#) (const char \*sequence, char \*structure, [vrna\\_param\\_t](#) \*parameters, int is\_constrained, int is\_circular)
 

*Compute minimum free energy and an appropriate secondary structure of an RNA sequence.*
- float [fold](#) (const char \*sequence, char \*structure)
 

*Compute minimum free energy and an appropriate secondary structure of an RNA sequence.*
- float [circfold](#) (const char \*sequence, char \*structure)
 

*Compute minimum free energy and an appropriate secondary structure of a circular RNA sequence.*
- void [free\\_arrays](#) (void)
 

*Free arrays for mfe folding.*
- void [update\\_fold\\_params](#) (void)
 

*Recalculate energy parameters.*
- void [update\\_fold\\_params\\_par](#) ([vrna\\_param\\_t](#) \*parameters)
 

*Recalculate energy parameters.*
- void [export\\_fold\\_arrays](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)
- void [export\\_fold\\_arrays\\_par](#) (int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, [vrna\\_param\\_t](#) \*\*P\_p)
- void [export\\_circfold\\_arrays](#) (int \*Fc\_p, int \*FcH\_p, int \*FcI\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p)
- void [export\\_circfold\\_arrays\\_par](#) (int \*Fc\_p, int \*FcH\_p, int \*FcI\_p, int \*FcM\_p, int \*\*fM2\_p, int \*\*f5\_p, int \*\*c\_p, int \*\*fML\_p, int \*\*fM1\_p, int \*\*indx\_p, char \*\*ptype\_p, [vrna\\_param\\_t](#) \*\*P\_p)
- int [LoopEnergy](#) (int n1, int n2, int type, int type\_2, int si1, int sj1, int sp1, int sq1)
- int [HairpinE](#) (int size, int type, int si1, int sj1, const char \*string)
- void [initialize\\_fold](#) (int length)

## 18.87.1 Detailed Description

MFE calculations for single RNA sequences.

## 18.88 fold.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_FOLD_H
2 #define VIENNA_RNA_PACKAGE_FOLD_H
3
4 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
5
6 #include <ViennaRNA/datastructures/basic.h>
7 #include <ViennaRNA/params/basic.h>
8 #include <ViennaRNA/mfe.h>
9 #include <ViennaRNA/eval.h>
10
11 #ifdef VRNA_WARN_DEPRECATED
12 # if defined(__clang__)
13 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
14 # elif defined(__GNUC__)
15 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
16 # else
17 #  define DEPRECATED(func, msg) func
18 # endif
19 #else
20 # define DEPRECATED(func, msg) func
21 #endif
22
23 DEPRECATED(float
24 fold_par( const char *sequence,
25          char *structure,
26          vrna_param_t *parameters,
27          int is_constrained,
28          int is_circular),
29 "Use the new API and vrna_mfe() instead");
30
31 DEPRECATED(float fold( const char *sequence, char *structure),
32 "Use vrna_fold() or vrna_mfe() instead");
33
34 DEPRECATED(float circfold( const char *sequence, char *structure),
35 "Use vrna_circfold() or vrna_mfe() instead");
36
37 DEPRECATED(void free_arrays(void),
38 "This function is obsolete");
39
40 DEPRECATED(void update_fold_params(void),
41 "This function is obsolete");
42
43 DEPRECATED(void update_fold_params_par(vrna_param_t *parameters),
44 "Use the new API with vrna_fold_compound_t datastructure instead");
45
46 DEPRECATED(void
47 export_fold_arrays( int **f5_p,
48                   int **c_p,
49                   int **fML_p,
50                   int **fM1_p,
51                   int **indx_p,
52                   char **ptype_p),
53 "Use the new API with vrna_fold_compound_t datastructure instead");
54
55 DEPRECATED(void
56 export_fold_arrays_par( int **f5_p,
57                      int **c_p,
58                      int **fML_p,
59                      int **fM1_p,
60                      int **indx_p,
61                      char **ptype_p,
62                      vrna_param_t **P_p),
63 "Use the new API with vrna_fold_compound_t datastructure instead");
64
65 DEPRECATED(void
66 export_circfold_arrays( int *Fc_p,
67                      int *FcH_p,
68                      int *FcI_p,
69                      int *FcM_p,
70                      int **fM2_p,
71                      int **f5_p,
72                      int **c_p,
73                      int **fML_p,
74                      int **fM1_p,
```

```

197             int **indx_p,
198             char **ptype_p),
199 "Use the new API with vrna_fold_compound_t datastructure instead");
200
201 DEPRECATED(void
202 export_circfold_arrays_par( int *Fc_p,
203                             int *FcH_p,
204                             int *FcI_p,
205                             int *FcM_p,
206                             int **fM2_p,
207                             int **f5_p,
208                             int **c_p,
209                             int **fML_p,
210                             int **fM1_p,
211                             int **indx_p,
212                             char **ptype_p,
213                             vrna_param_t **P_p),
214 "Use the new API with vrna_fold_compound_t datastructure instead");
215
216
217
218
219
220
221
222
223 /* finally moved the loop energy function declarations to this header... */
224 /* BUT: The functions only exist for backward compatibility reasons! */
225 /* You better include "loop_energies.h" and call the functions: */
226 /* E_Hairpin() and E_IntLoop() which are (almost) threadsafe as they get */
227 /* a pointer to the energy parameter data structure as additional argument */
228
229 DEPRECATED(int LoopEnergy(int n1,
230                          int n2,
231                          int type,
232                          int type_2,
233                          int sil,
234                          int sj1,
235                          int spl,
236                          int sql),
237 "This function is obsolete");
238
239 DEPRECATED(int HairpinE(int size,
240                       int type,
241                       int sil,
242                       int sj1,
243                       const char *string),
244 "Use E_Hairpin() instead");
245
246 DEPRECATED(void initialize_fold(int length),
247 "This function is obsolete");
248
249 DEPRECATED(char *backtrack_fold_from_pair(char *sequence,
250   int i,
251   int j),
252 "This function is obsolete. Consider using vrna_backtrack_from_intervals() instead");
253
254
255 #endif
256 #endif

```

## 18.89 ViennaRNA/fold\_compound.h File Reference

The Basic Fold Compound API.

Include dependency graph for fold\_compound.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_fc\\_s](#)

*The most basic data structure required by many functions throughout the RNAlib. [More...](#)*

### Macros

- #define [VRNA\\_STATUS\\_MFE\\_PRE](#) (unsigned char)1  
*Status message indicating that MFE computations are about to begin.*
- #define [VRNA\\_STATUS\\_MFE\\_POST](#) (unsigned char)2  
*Status message indicating that MFE computations are finished.*
- #define [VRNA\\_STATUS\\_PF\\_PRE](#) (unsigned char)3  
*Status message indicating that Partition function computations are about to begin.*



- #define [VRNA\\_STATUS\\_PF\\_POST](#) (unsigned char)4  
*Status message indicating that Partition function computations are finished.*
- #define [VRNA\\_OPTION\\_DEFAULT](#) 0U  
*Option flag to specify default settings/requirements.*
- #define [VRNA\\_OPTION\\_MFE](#) 1U  
*Option flag to specify requirement of Minimum Free Energy (MFE) DP matrices and corresponding set of energy parameters.*
- #define [VRNA\\_OPTION\\_PF](#) 2U  
*Option flag to specify requirement of Partition Function (PF) DP matrices and corresponding set of Boltzmann factors.*
- #define [VRNA\\_OPTION\\_HYBRID](#) 4U  
*Option flag to specify requirement of dimer DP matrices.*
- #define [VRNA\\_OPTION\\_EVAL\\_ONLY](#) 8U  
*Option flag to specify that neither MFE, nor PF DP matrices are required.*
- #define [VRNA\\_OPTION\\_WINDOW](#) 16U  
*Option flag to specify requirement of DP matrices for local folding approaches.*

## Typedefs

- typedef struct [vrna\\_fc\\_s](#) [vrna\\_fold\\_compound\\_t](#)  
*Typename for the fold\_compound data structure [vrna\\_fc\\_s](#).*
- typedef void() [vrna\\_callback\\_free\\_auxdata](#)(void \*data)  
*Callback to free memory allocated for auxiliary user-provided data.*
- typedef void() [vrna\\_callback\\_recursion\\_status](#)(unsigned char status, void \*data)  
*Callback to perform specific user-defined actions before, or after recursive computations.*

## Enumerations

- enum [vrna\\_fc\\_type\\_e](#) { [VRNA\\_FC\\_TYPE\\_SINGLE](#) , [VRNA\\_FC\\_TYPE\\_COMPARATIVE](#) }  
*An enumerator that is used to specify the type of a [vrna\\_fold\\_compound\\_t](#).*

## Functions

- [vrna\\_fold\\_compound\\_t](#) \* [vrna\\_fold\\_compound](#) (const char \*sequence, const [vrna\\_md\\_t](#) \*md\_p, unsigned int options)  
*Retrieve a [vrna\\_fold\\_compound\\_t](#) data structure for single sequences and hybridizing sequences.*
- [vrna\\_fold\\_compound\\_t](#) \* [vrna\\_fold\\_compound\\_comparative](#) (const char \*\*sequences, [vrna\\_md\\_t](#) \*md\_p, unsigned int options)  
*Retrieve a [vrna\\_fold\\_compound\\_t](#) data structure for sequence alignments.*
- void [vrna\\_fold\\_compound\\_free](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)  
*Free memory occupied by a [vrna\\_fold\\_compound\\_t](#).*
- void [vrna\\_fold\\_compound\\_add\\_auxdata](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, void \*data, [vrna\\_callback\\_free\\_auxdata](#) \*f)  
*Add auxiliary data to the [vrna\\_fold\\_compound\\_t](#).*
- void [vrna\\_fold\\_compound\\_add\\_callback](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, [vrna\\_callback\\_recursion\\_status](#) \*f)  
*Add a recursion status callback to the [vrna\\_fold\\_compound\\_t](#).*

### 18.89.1 Detailed Description

The Basic Fold Compound API.

## 18.90 fold\_compound.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_FOLD_COMPOUND_H
2 #define VIENNA_RNA_PACKAGE_FOLD_COMPOUND_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(" ", msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 typedef struct vrna_fc_s vrna_fold_compound_t;
17
18 typedef void (vrna_callback_free_auxdata)(void *data);
19
20 typedef void (vrna_callback_recursion_status)(unsigned char status,
21  void *data);
22
23 #define VRNA_STATUS_MFE_PRE      (unsigned char)1
24
25 #define VRNA_STATUS_MFE_POST     (unsigned char)2
26
27 #define VRNA_STATUS_PF_PRE      (unsigned char)3
28
29 #define VRNA_STATUS_PF_POST     (unsigned char)4
30
31 #include <ViennaRNA/model.h>
32 #include <ViennaRNA/params/basic.h>
33 #include <ViennaRNA/sequence.h>
34 #include <ViennaRNA/dp_matrices.h>
35 #include <ViennaRNA/constraints/hard.h>
36 #include <ViennaRNA/constraints/soft.h>
37 #include <ViennaRNA/grammar.h>
38 #include <ViennaRNA/structured_domains.h>
39 #include <ViennaRNA/unstructured_domains.h>
40
41 #ifdef VRNA_WITH_SVM
42 #include <ViennaRNA/zscore.h>
43 #endif
44
45 typedef enum {
46     VRNA_FC_TYPE_SINGLE,
47     VRNA_FC_TYPE_COMPARATIVE
48 } vrna_fc_type_e;
49
50 struct vrna_fc_s {
51     const vrna_fc_type_e type;
52     unsigned int length;
53 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
54     DEPRECATED(int cutpoint,
55               "Use strand_* members instead");
56 #endif
57     unsigned int *strand_number;
58     unsigned int *strand_order;
59     unsigned int *strand_order_uniq;
60     unsigned int *strand_start;
61     unsigned int *strand_end;
62     unsigned int *strands;
63     vrna_seq_t *nucleotides;
64     vrna_msa_t *alignment;
65     vrna_hc_t *hc;
66     vrna_mx_mfe_t *matrices;
67     vrna_mx_pf_t *exp_matrices;
68     vrna_param_t *params;
69     vrna_exp_param_t *exp_params;
70     int *iindx;
71     int *jindx;
72     vrna_callback_recursion_status *stat_cb;
73     void *auxdata;
74     vrna_callback_free_auxdata *free_auxdata;
75     /* data structure to adjust additional structural domains, such as G-quadruplexes */
76     vrna_sd_t *domains_struct;
77     /* data structure to adjust additional contributions to unpaired stretches, e.g. due to protein
78        binding */
79     vrna_ud_t *domains_up;
80     /* auxiliary (user-defined) extension to the folding grammar */
81

```

```

222  vrna_gr_aux_t *aux_grammar;
228  #ifndef VRNA_DISABLE_C11_FEATURES
229  /* C11 support for unnamed unions/structs */
230  union {
231      struct {
232  #endif
233
234      char *sequence;
241      short *sequence_encoding;
245      short *encoding5;
246      short *encoding3;
247
248      short *sequence_encoding2;
249
250
251      char *ptype;
260      char *ptype_pf_compat;
265      vrna_sc_t *sc;
273  #ifndef VRNA_DISABLE_C11_FEATURES
274  /* C11 support for unnamed unions/structs */
275  };
276  struct {
277  #endif
278
283      char          **sequences;
287      unsigned int  n_seq;
290      char          *cons_seq;
293      short         *S_cons;
296      short         **S;
299      short         **S5;
302      short         **S3;
305      char          **Ss;
306      unsigned int  **a2s;
307      int           *pscore;
310      int           **pscore_local;
313      short        *pscore_pf_compat;
317      vrna_sc_t     **scs;
320      int           oldAliEn;
321
325  #ifndef VRNA_DISABLE_C11_FEATURES
326  };
327  };
328  #endif
329
336  unsigned int  maxD1;
337  unsigned int  maxD2;
338  short        *reference_pt1;
339  short        *reference_pt2;
341  unsigned int  *referenceBPs1;
342  unsigned int  *referenceBPs2;
343  unsigned int  *bpdist;
345  unsigned int  *mm1;
346  unsigned int  *mm2;
358  int          window_size;
359  char **ptype_local;
360  #ifdef VRNA_WITH_SVM
361  vrna_zsc_dat_t zscore_data;
362  #endif
363
367  };
368
369
370  /* the definitions below should be used for functions that return/receive/destroy fold compound data
   structures */
371
375  #define VRNA_OPTION_DEFAULT          0U
376
383  #define VRNA_OPTION_MFE              1U
384
391  #define VRNA_OPTION_PF                2U
392
396  #define VRNA_OPTION_HYBRID           4U
397
407  #define VRNA_OPTION_EVAL_ONLY        8U
408
412  #define VRNA_OPTION_WINDOW           16U
413
451  vrna_fold_compound_t *
452  vrna_fold_compound(const char *sequence,
453                    const vrna_md_t *md_p,
454                    unsigned int options);
455
456
494  vrna_fold_compound_t *
495  vrna_fold_compound_comparative(const char **sequences,
496                                vrna_md_t *md_p,
497                                unsigned int options);

```

```

498
499
500 vrna_fold_compound_t *
501 vrna_fold_compound_comparative2(const char          **sequences,
502                                const char          **names,
503                                const unsigned char  *orientation,
504                                const unsigned long long *start,
505                                const unsigned long long *genome_size,
506                                vrna_md_t            *md_p,
507                                unsigned int          options);
508
509
510 vrna_fold_compound_t *
511 vrna_fold_compound_TwoD(const char  *sequence,
512                        const char  *s1,
513                        const char  *s2,
514                        vrna_md_t    *md_p,
515                        unsigned int  options);
516
517
518 int
519 vrna_fold_compound_prepare(vrna_fold_compound_t *fc,
520                           unsigned int          options);
521
522
523 void
524 vrna_fold_compound_free(vrna_fold_compound_t *fc);
525
526
527 void
528 vrna_fold_compound_add_auxdata(vrna_fold_compound_t *fc,
529                               void                  *data,
530                               vrna_callback_free_auxdata *f);
531
532
533 void
534 vrna_fold_compound_add_callback(vrna_fold_compound_t *fc,
535                                vrna_callback_recursion_status *f);
536
537
538 #endif

```

## 18.91 ViennaRNA/fold\_vars.h File Reference

Here all all declarations of the global variables used throughout RNAlib.

Include dependency graph for fold\_vars.h: This graph shows which files directly or indirectly include this file:

### Variables

- int **fold\_constrained**  
*Global switch to activate/deactivate folding with structure constraints.*
- int **csv**  
*generate comma seperated output*
- char \* **RibosumFile**
- int **james\_rule**
- int **logML**
- int **cut\_point**  
*Marks the position (starting from 1) of the first nucleotide of the second molecule within the concatenated sequence.*
- **bondT** \* **base\_pair**  
*Contains a list of base pairs after a call to [fold\(\)](#).*
- **FLT\_OR\_DBL** \* **pr**  
*A pointer to the base pair probability matrix.*
- int \* **iindx**  
*index array to move through pr.*

### 18.91.1 Detailed Description

Here all all declarations of the global variables used throughout RNAlib.

## 18.91.2 Variable Documentation

### 18.91.2.1 RibosumFile

```
char* RibosumFile [extern]
```

warning this variable will vanish in the future ribosums will be compiled in instead

### 18.91.2.2 james\_rule

```
int james_rule [extern]
```

interior loops of size 2 get energy 0.8Kcal and no mismatches, default 1

### 18.91.2.3 logML

```
int logML [extern]
```

use logarithmic multiloop energy function

### 18.91.2.4 cut\_point

```
int cut_point [extern]
```

Marks the position (starting from 1) of the first nucleotide of the second molecule within the concatenated sequence. To evaluate the energy of a duplex structure (a structure formed by two strands), concatenate the two sequences and set it to the first base of the second strand in the concatenated sequence. The default value of -1 stands for single molecule folding. The cut\_point variable is also used by [vrna\\_file\\_PS\\_rnaplot\(\)](#) and [PS\\_dot\\_plot\(\)](#) to mark the chain break in postscript plots.

### 18.91.2.5 base\_pair

```
bondT* base_pair [extern]
```

Contains a list of base pairs after a call to [fold\(\)](#).

base\_pair[0].i contains the total number of pairs.

**Deprecated** Do not use this variable anymore!

### 18.91.2.6 pr

```
FLT_OR_DBL* pr [extern]
```

A pointer to the base pair probability matrix.

**Deprecated** Do not use this variable anymore!

### 18.91.2.7 iindx

```
int* iindx [extern]
```

index array to move through pr.

The probability for base i and j to form a pair is in pr[iindx[i]-j].

**Deprecated** Do not use this variable anymore!

## 18.92 fold\_vars.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_FOLD_VARS_H
2 #define VIENNA_RNA_PACKAGE_FOLD_VARS_H
3
4 #include <ViennaRNA/datastructures/basic.h>
```

```

5 /* For now, we include model.h by default to provide backwards compatibility
6    However, this will most likely change, since fold_vars.h is scheduled to
7    vanish from the sources at latest in ViennaRNA Package v3
8 */
9 #include <ViennaRNA/model.h>
10
11
12 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
13
14 extern int    fold_constrained;
15
16 extern int    csv;
17
18 extern char *RibosumFile;
19
20 extern int    james_rule;
21
22 extern int    logML;
23
24 extern int    cut_point;
25
26 extern bondT *base_pair;
27
28 extern FLT_OR_DBL *pr;
29
30 extern int    *iindx;
31
32 #endif
33
34 #endif

```

## 18.93 ViennaRNA/gquad.h File Reference

G-quadruplexes.

Include dependency graph for gquad.h:

### Functions

- int [get\\_gquad\\_matrix](#) (short \*S, [vrna\\_param\\_t](#) \*P)  
*Get a triangular matrix prefilled with minimum free energy contributions of G-quadruplexes.*
- int [parse\\_gquad](#) (const char \*struc, int \*L, int l[3])
- PRIVATE int [backtrack\\_GQuad\\_IntLoop](#) (int c, int i, int j, int type, short \*S, int \*ggg, int \*index, int \*p, int \*q, [vrna\\_param\\_t](#) \*P)
- PRIVATE int [backtrack\\_GQuad\\_IntLoop\\_L](#) (int c, int i, int j, int type, short \*S, int \*\*ggg, int maxdist, int \*p, int \*q, [vrna\\_param\\_t](#) \*P)

### 18.93.1 Detailed Description

G-quadruplexes.

## 18.94 gquad.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_GQUAD_H
2 #define VIENNA_RNA_PACKAGE_GQUAD_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/fold_compound.h>
6 #include <ViennaRNA/params/basic.h>
7
8 #ifndef INLINE
9 #ifdef __GNUC__
10 # define INLINE inline
11 #else
12 # define INLINE
13 #endif
14 #endif
15
16 int    E_gquad(int    L,
17               int    l[3],
18               vrna\_param\_t *P);

```

```

33
34
35 FLT_OR_DBL exp_E_gquad(int          L,
36                        int          l[3],
37                        vrna_exp_param_t *pf);
38
39
40 void E_gquad_ali_en(int          i,
41                   int          L,
42                   int          l[3],
43                   const short **S,
44                   unsigned int **a2s,
45                   unsigned int n_seq,
46                   vrna_param_t *P,
47                   int          en[2]);
48
49
66 int *get_gquad_matrix(short      *S,
67                      vrna_param_t *P);
68
69
70 int *get_gquad_ali_matrix(unsigned int n,
71                          short      *S_cons,
72                          short      **S,
73                          unsigned int **a2s,
74                          int          n_seq,
75                          vrna_param_t *P);
76
77
78 FLT_OR_DBL *get_gquad_pf_matrix(short      *S,
79                                FLT_OR_DBL *scale,
80                                vrna_exp_param_t *pf);
81
82
83 FLT_OR_DBL *get_gquad_pf_matrix_comparative(unsigned int n,
84   short      *S_cons,
85   short      **S,
86   unsigned int **a2s,
87   FLT_OR_DBL *scale,
88   unsigned int n_seq,
89   vrna_exp_param_t *pf);
90
91
92 int **get_gquad_L_matrix(short      *S,
93                        int          start,
94                        int          maxdist,
95                        int          n,
96                        int          **g,
97                        vrna_param_t *P);
98
99
100 void      vrna_gquad_mx_local_update(vrna_fold_compound_t *vc,
101                                     int          start);
102
103
104 void get_gquad_pattern_mfe(short      *S,
105                        int          i,
106                        int          j,
107                        vrna_param_t *P,
108                        int          *L,
109                        int          l[3]);
110
111
112 void
113 get_gquad_pattern_exhaustive(short      *S,
114                        int          i,
115                        int          j,
116                        vrna_param_t *P,
117                        int          *L,
118                        int          *l,
119                        int          threshold);
120
121
122 void get_gquad_pattern_pf(short      *S,
123                        int          i,
124                        int          j,
125                        vrna_exp_param_t *pf,
126                        int          *L,
127                        int          l[3]);
128
129
130 plist *get_plist_gquad_from_pr(short      *S,
131                              int          gi,
132                              int          gj,
133                              FLT_OR_DBL *G,
134                              FLT_OR_DBL *probs,
135                              FLT_OR_DBL *scale,

```

```

136             vrna_exp_param_t *pf);
137
138
139 plist *get_plist_gquad_from_pr_max(short      *S,
140                                   int         gi,
141                                   int         gj,
142                                   FLT_OR_DBL *G,
143                                   FLT_OR_DBL *probs,
144                                   FLT_OR_DBL *scale,
145                                   int         *L,
146                                   int         l[3],
147                                   vrna_exp_param_t *pf);
148
149
150 plist *get_plist_gquad_from_db(const char *structure,
151                               float      pr);
152
153
154 plist *
155 vrna_get_plist_gquad_from_pr(vrna_fold_compound_t *fc,
156                             int                 gi,
157                             int                 gj);
158
159
160 plist *
161 vrna_get_plist_gquad_from_pr_max(vrna_fold_compound_t *fc,
162                                  int                 gi,
163                                  int                 gj,
164                                  int                 *Lmax,
165                                  int                 lmax[3]);
166
167
168 int get_gquad_count(short *S,
169                    int   i,
170                    int   j);
171
172
173 int get_gquad_layer_count(short *S,
174                          int   i,
175                          int   j);
176
177
178 void get_gquad_pattern_mfe_all(short **S,
179                               unsigned int **a2s,
180                               short *S_cons,
181                               int n_seq,
182                               int i,
183                               int j,
184                               vrna_param_t *P,
185                               int *L,
186                               int l[3]);
187
188
189 int parse_gquad(const char *struc,
190                int *L,
191                int l[3]);
192
193
194
195
196
197
198
199
200
201
202
203
204 INLINE PRIVATE int backtrack_GQuad_IntLoop(int c,
205   int i,
206   int j,
207   int type,
208   short *S,
209   int *ggg,
210   int *index,
211   int *p,
212   int *q,
213   vrna_param_t *P);
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232 INLINE PRIVATE int backtrack_GQuad_IntLoop_L(int c,

```



```

233                                     int          i,
234                                     int          j,
235                                     int          type,
236                                     short         *S,
237                                     int          **ggg,
238                                     int          maxdist,
239                                     int          *p,
240                                     int          *q,
241                                     vrna_param_t *P);
242
243
244 PRIVATE INLINE int
245 vrna_BT_gquad_int(vrna_fold_compound_t *vc,
246                  int i,
247                  int j,
248                  int en,
249                  vrna_bp_stack_t *bp_stack,
250                  int *stack_count);
251
252
253 PRIVATE INLINE int
254 vrna_BT_gquad_mfe(vrna_fold_compound_t *vc,
255                  int i,
256                  int j,
257                  vrna_bp_stack_t *bp_stack,
258                  int *stack_count)
259 {
260     /*
261      * here we do some fancy stuff to backtrace the stacksize and linker lengths
262      * of the g-quadruplex that should reside within position i,j
263      */
264     short *S;
265     int l[3], L, a, n_seq;
266     vrna_param_t *P;
267
268     if (vc) {
269         P = vc->params;
270         switch (vc->type) {
271             case VRNA_FC_TYPE_SINGLE:
272                 S = vc->sequence_encoding2;
273                 L = -1;
274
275                 get_gquad_pattern_mfe(S, i, j, P, &L, l);
276                 break;
277
278             case VRNA_FC_TYPE_COMPARATIVE:
279                 n_seq = vc->n_seq;
280                 L = -1;
281                 get_gquad_pattern_mfe_aln(vc->S, vc->a2s, vc->S_cons, n_seq, i, j, P, &L, l);
282                 break;
283         }
284
285         if (L != -1) {
286             /* fill the G's of the quadruplex into base_pair2 */
287             for (a = 0; a < L; a++) {
288                 bp_stack[+(*stack_count)].i = i + a;
289                 bp_stack[(*stack_count)].j = i + a;
290                 bp_stack[+(*stack_count)].i = i + L + l[0] + a;
291                 bp_stack[(*stack_count)].j = i + L + l[0] + a;
292                 bp_stack[+(*stack_count)].i = i + L + l[0] + L + l[1] + a;
293                 bp_stack[(*stack_count)].j = i + L + l[0] + L + l[1] + a;
294                 bp_stack[+(*stack_count)].i = i + L + l[0] + L + l[1] + L + l[2] + a;
295                 bp_stack[(*stack_count)].j = i + L + l[0] + L + l[1] + L + l[2] + a;
296             }
297             return 1;
298         } else {
299             return 0;
300         }
301     }
302
303     return 0;
304 }
305
306
307 PRIVATE INLINE int
308 vrna_BT_gquad_int(vrna_fold_compound_t *vc,
309                  int i,
310                  int j,
311                  int en,
312                  vrna_bp_stack_t *bp_stack,
313                  int *stack_count)
314 {
315     int energy, dangles, *idx, ij, p, q, maxl, minl, c0, l1, *ggg;
316     unsigned char type;
317     char *ptype;
318     short si, sj, *S, *S1;
319

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320 vrna_param_t *P;
321 vrna_md_t *md;
322
323 idx = vc->jindx;
324 ij = idx[j] + i;
325 P = vc->params;
326 md = &(P->model_details);
327 ptype = vc->ptype;
328 type = (unsigned char)ptype[ij];
329 S1 = vc->sequence_encoding;
330 S = vc->sequence_encoding2;
331 dangles = md->dangles;
332 si = S1[i + 1];
333 sj = S1[j - 1];
334 ggg = vc->matrices->ggg;
335 energy = 0;
336
337 if (dangles == 2)
338     energy += P->mismatchI[type][si][sj];
339
340 if (type > 2)
341     energy += P->TerminalAU;
342
343 p = i + 1;
344 if (S1[p] == 3) {
345     if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
346         minl = j - i + p - MAXLOOP - 2;
347         c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
348         minl = MAX2(c0, minl);
349         c0 = j - 3;
350         maxl = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
351         maxl = MIN2(c0, maxl);
352         for (q = minl; q < maxl; q++) {
353             if (S[q] != 3)
354                 continue;
355
356             if (en == energy + ggg[idx[q] + p] + P->internal_loop[j - q - 1])
357                 return vrna_BT_gquad_mfe(vc, p, q, bp_stack, stack_count);
358         }
359     }
360 }
361
362 for (p = i + 2;
363      p < j - VRNA_GQUAD_MIN_BOX_SIZE;
364      p++) {
365     l1 = p - i - 1;
366     if (l1 > MAXLOOP)
367         break;
368
369     if (S1[p] != 3)
370         continue;
371
372     minl = j - i + p - MAXLOOP - 2;
373     c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
374     minl = MAX2(c0, minl);
375     c0 = j - 1;
376     maxl = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
377     maxl = MIN2(c0, maxl);
378     for (q = minl; q < maxl; q++) {
379         if (S1[q] != 3)
380             continue;
381
382         if (en == energy + ggg[idx[q] + p] + P->internal_loop[l1 + j - q - 1])
383             return vrna_BT_gquad_mfe(vc, p, q, bp_stack, stack_count);
384     }
385 }
386
387 q = j - 1;
388 if (S1[q] == 3)
389     for (p = i + 4;
390          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
391          p++) {
392         l1 = p - i - 1;
393         if (l1 > MAXLOOP)
394             break;
395
396         if (S1[p] != 3)
397             continue;
398
399         if (en == energy + ggg[idx[q] + p] + P->internal_loop[l1])
400             return vrna_BT_gquad_mfe(vc, p, q, bp_stack, stack_count);
401     }
402
403 return 0;
404 }
405
406

```

```

424 INLINE PRIVATE int
425 backtrack_GQuad_IntLoop(int          c,
426                          int          i,
427                          int          j,
428                          int          type,
429                          short        *S,
430                          int          *ggg,
431                          int          *index,
432                          int          *p,
433                          int          *q,
434                          vrna_param_t *P)
435 {
436     int  energy, dangles, k, l, maxl, minl, c0, ll;
437     short si, sj;
438
439     dangles = P->model_details.dangles;
440     si      = S[i + 1];
441     sj      = S[j - 1];
442     energy  = 0;
443
444     if (dangles == 2)
445         energy += P->mismatchI[type][si][sj];
446
447     if (type > 2)
448         energy += P->TerminalAU;
449
450     k = i + 1;
451     if (S[k] == 3) {
452         if (k < j - VRNA_GQUAD_MIN_BOX_SIZE) {
453             minl = j - i + k - MAXLOOP - 2;
454             c0   = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
455             minl = MAX2(c0, minl);
456             c0   = j - 3;
457             maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
458             maxl = MIN2(c0, maxl);
459             for (l = minl; l < maxl; l++) {
460                 if (S[l] != 3)
461                     continue;
462
463                 if (c == energy + ggg[index[l] + k] + P->internal_loop[j - l - 1]) {
464                     *p = k;
465                     *q = l;
466                     return 1;
467                 }
468             }
469         }
470     }
471
472     for (k = i + 2;
473          k < j - VRNA_GQUAD_MIN_BOX_SIZE;
474          k++) {
475         ll = k - i - 1;
476         if (ll > MAXLOOP)
477             break;
478
479         if (S[k] != 3)
480             continue;
481
482         minl = j - i + k - MAXLOOP - 2;
483         c0   = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
484         minl = MAX2(c0, minl);
485         c0   = j - 1;
486         maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
487         maxl = MIN2(c0, maxl);
488         for (l = minl; l < maxl; l++) {
489             if (S[l] != 3)
490                 continue;
491
492             if (c == energy + ggg[index[l] + k] + P->internal_loop[ll + j - l - 1]) {
493                 *p = k;
494                 *q = l;
495                 return 1;
496             }
497         }
498     }
499
500     l = j - 1;
501     if (S[l] == 3)
502         for (k = i + 4;
503              k < j - VRNA_GQUAD_MIN_BOX_SIZE;
504              k++) {
505             ll = k - i - 1;
506             if (ll > MAXLOOP)
507                 break;
508
509             if (S[k] != 3)
510                 continue;

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511
512     if (c == energy + ggg[index[l] + k] + P->internal_loop[l1]) {
513         *p = k;
514         *q = l;
515         return 1;
516     }
517 }
518
519 return 0;
520 }
521
522
523 INLINE PRIVATE int
524 backtrack_GQuad_IntLoop_comparative(int          c,
525                                     int           i,
526                                     int           j,
527                                     unsigned int  *type,
528                                     short         *S_cons,
529                                     short         **S5,
530                                     short         **S3,
531                                     unsigned int  **a2s,
532                                     int           *ggg,
533                                     int           *index,
534                                     int           *p,
535                                     int           *q,
536                                     int           n_seq,
537                                     vrna_param_t *P)
538 {
539     int energy, dangles, k, l, maxl, minl, c0, l1, ss, tt, u1, u2, eee;
540
541     dangles = P->model_details.dangles;
542     energy = 0;
543
544     for (ss = 0; ss < n_seq; ss++) {
545         tt = type[ss];
546         if (tt == 0)
547             tt = 7;
548
549         if (dangles == 2)
550             energy += P->mismatchI[tt][S3[ss][i]][S5[ss][j]];
551
552         if (tt > 2)
553             energy += P->TerminalAU;
554     }
555
556     k = i + 1;
557     if (S_cons[k] == 3) {
558         if (k < j - VRNA_GQUAD_MIN_BOX_SIZE) {
559             minl = j - i + k - MAXLOOP - 2;
560             c0 = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
561             minl = MAX2(c0, minl);
562             c0 = j - 3;
563             maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
564             maxl = MIN2(c0, maxl);
565             for (l = minl; l < maxl; l++) {
566                 if (S_cons[l] != 3)
567                     continue;
568
569                 eee = 0;
570
571                 for (ss = 0; ss < n_seq; ss++) {
572                     u1 = a2s[ss][j - 1] - a2s[ss][l];
573                     eee += P->internal_loop[u1];
574                 }
575
576                 if (c == energy + ggg[index[l] + k] + eee) {
577                     *p = k;
578                     *q = l;
579                     return 1;
580                 }
581             }
582         }
583     }
584
585     for (k = i + 2;
586          k < j - VRNA_GQUAD_MIN_BOX_SIZE;
587          k++) {
588         l1 = k - i - 1;
589         if (l1 > MAXLOOP)
590             break;
591
592         if (S_cons[k] != 3)
593             continue;
594
595         minl = j - i + k - MAXLOOP - 2;
596         c0 = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
597         minl = MAX2(c0, minl);

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598     c0    = j - 1;
599     maxl   = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
600     maxl   = MIN2(c0, maxl);
601     for (l = minl; l < maxl; l++) {
602         if (S_cons[l] != 3)
603             continue;
604
605         eee = 0;
606
607         for (ss = 0; ss < n_seq; ss++) {
608             u1 = a2s[ss][k - 1] - a2s[ss][i];
609             u2 = a2s[ss][j - 1] - a2s[ss][l];
610             eee += P->internal_loop[u1 + u2];
611         }
612
613         if (c == energy + ggg[index[l] + k] + eee) {
614             *p = k;
615             *q = l;
616             return 1;
617         }
618     }
619 }
620
621 l = j - 1;
622 if (S_cons[l] == 3)
623     for (k = i + 4;
624          k < j - VRNA_GQUAD_MIN_BOX_SIZE;
625          k++) {
626         ll = k - i - 1;
627         if (ll > MAXLOOP)
628             break;
629
630         if (S_cons[k] != 3)
631             continue;
632
633         eee = 0;
634
635         for (ss = 0; ss < n_seq; ss++) {
636             u1 = a2s[ss][k - 1] - a2s[ss][i];
637             eee += P->internal_loop[u1];
638         }
639
640         if (c == energy + ggg[index[l] + k] + eee) {
641             *p = k;
642             *q = l;
643             return 1;
644         }
645     }
646
647 return 0;
648 }
649
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```

701     maxl = MIN2(c0, maxl);
702     for (l = minl; l < maxl; l++) {
703         if (S[l] != 3)
704             continue;
705
706         if (c == energy + ggg[k][l - k] + P->internal_loop[j - l - 1]) {
707             *p = k;
708             *q = l;
709             return 1;
710         }
711     }
712 }
713 }
714
715 for (k = i + 2;
716      k < j - VRNA_GQUAD_MIN_BOX_SIZE;
717      k++) {
718     ll = k - i - 1;
719     if (ll > MAXLOOP)
720         break;
721
722     if (S[k] != 3)
723         continue;
724
725     minl = j - i + k - MAXLOOP - 2;
726     c0 = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
727     minl = MAX2(c0, minl);
728     c0 = j - 1;
729     maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
730     maxl = MIN2(c0, maxl);
731     for (l = minl; l < maxl; l++) {
732         if (S[l] != 3)
733             continue;
734
735         if (c == energy + ggg[k][l - k] + P->internal_loop[ll + j - l - 1]) {
736             *p = k;
737             *q = l;
738             return 1;
739         }
740     }
741 }
742
743 l = j - 1;
744 if (S[l] == 3)
745     for (k = i + 4;
746          k < j - VRNA_GQUAD_MIN_BOX_SIZE;
747          k++) {
748         ll = k - i - 1;
749         if (ll > MAXLOOP)
750             break;
751
752         if (S[k] != 3)
753             continue;
754
755         if (c == energy + ggg[k][l - k] + P->internal_loop[ll]) {
756             *p = k;
757             *q = l;
758             return 1;
759         }
760     }
761
762 return 0;
763 }
764
765
766 INLINE PRIVATE int
767 backtrack_GQuad_IntLoop_L_comparative(int c,
768                                       int i,
769                                       int j,
770                                       unsigned int *ttype,
771                                       short *S_cons,
772                                       short **S5,
773                                       short **S3,
774                                       unsigned int **a2s,
775                                       int **ggg,
776                                       int *p,
777                                       int *q,
778                                       int n_seq,
779                                       vrna_param_t *P)
780 {
781     /*
782     * The case that is handled here actually resembles something like
783     * an interior loop where the enclosing base pair is of regular
784     * kind and the enclosed pair is not a canonical one but a g-quadruplex
785     * that should then be decomposed further...
786     */
787     int mm, dangle_model, k, l, maxl, minl, c0, ll, ss, tt, eee, ul, u2;

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788
789 dangle_model = P->model_details.dangles;
790
791 mm = 0;
792 for (ss = 0; ss < n_seq; ss++) {
793     tt = type[ss];
794
795     if (dangle_model == 2)
796         mm += P->mismatchI[tt][S3[ss][i]][S5[ss][j]];
797
798     if (tt > 2)
799         mm += P->TerminalAU;
800 }
801
802 for (k = i + 2;
803      k < j - VRNA_GQUAD_MIN_BOX_SIZE;
804      k++) {
805     if (S_cons[k] != 3)
806         continue;
807
808     l1 = k - i - 1;
809     if (l1 > MAXLOOP)
810         break;
811
812     minl = j - i + k - MAXLOOP - 2;
813     c0 = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
814     minl = MAX2(c0, minl);
815     c0 = j - 1;
816     maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
817     maxl = MIN2(c0, maxl);
818     for (l = minl; l < maxl; l++) {
819         if (S_cons[l] != 3)
820             continue;
821
822         eee = 0;
823
824         for (ss = 0; ss < n_seq; ss++) {
825             u1 = a2s[ss][k - 1] - a2s[ss][i];
826             u2 = a2s[ss][j - 1] - a2s[ss][l];
827             eee += P->internal_loop[u1 + u2];
828         }
829
830         c0 = mm +
831             ggg[k][l - k] +
832             eee;
833
834         if (c == c0) {
835             *p = k;
836             *q = l;
837             return 1;
838         }
839     }
840 }
841 k = i + 1;
842 if (S_cons[k] == 3) {
843     if (k < j - VRNA_GQUAD_MIN_BOX_SIZE) {
844         minl = j - i + k - MAXLOOP - 2;
845         c0 = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
846         minl = MAX2(c0, minl);
847         c0 = j - 3;
848         maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
849         maxl = MIN2(c0, maxl);
850         for (l = minl; l < maxl; l++) {
851             if (S_cons[l] != 3)
852                 continue;
853
854             eee = 0;
855
856             for (ss = 0; ss < n_seq; ss++) {
857                 u1 = a2s[ss][j - 1] - a2s[ss][l];
858                 eee += P->internal_loop[u1];
859             }
860
861             if (c == mm + ggg[k][l - k] + eee) {
862                 *p = k;
863                 *q = l;
864                 return 1;
865             }
866         }
867     }
868 }
869
870 l = j - 1;
871 if (S_cons[l] == 3) {
872     for (k = i + 4; k < j - VRNA_GQUAD_MIN_BOX_SIZE; k++) {
873         l1 = k - i - 1;
874         if (l1 > MAXLOOP)

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875         break;
876
877     if (S_cons[k] != 3)
878         continue;
879
880     eee = 0;
881
882     for (ss = 0; ss < n_seq; ss++) {
883         u1 = a2s[ss][k - 1] - a2s[ss][i];
884         eee += P->internal_loop[u1];
885     }
886
887     if (c == mm + ggg[k][l - k] + eee) {
888         *p = k;
889         *q = l;
890         return 1;
891     }
892 }
893 }
894
895 return 0;
896 }
897
898
899 PRIVATE INLINE
900 int
901 E_GQuad_IntLoop(int      i,
902                 int      j,
903                 int      type,
904                 short     *S,
905                 int       *ggg,
906                 int       *index,
907                 vrna_param_t *P)
908 {
909     int  energy, ge, dangles, p, q, l1, minq, maxq, c0;
910     short si, sj;
911
912     dangles = P->model_details.dangles;
913     si = S[i + 1];
914     sj = S[j - 1];
915     energy = 0;
916
917     if (dangles == 2)
918         energy += P->mismatchI[type][si][sj];
919
920     if (type > 2)
921         energy += P->TerminalAU;
922
923     ge = INF;
924
925     p = i + 1;
926     if (S[p] == 3) {
927         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
928             minq = j - i + p - MAXLOOP - 2;
929             c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
930             minq = MAX2(c0, minq);
931             c0 = j - 3;
932             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
933             maxq = MIN2(c0, maxq);
934             for (q = minq; q < maxq; q++) {
935                 if (S[q] != 3)
936                     continue;
937
938                 c0 = energy + ggg[index[q] + p] + P->internal_loop[j - q - 1];
939                 ge = MIN2(ge, c0);
940             }
941         }
942     }
943
944     for (p = i + 2;
945          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
946          p++) {
947         l1 = p - i - 1;
948         if (l1 > MAXLOOP)
949             break;
950
951         if (S[p] != 3)
952             continue;
953
954         minq = j - i + p - MAXLOOP - 2;
955         c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
956         minq = MAX2(c0, minq);
957         c0 = j - 1;
958         maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
959         maxq = MIN2(c0, maxq);
960         for (q = minq; q < maxq; q++) {
961             if (S[q] != 3)

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962         continue;
963
964         c0 = energy + ggg[index[q] + p] + P->internal_loop[l1 + j - q - 1];
965         ge = MIN2(ge, c0);
966     }
967 }
968
969 q = j - 1;
970 if (S[q] == 3)
971     for (p = i + 4;
972          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
973          p++) {
974         l1 = p - i - 1;
975         if (l1 > MAXLOOP)
976             break;
977
978         if (S[p] != 3)
979             continue;
980
981         c0 = energy + ggg[index[q] + p] + P->internal_loop[l1];
982         ge = MIN2(ge, c0);
983     }
984
985 #if 0
986 /* here comes the additional stuff for the odd dangle models */
987 if (dangles % 1) {
988     en1 = energy + P->dangle5[type][si];
989     en2 = energy + P->dangle5[type][sj];
990     en3 = energy + P->mismatchI[type][si][sj];
991
992     /* first case with 5' dangle (i.e. j-1) onto enclosing pair */
993     p = i + 1;
994     if (S[p] == 3) {
995         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
996             minq = j - i + p - MAXLOOP - 2;
997             c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
998             minq = MAX2(c0, minq);
999             c0 = j - 4;
1000             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1001             maxq = MIN2(c0, maxq);
1002             for (q = minq; q < maxq; q++) {
1003                 if (S[q] != 3)
1004                     continue;
1005
1006                 c0 = en1 + ggg[index[q] + p] + P->internal_loop[j - q - 1];
1007                 ge = MIN2(ge, c0);
1008             }
1009         }
1010     }
1011
1012     for (p = i + 2; p < j - VRNA_GQUAD_MIN_BOX_SIZE; p++) {
1013         l1 = p - i - 1;
1014         if (l1 > MAXLOOP)
1015             break;
1016
1017         if (S[p] != 3)
1018             continue;
1019
1020         minq = j - i + p - MAXLOOP - 2;
1021         c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1022         minq = MAX2(c0, minq);
1023         c0 = j - 2;
1024         maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1025         maxq = MIN2(c0, maxq);
1026         for (q = minq; q < maxq; q++) {
1027             if (S[q] != 3)
1028                 continue;
1029
1030             c0 = en1 + ggg[index[q] + p] + P->internal_loop[l1 + j - q - 1];
1031             ge = MIN2(ge, c0);
1032         }
1033     }
1034
1035     q = j - 2;
1036     if (S[q] == 3)
1037         for (p = i + 4; p < j - VRNA_GQUAD_MIN_BOX_SIZE; p++) {
1038             l1 = p - i - 1;
1039             if (l1 > MAXLOOP)
1040                 break;
1041
1042             if (S[p] != 3)
1043                 continue;
1044
1045             c0 = en1 + ggg[index[q] + p] + P->internal_loop[l1 + 1];
1046             ge = MIN2(ge, c0);
1047         }
1048 }

```

```

1049     /* second case with 3' dangle (i.e. i+1) onto enclosing pair */
1050 }
1051
1052 #endif
1053 return ge;
1054 }
1055
1056
1057 PRIVATE INLINE
1058 int
1059 E_GQuad_IntLoop_comparative(int i,
1060                               int j,
1061                               unsigned int *tt,
1062                               short *S_cons,
1063                               short **S5,
1064                               short **S3,
1065                               unsigned int **a2s,
1066                               int *ggg,
1067                               int *index,
1068                               int n_seq,
1069                               vrna_param_t *P)
1070 {
1071     unsigned int type;
1072     int eee, energy, ge, p, q, l1, u1, u2, minq, maxq, c0, s;
1073     vrna_md_t *md;
1074
1075     md = &(P->model_details);
1076     energy = 0;
1077
1078     for (s = 0; s < n_seq; s++) {
1079         type = tt[s];
1080         if (md->dangles == 2)
1081             energy += P->mismatchI[type][S3[s][i]][S5[s][j]];
1082
1083         if (type > 2)
1084             energy += P->TerminalAU;
1085     }
1086
1087     ge = INF;
1088
1089     p = i + 1;
1090     if (S_cons[p] == 3) {
1091         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1092             minq = j - i + p - MAXLOOP - 2;
1093             c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1094             minq = MAX2(c0, minq);
1095             c0 = j - 3;
1096             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1097             maxq = MIN2(c0, maxq);
1098             for (q = minq; q < maxq; q++) {
1099                 if (S_cons[q] != 3)
1100                     continue;
1101
1102                 eee = 0;
1103
1104                 for (s = 0; s < n_seq; s++) {
1105                     u1 = a2s[s][j - 1] - a2s[s][q];
1106                     eee += P->internal_loop[u1];
1107                 }
1108
1109                 c0 = energy +
1110                     ggg[index[q] + p] +
1111                     eee;
1112                 ge = MIN2(ge, c0);
1113             }
1114         }
1115     }
1116
1117     for (p = i + 2;
1118          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1119          p++) {
1120         l1 = p - i - 1;
1121         if (l1 > MAXLOOP)
1122             break;
1123
1124         if (S_cons[p] != 3)
1125             continue;
1126
1127         minq = j - i + p - MAXLOOP - 2;
1128         c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1129         minq = MAX2(c0, minq);
1130         c0 = j - 1;
1131         maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1132         maxq = MIN2(c0, maxq);
1133         for (q = minq; q < maxq; q++) {
1134             if (S_cons[q] != 3)
1135                 continue;

```

```

1136
1137     eee = 0;
1138
1139     for (s = 0; s < n_seq; s++) {
1140         u1 = a2s[s][p - 1] - a2s[s][i];
1141         u2 = a2s[s][j - 1] - a2s[s][q];
1142         eee += P->internal_loop[u1 + u2];
1143     }
1144
1145     c0 = energy +
1146         ggg[index[q] + p] +
1147         eee;
1148     ge = MIN2(ge, c0);
1149 }
1150 }
1151
1152 q = j - 1;
1153 if (S_cons[q] == 3)
1154     for (p = i + 4;
1155          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1156          p++) {
1157         l1 = p - i - 1;
1158         if (l1 > MAXLOOP)
1159             break;
1160
1161         if (S_cons[p] != 3)
1162             continue;
1163
1164         eee = 0;
1165
1166         for (s = 0; s < n_seq; s++) {
1167             u1 = a2s[s][p - 1] - a2s[s][i];
1168             eee += P->internal_loop[u1];
1169         }
1170
1171         c0 = energy +
1172             ggg[index[q] + p] +
1173             eee;
1174         ge = MIN2(ge, c0);
1175     }
1176
1177     return ge;
1178 }
1179
1180
1181 PRIVATE INLINE
1182 int
1183 E_GQuad_IntLoop_L_comparative(int i,
1184                                int j,
1185                                unsigned int *tt,
1186                                short *S_cons,
1187                                short **S5,
1188                                short **S3,
1189                                unsigned int **a2s,
1190                                int **ggg,
1191                                int n_seq,
1192                                vrna_param_t *P)
1193 {
1194     unsigned int type;
1195     int eee, energy, ge, p, q, l1, u1, u2, minq, maxq, c0, s;
1196     vrna_md_t *md;
1197
1198     md = &(P->model_details);
1199     energy = 0;
1200
1201     for (s = 0; s < n_seq; s++) {
1202         type = tt[s];
1203         if (md->dangles == 2)
1204             energy += P->mismatchI[type][S3[s][i]][S5[s][j]];
1205
1206         if (type > 2)
1207             energy += P->TerminalAU;
1208     }
1209
1210     ge = INF;
1211
1212     p = i + 1;
1213     if (S_cons[p] == 3) {
1214         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1215             minq = j - i + p - MAXLOOP - 2;
1216             c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1217             minq = MAX2(c0, minq);
1218             c0 = j - 3;
1219             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1220             maxq = MIN2(c0, maxq);
1221             for (q = minq; q < maxq; q++) {
1222                 if (S_cons[q] != 3)

```

```

1223         continue;
1224
1225         eee = 0;
1226
1227         for (s = 0; s < n_seq; s++) {
1228             u1 = a2s[s][j - 1] - a2s[s][q];
1229             eee += P->internal_loop[u1];
1230         }
1231
1232         c0 = energy +
1233             ggg[p][q - p] +
1234             eee;
1235         ge = MIN2(ge, c0);
1236     }
1237 }
1238 }
1239
1240 for (p = i + 2;
1241      p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1242      p++) {
1243     l1 = p - i - 1;
1244     if (l1 > MAXLOOP)
1245         break;
1246
1247     if (S_cons[p] != 3)
1248         continue;
1249
1250     minq = j - i + p - MAXLOOP - 2;
1251     c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1252     minq = MAX2(c0, minq);
1253     c0 = j - 1;
1254     maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1255     maxq = MIN2(c0, maxq);
1256     for (q = minq; q < maxq; q++) {
1257         if (S_cons[q] != 3)
1258             continue;
1259
1260         eee = 0;
1261
1262         for (s = 0; s < n_seq; s++) {
1263             u1 = a2s[s][p - 1] - a2s[s][i];
1264             u2 = a2s[s][j - 1] - a2s[s][q];
1265             eee += P->internal_loop[u1 + u2];
1266         }
1267
1268         c0 = energy +
1269             ggg[p][q - p] +
1270             eee;
1271         ge = MIN2(ge, c0);
1272     }
1273 }
1274
1275 q = j - 1;
1276 if (S_cons[q] == 3)
1277     for (p = i + 4;
1278          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1279          p++) {
1280         l1 = p - i - 1;
1281         if (l1 > MAXLOOP)
1282             break;
1283
1284         if (S_cons[p] != 3)
1285             continue;
1286
1287         eee = 0;
1288
1289         for (s = 0; s < n_seq; s++) {
1290             u1 = a2s[s][p - 1] - a2s[s][i];
1291             eee += P->internal_loop[u1];
1292         }
1293
1294         c0 = energy +
1295             ggg[p][q - p] +
1296             eee;
1297         ge = MIN2(ge, c0);
1298     }
1299
1300 return ge;
1301 }
1302
1303
1304 PRIVATE INLINE
1305 int *
1306 E_GQuad_IntLoop_exhaustive(int i,
1307                             int j,
1308                             int **p_p,
1309                             int **q_p,

```

```

1310             int            type,
1311             short          *S,
1312             int            *ggg,
1313             int            threshold,
1314             int            *index,
1315             vrna_param_t  *P)
1316 {
1317     int    energy, *ge, dangles, p, q, l1, minq, maxq, c0;
1318     short si, sj;
1319     int    cnt = 0;
1320
1321     dangles = P->model_details.dangles;
1322     si      = S[i + 1];
1323     sj      = S[j - 1];
1324     energy  = 0;
1325
1326     if (dangles == 2)
1327         energy += P->mismatchI[type][si][sj];
1328
1329     if (type > 2)
1330         energy += P->TerminalAU;
1331
1332     /* guess how many gquads are possible in interval [i+1,j-1] */
1333     *p_p = (int *)vrna_alloc(sizeof(int) * 256);
1334     *q_p = (int *)vrna_alloc(sizeof(int) * 256);
1335     ge   = (int *)vrna_alloc(sizeof(int) * 256);
1336
1337     p = i + 1;
1338     if (S[p] == 3) {
1339         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1340             minq = j - i + p - MAXLOOP - 2;
1341             c0   = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1342             minq = MAX2(c0, minq);
1343             c0   = j - 3;
1344             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1345             maxq = MIN2(c0, maxq);
1346             for (q = minq; q < maxq; q++) {
1347                 if (S[q] != 3)
1348                     continue;
1349
1350                 c0 = energy + ggg[index[q] + p] + P->internal_loop[j - q - 1];
1351                 if (c0 <= threshold) {
1352                     ge[cnt] = energy + P->internal_loop[j - q - 1];
1353                     (*p_p)[cnt] = p;
1354                     (*q_p)[cnt++] = q;
1355                 }
1356             }
1357         }
1358     }
1359
1360     for (p = i + 2;
1361          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1362          p++) {
1363         l1 = p - i - 1;
1364         if (l1 > MAXLOOP)
1365             break;
1366
1367         if (S[p] != 3)
1368             continue;
1369
1370         minq = j - i + p - MAXLOOP - 2;
1371         c0   = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1372         minq = MAX2(c0, minq);
1373         c0   = j - 1;
1374         maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1375         maxq = MIN2(c0, maxq);
1376         for (q = minq; q < maxq; q++) {
1377             if (S[q] != 3)
1378                 continue;
1379
1380             c0 = energy + ggg[index[q] + p] + P->internal_loop[l1 + j - q - 1];
1381             if (c0 <= threshold) {
1382                 ge[cnt] = energy + P->internal_loop[l1 + j - q - 1];
1383                 (*p_p)[cnt] = p;
1384                 (*q_p)[cnt++] = q;
1385             }
1386         }
1387     }
1388
1389     q = j - 1;
1390     if (S[q] == 3)
1391         for (p = i + 4;
1392              p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1393              p++) {
1394             l1 = p - i - 1;
1395             if (l1 > MAXLOOP)
1396                 break;

```

```

1397
1398     if (S[p] != 3)
1399         continue;
1400
1401     c0 = energy + ggg[index[q] + p] + P->internal_loop[l1];
1402     if (c0 <= threshold) {
1403         ge[cnt] = energy + P->internal_loop[l1];
1404         (*p_p)[cnt] = p;
1405         (*q_p)[cnt++] = q;
1406     }
1407 }
1408
1409 (*p_p)[cnt] = -1;
1410
1411 return ge;
1412 }
1413
1414
1415 PRIVATE INLINE
1416 int
1417 E_GQuad_IntLoop_L(int i,
1418                   int j,
1419                   int type,
1420                   short *S,
1421                   int **ggg,
1422                   int maxdist,
1423                   vrna_param_t *P)
1424 {
1425     int energy, ge, dangles, p, q, l1, minq, maxq, c0;
1426     short si, sj;
1427
1428     dangles = P->model_details.dangles;
1429     si = S[i + 1];
1430     sj = S[j - 1];
1431     energy = 0;
1432
1433     if (dangles == 2)
1434         energy += P->mismatchI[type][si][sj];
1435
1436     if (type > 2)
1437         energy += P->TerminalAU;
1438
1439     ge = INF;
1440
1441     p = i + 1;
1442     if (S[p] == 3) {
1443         if (p < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1444             minq = j - i + p - MAXLOOP - 2;
1445             c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1446             minq = MAX2(c0, minq);
1447             c0 = j - 3;
1448             maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1449             maxq = MIN2(c0, maxq);
1450             for (q = minq; q < maxq; q++) {
1451                 if (S[q] != 3)
1452                     continue;
1453
1454                 c0 = energy + ggg[p][q - p] + P->internal_loop[j - q - 1];
1455                 ge = MIN2(ge, c0);
1456             }
1457         }
1458     }
1459
1460     for (p = i + 2;
1461          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1462          p++) {
1463         l1 = p - i - 1;
1464         if (l1 > MAXLOOP)
1465             break;
1466
1467         if (S[p] != 3)
1468             continue;
1469
1470         minq = j - i + p - MAXLOOP - 2;
1471         c0 = p + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1472         minq = MAX2(c0, minq);
1473         c0 = j - 1;
1474         maxq = p + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1475         maxq = MIN2(c0, maxq);
1476         for (q = minq; q < maxq; q++) {
1477             if (S[q] != 3)
1478                 continue;
1479
1480             c0 = energy + ggg[p][q - p] + P->internal_loop[l1 + j - q - 1];
1481             ge = MIN2(ge, c0);
1482         }
1483     }

```

```

1484
1485 q = j - 1;
1486 if (S[q] == 3)
1487     for (p = i + 4;
1488          p < j - VRNA_GQUAD_MIN_BOX_SIZE;
1489          p++) {
1490         ll = p - i - 1;
1491         if (ll > MAXLOOP)
1492             break;
1493
1494         if (S[p] != 3)
1495             continue;
1496
1497         c0 = energy + ggg[p][q - p] + P->internal_loop[ll];
1498         ge = MIN2(ge, c0);
1499     }
1500
1501     return ge;
1502 }
1503
1504
1505 PRIVATE INLINE
1506 FLT_OR_DBL
1507 exp_E_GQuad_IntLoop(int i,
1508                     int j,
1509                     int type,
1510                     short *S,
1511                     FLT_OR_DBL *G,
1512                     FLT_OR_DBL *scale,
1513                     int *index,
1514                     vrna_exp_param_t *pf)
1515 {
1516     int k, l, minl, maxl, u, r;
1517     FLT_OR_DBL q, qe;
1518     double *expintern;
1519     short si, sj;
1520
1521     q = 0;
1522     si = S[i + 1];
1523     sj = S[j - 1];
1524     qe = (FLT_OR_DBL)pf->expmismatchI[type][si][sj];
1525     expintern = &(pf->expinternal[0]);
1526
1527     if (type > 2)
1528         qe *= (FLT_OR_DBL)pf->expTermAU;
1529
1530     k = i + 1;
1531     if (S[k] == 3) {
1532         if (k < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1533             minl = j - MAXLOOP - 1;
1534             u = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1535             minl = MAX2(u, minl);
1536             u = j - 3;
1537             maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1538             maxl = MIN2(u, maxl);
1539             for (l = minl; l < maxl; l++) {
1540                 if (S[l] != 3)
1541                     continue;
1542
1543                 if (G[index[k] - 1] == 0.)
1544                     continue;
1545
1546                 q += qe
1547                     * G[index[k] - 1]
1548                     * (FLT_OR_DBL)expintern[j - 1 - l]
1549                     * scale[j - 1 + l];
1550             }
1551         }
1552     }
1553
1554     for (k = i + 2;
1555          k <= j - VRNA_GQUAD_MIN_BOX_SIZE;
1556          k++) {
1557         u = k - i - 1;
1558         if (u > MAXLOOP)
1559             break;
1560
1561         if (S[k] != 3)
1562             continue;
1563
1564         minl = j - i + k - MAXLOOP - 2;
1565         r = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1566         minl = MAX2(r, minl);
1567         maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1568         r = j - 1;
1569         maxl = MIN2(r, maxl);
1570         for (l = minl; l < maxl; l++) {

```

```

1571     if (S[l] != 3)
1572         continue;
1573
1574     if (G[index[k] - 1] == 0.)
1575         continue;
1576
1577     q += qe
1578         * G[index[k] - 1]
1579         * (FLT_OR_DBL)expintern[u + j - 1 - 1]
1580         * scale[u + j - 1 + 1];
1581 }
1582 }
1583
1584 l = j - 1;
1585 if (S[l] == 3)
1586     for (k = i + 4; k <= j - VRNA_GQUAD_MIN_BOX_SIZE; k++) {
1587         u = k - i - 1;
1588         if (u > MAXLOOP)
1589             break;
1590
1591         if (S[k] != 3)
1592             continue;
1593
1594         if (G[index[k] - 1] == 0.)
1595             continue;
1596
1597         q += qe
1598             * G[index[k] - 1]
1599             * (FLT_OR_DBL)expintern[u]
1600             * scale[u + 2];
1601     }
1602
1603     return q;
1604 }
1605
1606
1607 PRIVATE INLINE
1608 FLT_OR_DBL
1609 exp_E_GQuad_IntLoop_comparative(int i,
1610                                   int j,
1611                                   unsigned int *tt,
1612                                   short *S_cons,
1613                                   short **S5,
1614                                   short **S3,
1615                                   unsigned int **a2s,
1616                                   FLT_OR_DBL *G,
1617                                   FLT_OR_DBL *scale,
1618                                   int *index,
1619                                   int n_seq,
1620                                   vrna_exp_param_t *pf)
1621 {
1622     unsigned int type;
1623     int k, l, minl, maxl, u, u1, u2, r, s;
1624     FLT_OR_DBL q, qe, qqq;
1625     double *expintern;
1626     vrna_md_t *md;
1627
1628     q = 0;
1629     qe = 1.;
1630     md = &(pf->model_details);
1631     expintern = &(pf->expinternal[0]);
1632
1633     for (s = 0; s < n_seq; s++) {
1634         type = tt[s];
1635         if (md->dangles == 2)
1636             qe *= (FLT_OR_DBL)pf->expmismatchI[type][S3[s][i]][S5[s][j]];
1637
1638         if (type > 2)
1639             qe *= (FLT_OR_DBL)pf->expTermAU;
1640     }
1641
1642     k = i + 1;
1643     if (S_cons[k] == 3) {
1644         if (k < j - VRNA_GQUAD_MIN_BOX_SIZE) {
1645             minl = j - MAXLOOP - 1;
1646             u = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1647             minl = MAX2(u, minl);
1648             u = j - 3;
1649             maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1650             maxl = MIN2(u, maxl);
1651             for (l = minl; l < maxl; l++) {
1652                 if (S_cons[l] != 3)
1653                     continue;
1654
1655                 if (G[index[k] - 1] == 0.)
1656                     continue;
1657

```



```

1658         qqg = 1.;
1659
1660         for (s = 0; s < n_seq; s++) {
1661             u1 = a2s[s][j - 1] - a2s[s][l];
1662             qqg *= expintern[u1];
1663         }
1664
1665         q += qe *
1666             G[index[k] - 1] *
1667             qqg *
1668             scale[j - 1 + 1];
1669     }
1670 }
1671 }
1672
1673 for (k = i + 2;
1674      k <= j - VRNA_GQUAD_MIN_BOX_SIZE;
1675      k++) {
1676     u = k - i - 1;
1677     if (u > MAXLOOP)
1678         break;
1679
1680     if (S_cons[k] != 3)
1681         continue;
1682
1683     minl = j - i + k - MAXLOOP - 2;
1684     r = k + VRNA_GQUAD_MIN_BOX_SIZE - 1;
1685     minl = MAX2(r, minl);
1686     maxl = k + VRNA_GQUAD_MAX_BOX_SIZE + 1;
1687     r = j - 1;
1688     maxl = MIN2(r, maxl);
1689     for (l = minl; l < maxl; l++) {
1690         if (S_cons[l] != 3)
1691             continue;
1692
1693         if (G[index[k] - 1] == 0.)
1694             continue;
1695
1696         qqg = 1.;
1697
1698         for (s = 0; s < n_seq; s++) {
1699             u1 = a2s[s][k - 1] - a2s[s][i];
1700             u2 = a2s[s][j - 1] - a2s[s][l];
1701             qqg *= expintern[u1 + u2];
1702         }
1703
1704         q += qe *
1705             G[index[k] - 1] *
1706             qqg *
1707             scale[u + j - 1 + 1];
1708     }
1709 }
1710
1711 l = j - 1;
1712 if (S_cons[l] == 3)
1713     for (k = i + 4; k <= j - VRNA_GQUAD_MIN_BOX_SIZE; k++) {
1714         u = k - i - 1;
1715         if (u > MAXLOOP)
1716             break;
1717
1718         if (S_cons[k] != 3)
1719             continue;
1720
1721         if (G[index[k] - 1] == 0.)
1722             continue;
1723
1724         qqg = 1.;
1725
1726         for (s = 0; s < n_seq; s++) {
1727             u1 = a2s[s][k - 1] - a2s[s][i];
1728             qqg *= expintern[u1];
1729         }
1730
1731         q += qe *
1732             G[index[k] - 1] *
1733             qqg *
1734             scale[u + 2];
1735     }
1736
1737 return q;
1738 }
1739
1740
1746 #endif

```

## 18.95 ViennaRNA/grammar.h File Reference

Implementations for the RNA folding grammar.

Include dependency graph for grammar.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_gr\\_aux\\_s](#)

### 18.95.1 Detailed Description

Implementations for the RNA folding grammar.

## 18.96 grammar.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_GRAMMAR_H
2 #define VIENNA_RNA_PACKAGE_GRAMMAR_H
3
16 #include <ViennaRNA/fold_compound.h>
17
18 typedef int (vrna_callback_gr_rule)(vrna_fold_compound_t *vc,
19                                     int i,
20                                     int j,
21                                     void *data);
22
23
24 typedef void (vrna_callback_gr_rule_aux)(vrna_fold_compound_t *vc,
25   int i,
26   int j,
27   void *data);
28
29
30 typedef FLT_OR_DBL (vrna_callback_gr_rule_exp)(vrna_fold_compound_t *vc,
31   int i,
32   int j,
33   void *data);
34
35
36 typedef void (vrna_callback_gr_rule_aux_exp)(vrna_fold_compound_t *vc,
37   int i,
38   int j,
39   void *data);
40
41
42 typedef void (vrna_callback_gr_cond)(vrna_fold_compound_t *fc,
43                                       unsigned char stage,
44                                       void *data);
45
46
47 typedef void (vrna_callback_gr_free_data)(void *data);
48
49
50 typedef struct vrna_gr_aux_s vrna_gr_aux_t;
51
52
53 struct vrna_gr_aux_s {
54     vrna_callback_gr_cond      *cb_proc;
55     vrna_callback_gr_rule      *cb_aux_f;
56     vrna_callback_gr_rule      *cb_aux_c;
57     vrna_callback_gr_rule      *cb_aux_m;
58     vrna_callback_gr_rule      *cb_aux_ml;
59     vrna_callback_gr_rule_aux  *cb_aux;
60
61     vrna_callback_gr_rule_exp   *cb_aux_exp_f;
62     vrna_callback_gr_rule_exp   *cb_aux_exp_c;
63     vrna_callback_gr_rule_exp   *cb_aux_exp_m;
64     vrna_callback_gr_rule_exp   *cb_aux_exp_ml;
65     vrna_callback_gr_rule_aux_exp *cb_aux_exp;
66
67     void *data;
68     vrna_callback_gr_free_data *free_data;
69 };
70
71
72
73 int
74 vrna_gr_set_aux_f(vrna_fold_compound_t *fc,
75                   vrna_callback_gr_rule *cb);
76

```

```

77
78 int
79 vrna_gr_set_aux_exp_f(vrna_fold_compound_t *fc,
80                       vrna_callback_gr_rule_exp *cb);
81
82
83 int
84 vrna_gr_set_aux_c(vrna_fold_compound_t *fc,
85                  vrna_callback_gr_rule *cb);
86
87
88 int
89 vrna_gr_set_aux_exp_c(vrna_fold_compound_t *fc,
90                      vrna_callback_gr_rule_exp *cb);
91
92
93 int
94 vrna_gr_set_aux_m(vrna_fold_compound_t *fc,
95                  vrna_callback_gr_rule *cb);
96
97
98 int
99 vrna_gr_set_aux_exp_m(vrna_fold_compound_t *fc,
100                     vrna_callback_gr_rule_exp *cb);
101
102
103 int
104 vrna_gr_set_aux_ml(vrna_fold_compound_t *fc,
105                   vrna_callback_gr_rule *cb);
106
107
108 int
109 vrna_gr_set_aux_exp_ml(vrna_fold_compound_t *fc,
110                       vrna_callback_gr_rule_exp *cb);
111
112
113 int
114 vrna_gr_set_aux(vrna_fold_compound_t *fc,
115                vrna_callback_gr_rule_aux *cb);
116
117
118 int
119 vrna_gr_set_aux_exp(vrna_fold_compound_t *fc,
120                    vrna_callback_gr_rule_aux_exp *cb);
121
122
123 int
124 vrna_gr_set_data(vrna_fold_compound_t *fc,
125                 void *data,
126                 vrna_callback_gr_free_data *free_data);
127
128
129 int
130 vrna_gr_set_cond(vrna_fold_compound_t *fc,
131                 vrna_callback_gr_cond *cb);
132
133
134 int
135 vrna_gr_reset(vrna_fold_compound_t *fc);
136
137
138 #endif

```

## 18.97 ViennaRNA/hairpin\_loops.h File Reference

Use [ViennaRNA/loops/hairpin.h](#) instead.

Include dependency graph for hairpin\_loops.h:

### 18.97.1 Detailed Description

Use [ViennaRNA/loops/hairpin.h](#) instead.

**Deprecated** Use [ViennaRNA/loops/hairpin.h](#) instead

## 18.98 hairpin\_loops.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_HAIRPIN_DEPRECATED_H
```

```

2 #define VIENNA_RNA_PACKAGE_LOOPS_HAIRPIN_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/loops.h>! Use <ViennaRNA/loops/loop.h>
    instead!"
13 # endif
14 #include <ViennaRNA/loops/loop.h>
15 #endif
16
17 #endif

```

## 18.99 ViennaRNA/heat\_capacity.h File Reference

Compute heat capacity for an RNA.

Include dependency graph for heat\_capacity.h:

### Data Structures

- struct [vrna\\_heat\\_capacity\\_s](#)  
A single result from heat capacity computations. [More...](#)

### Typedefs

- typedef void() [vrna\\_heat\\_capacity\\_callback](#)(float temp, float heat\_capacity, void \*data)  
The callback for heat capacity predictions.
- typedef struct [vrna\\_heat\\_capacity\\_s](#) [vrna\\_heat\\_capacity\\_t](#)  
A single result from heat capacity computations.

### Functions

#### Basic heat capacity function interface

- [vrna\\_heat\\_capacity\\_t](#) \* [vrna\\_heat\\_capacity](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, float T\_min, float T\_max, float T\_increment, unsigned int mpoints)  
Compute the specific heat for an RNA.
- int [vrna\\_heat\\_capacity\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, float T\_min, float T\_max, float T\_increment, unsigned int mpoints, [vrna\\_heat\\_capacity\\_callback](#) \*cb, void \*data)  
Compute the specific heat for an RNA (callback variant)

#### Simplified heat capacity computation

- [vrna\\_heat\\_capacity\\_t](#) \* [vrna\\_heat\\_capacity\\_simple](#) (const char \*sequence, float T\_min, float T\_max, float T\_increment, unsigned int mpoints)  
Compute the specific heat for an RNA (simplified variant)

### 18.99.1 Detailed Description

Compute heat capacity for an RNA.

This file includes the interface to all functions related to predicting the heat capacity for an RNA.

## 18.100 heat\_capacity.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_MELTING_H
2 #define VIENNA_RNA_PACKAGE_MELTING_H
3
4 #include <stdio.h>
5
6 #include <ViennaRNA/datastructures/basic.h>
7
38 typedef void (vrna_heat_capacity_callback) (float temp,
39   float heat_capacity,

```

```

40                                     void    *data);
41
42
43 typedef struct vrna_heat_capacity_s vrna_heat_capacity_t;
44
45
46 struct vrna_heat_capacity_s {
47     float temperature;
48     float heat_capacity;
49 };
50
51
52 vrna_heat_capacity_t *
53 vrna_heat_capacity(vrna_fold_compound_t *fc,
54                  float T_min,
55                  float T_max,
56                  float T_increment,
57                  unsigned int mpoints);
58
59
60
61
62 int
63 vrna_heat_capacity_cb(vrna_fold_compound_t *fc,
64                     float T_min,
65                     float T_max,
66                     float T_increment,
67                     unsigned int mpoints,
68                     vrna_heat_capacity_callback *cb,
69                     void *data);
70
71
72
73
74 /* End basic interface */
75 vrna_heat_capacity_t *
76 vrna_heat_capacity_simple(const char *sequence,
77                          float T_min,
78                          float T_max,
79                          float T_increment,
80                          unsigned int mpoints);
81
82 /* End basic interface */
83 /* End thermodynamics */
84 #endif

```

## 18.101 ViennaRNA/interior\_loops.h File Reference

Use [ViennaRNA/loops/internal.h](#) instead.

Include dependency graph for interior\_loops.h:

### 18.101.1 Detailed Description

Use [ViennaRNA/loops/internal.h](#) instead.

**Deprecated** Use [ViennaRNA/loops/internal.h](#) instead

## 18.102 interior\_loops.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_INTERNAL_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_INTERNAL_DEPRECATED_H
3
4 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
5 # ifdef VRNA_WARN_DEPRECATED
6 #warning "Including deprecated header file <ViennaRNA/interior_loops.h>! Use <ViennaRNA/loops/internal.h>
7         instead!"
8 # endif
9 #include <ViennaRNA/loops/internal.h>
10 #endif
11 #endif

```

## 18.103 ViennaRNA/inverse.h File Reference

Inverse folding routines.

## Functions

- float [inverse\\_fold](#) (char \*start, const char \*target)  
*Find sequences with predefined structure.*
- float [inverse\\_pf\\_fold](#) (char \*start, const char \*target)  
*Find sequence that maximizes probability of a predefined structure.*

## Variables

- char \* [symbolset](#)  
*This global variable points to the allowed bases, initially "AUGC". It can be used to design sequences from reduced alphabets.*
- float [final\\_cost](#)
- int [give\\_up](#)
- int [inv\\_verbose](#)

### 18.103.1 Detailed Description

Inverse folding routines.

## 18.104 [inverse.h](#)

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_INVERSE_H
2 #define VIENNA_RNA_PACKAGE_INVERSE_H
3
21 extern char *symbolset;
23 extern float final_cost;
25 extern int give_up;
27 extern int inv_verbose;
28
45 float inverse_fold( char *start,
46                     const char *target);
47
61 float inverse_pf_fold(char *start,
62                       const char *target);
63
67 #endif
```

## 18.105 [ViennaRNA/landscape/move.h](#) File Reference

Methods to operate with structural neighbors of RNA secondary structures.  
This graph shows which files directly or indirectly include this file:

## Data Structures

- struct [vrna\\_move\\_s](#)  
*An atomic representation of the transition / move from one structure to its neighbor. [More...](#)*

## Macros

- #define [VRNA\\_MOVESET\\_INSERTION](#) 4  
*Option flag indicating insertion move.*
- #define [VRNA\\_MOVESET\\_DELETION](#) 8  
*Option flag indicating deletion move.*
- #define [VRNA\\_MOVESET\\_SHIFT](#) 16  
*Option flag indicating shift move.*
- #define [VRNA\\_MOVESET\\_NO\\_LP](#) 32  
*Option flag indicating moves without lonely base pairs.*
- #define [VRNA\\_MOVESET\\_DEFAULT](#) ([VRNA\\_MOVESET\\_INSERTION](#) | [VRNA\\_MOVESET\\_DELETION](#))  
*Option flag indicating default move set, i.e. insertions/deletion of a base pair.*

## Typedefs

- typedef struct [vrna\\_move\\_s](#) [vrna\\_move\\_t](#)  
A single move that transforms a secondary structure into one of its neighbors.

## Functions

- [vrna\\_move\\_t](#) [vrna\\_move\\_init](#) (int pos\_5, int pos\_3)  
Create an atomic move.
- void [vrna\\_move\\_list\\_free](#) ([vrna\\_move\\_t](#) \*moves)
- void [vrna\\_move\\_apply](#) (short \*pt, const [vrna\\_move\\_t](#) \*m)  
Apply a particular move / transition to a secondary structure, i.e. transform a structure.
- int [vrna\\_move\\_is\\_removal](#) (const [vrna\\_move\\_t](#) \*m)  
Test whether a move is a base pair removal.
- int [vrna\\_move\\_is\\_insertion](#) (const [vrna\\_move\\_t](#) \*m)  
Test whether a move is a base pair insertion.
- int [vrna\\_move\\_is\\_shift](#) (const [vrna\\_move\\_t](#) \*m)  
Test whether a move is a base pair shift.
- int [vrna\\_move\\_compare](#) (const [vrna\\_move\\_t](#) \*a, const [vrna\\_move\\_t](#) \*b, const short \*pt)  
Compare two moves.

### 18.105.1 Detailed Description

Methods to operate with structural neighbors of RNA secondary structures.

## 18.106 move.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_MOVE_H
2 #define VIENNA_RNA_PACKAGE_MOVE_H
3
4
20 typedef struct vrna_move_s vrna_move_t;
21
26 #define VRNA_MOVESET_INSERTION 4
27
32 #define VRNA_MOVESET_DELETION 8
33
38 #define VRNA_MOVESET_SHIFT 16
43 #define VRNA_MOVESET_NO_LP 32
44
49 #define VRNA_MOVESET_DEFAULT (VRNA_MOVESET_INSERTION | VRNA_MOVESET_DELETION)
50
51
73 struct vrna_move_s {
74     int pos_5;
75     int pos_3;
76     vrna_move_t *next;
79 };
80
81
91 vrna_move_t
92 vrna_move_init(int pos_5,
93               int pos_3);
94
95
99 void
100 vrna_move_list_free(vrna_move_t *moves);
101
102
109 void
110 vrna_move_apply(short *pt,
111                 const vrna_move_t *m);
112
113
114 void
115 vrna_move_apply_db(char *structure,
116                   const short *pt,
117                   const vrna_move_t *m);
118

```

```

119
126 int
127 vrna_move_is_removal(const vrna_move_t *m);
128
129
136 int
137 vrna_move_is_insertion(const vrna_move_t *m);
138
139
146 int
147 vrna_move_is_shift(const vrna_move_t *m);
148
149
170 int
171 vrna_move_compare(const vrna_move_t *a,
172                  const vrna_move_t *b,
173                  const short *pt);
174
175
180 #endif

```

## 18.107 ViennaRNA/landscape/paths.h File Reference

API for computing (optimal) (re-)folding paths between secondary structures.

Include dependency graph for paths.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_path\\_s](#)  
An element of a refolding path list. [More...](#)

### Macros

- #define [VRNA\\_PATH\\_TYPE\\_DOT\\_BRACKET](#) 1U  
Flag to indicate producing a (re-)folding path as list of dot-bracket structures.
- #define [VRNA\\_PATH\\_TYPE\\_MOVES](#) 2U  
Flag to indicate producing a (re-)folding path as list of transition moves.

### Typedefs

- typedef struct [vrna\\_path\\_s](#) [vrna\\_path\\_t](#)  
Typename for the refolding path data structure [vrna\\_path\\_s](#).
- typedef struct vrna\_path\_options\_s \* [vrna\\_path\\_options\\_t](#)  
Options data structure for (re-)folding path implementations.
- typedef struct [vrna\\_path\\_s](#) [path\\_t](#)  
Old typename of [vrna\\_path\\_s](#).

### Functions

- void [vrna\\_path\\_free](#) ([vrna\\_path\\_t](#) \*path)  
Release (free) memory occupied by a (re-)folding path.
- void [vrna\\_path\\_options\\_free](#) ([vrna\\_path\\_options\\_t](#) options)  
Release (free) memory occupied by an options data structure for (re-)folding path implementations.
- [vrna\\_path\\_options\\_t](#) [vrna\\_path\\_options\\_findpath](#) (int width, unsigned int type)  
Create options data structure for findpath direct (re-)folding path heuristic.
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_direct](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, [vrna\\_path\\_options\\_t](#) options)  
Determine an optimal direct (re-)folding path between two secondary structures.
- [vrna\\_path\\_t](#) \* [vrna\\_path\\_direct\\_ub](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*s1, const char \*s2, int maxE, [vrna\\_path\\_options\\_t](#) options)  
Determine an optimal direct (re-)folding path between two secondary structures.



### 18.107.1 Detailed Description

API for computing (optimal) (re-)folding paths between secondary structures.

## 18.108 paths.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PATHS_H
2 #define VIENNA_RNA_PACKAGE_PATHS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 typedef struct vrna_path_s vrna_path_t;
17
18 typedef struct vrna_path_options_s *vrna_path_options_t;
19
20 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
21 DEPRECATED(typedef struct vrna_path_s path_t,
22           "Use vrna_path_t instead!");
23 #endif
24
25 #include <ViennaRNA/fold_compound.h>
26 #include <ViennaRNA/landscape/move.h>
27
28 #define VRNA_PATH_TYPE_DOT_BRACKET 1U
29
30 #define VRNA_PATH_TYPE_MOVES 2U
31
32 struct vrna_path_s {
33     unsigned int type;
34     double en;
35     char *s;
36     vrna_move_t move;
37 };
38
39 void
40 vrna_path_free(vrna_path_t *path);
41
42 void
43 vrna_path_options_free(vrna_path_options_t options);
44
45 vrna_path_options_t
46 vrna_path_options_findpath(int width,
47                            unsigned int type);
48
49 vrna_path_t *
50 vrna_path_direct(vrna_fold_compound_t *fc,
51                  const char *s1,
52                  const char *s2,
53                  vrna_path_options_t options);
54
55 vrna_path_t *
56 vrna_path_direct_ub(vrna_fold_compound_t *fc,
57                     const char *s1,
58                     const char *s2,
59                     int maxE,
60                     vrna_path_options_t options);
61
62 #endif

```

## 18.109 ViennaRNA/Lfold.h File Reference

Functions for locally optimal MFE structure prediction.

Include dependency graph for Lfold.h:

### Functions

- float [Lfold](#) (const char \*string, const char \*structure, int maxdist)  
*The local analog to [fold\(\)](#).*
- float [Lfoldz](#) (const char \*string, const char \*structure, int maxdist, int zsc, double min\_z)

### 18.109.1 Detailed Description

Functions for locally optimal MFE structure prediction.

## 18.110 Lfold.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LFOLD_H
2 #define VIENNA_RNA_PACKAGE_LFOLD_H
3
4 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
5
6 #ifdef VRNA_WARN_DEPRECATED
7 # if defined(__clang__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # elif defined(__GNUC__)
10 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
11 # else
12 #  define DEPRECATED(func, msg) func
13 # endif
14 #else
15 # define DEPRECATED(func, msg) func
16 #endif
17
18 #include <ViennaRNA/mfe_window.h>
19
20 DEPRECATED(float Lfold(const char *string,
21                       const char *structure,
22                       int maxdist),
23           "Use vrna_Lfold() or vrna_Lfold_cb() instead");
24
25 #ifdef VRNA_WITH_SVM
26 DEPRECATED(float Lfoldz(const char *string,
27                        const char *structure,
28                        int maxdist,
29                        int zsc,
30                        double min_z),
31           "Use vrna_Lfoldz() or vrna_Lfoldz_cb() instead");
32 #endif
33
34 DEPRECATED(float aliLfold(const char **AS,
35                          const char *structure,
36                          int maxdist),
37           "Use vrna_aliLfold() or vrna_aliLfold_cb() instead");
38
39 DEPRECATED(float aliLfold_cb(const char **AS,
40                             int maxdist,
41                             vrna_mfe_window_callback *cb,
42                             void *data),
43           "Use vrna_aliLfold() or vrna_aliLfold_cb() instead");
44
45 #endif
46 #endif

```

## 18.111 ViennaRNA/loop\_energies.h File Reference

Use [ViennaRNA/loops/all.h](#) instead.

Include dependency graph for loop\_energies.h:

### 18.111.1 Detailed Description

Use [ViennaRNA/loops/all.h](#) instead.

**Deprecated** Use [ViennaRNA/loops/all.h](#) instead

## 18.112 loop\_energies.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_ALL_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_ALL_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/loop_energies.h>! Use <ViennaRNA/loops/all.h>
    instead!"
13 # endif
14 #include <ViennaRNA/loops/all.h>
15 #endif
16
17 #endif
```

## 18.113 ViennaRNA/loops/all.h File Reference

Energy evaluation for MFE and partition function calculations.

Include dependency graph for all.h: This graph shows which files directly or indirectly include this file:

### 18.113.1 Detailed Description

Energy evaluation for MFE and partition function calculations.

,  
This file contains functions for the calculation of the free energy  $\Delta G$  of a hairpin- [ [E\\_Hairpin\(\)](#) ] or interior-loop [ [E\\_IntLoop\(\)](#) ].

The unit of the free energy returned is  $10^{-2} * \text{kcal/mol}$

In case of computing the partition function, this file also supplies functions which return the Boltzmann weights  $e^{-\Delta G/kT}$  for a hairpin- [ [exp\\_E\\_Hairpin\(\)](#) ] or interior-loop [ [exp\\_E\\_IntLoop\(\)](#) ].

## 18.114 all.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_ALL_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_ALL_H
3
27 /* below we include the loop type specific energy evaluation functions */
28
29 #include <ViennaRNA/loops/external.h>
30
31 #include <ViennaRNA/loops/hairpin.h>
32
33 #include <ViennaRNA/loops/internal.h>
34
35 #include <ViennaRNA/loops/multibranch.h>
36
41 #endif
```

## 18.115 ViennaRNA/loops/external.h File Reference

Energy evaluation of exterior loops for MFE and partition function calculations.

Include dependency graph for external.h: This graph shows which files directly or indirectly include this file:

### Functions

- int [E\\_Stem](#) (int type, int si1, int sj1, int extLoop, [vrna\\_param\\_t](#) \*P)  
*Compute the energy contribution of a stem branching off a loop-region.*

- [FLT\\_OR\\_DBL exp\\_E\\_ExtLoop](#) (int type, int si1, int sj1, [vrna\\_exp\\_param\\_t](#) \*P)
- [FLT\\_OR\\_DBL exp\\_E\\_Stem](#) (int type, int si1, int sj1, int extLoop, [vrna\\_exp\\_param\\_t](#) \*P)

### Basic free energy interface

- int [vrna\\_E\\_ext\\_stem](#) (unsigned int type, int n5d, int n3d, [vrna\\_param\\_t](#) \*p)  
*Evaluate a stem branching off the exterior loop.*
- int [vrna\\_eval\\_ext\\_stem](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of a base pair in the exterior loop.*
- int [vrna\\_E\\_ext\\_loop\\_5](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- int [vrna\\_E\\_ext\\_loop\\_3](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i)

### Boltzmann weight (partition function) interface

- typedef struct [vrna\\_mx\\_pf\\_aux\\_el\\_s](#) \* [vrna\\_mx\\_pf\\_aux\\_el\\_t](#)  
*Auxiliary helper arrays for fast exterior loop computations.*
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ext\\_stem](#) (unsigned int type, int n5d, int n3d, [vrna\\_exp\\_param\\_t](#) \*p)  
*Evaluate a stem branching off the exterior loop (Boltzmann factor version)*
- [vrna\\_mx\\_pf\\_aux\\_el\\_t vrna\\_exp\\_E\\_ext\\_fast\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_rotate](#) ([vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_free](#) ([vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ext\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ext\\_fast\\_update](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int j, [vrna\\_mx\\_pf\\_aux\\_el\\_t](#) aux\_mx)

#### 18.115.1 Detailed Description

Energy evaluation of exterior loops for MFE and partition function calculations.

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### 18.116 external.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_EXTERNAL_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_EXTERNAL_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/fold_compound.h>
6 #include <ViennaRNA/params/basic.h>
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(DEPRECATED)
10 #  undef DEPRECATED
11 # endif
12 # if defined(__clang__)
13 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
14 # elif defined(__GNUC__)
15 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
16 # else
17 #  define DEPRECATED(func, msg) func
18 # endif
19 #else
20 # define DEPRECATED(func, msg) func
21 #endif
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59 int
60 vrna_E_ext_stem(unsigned int  type,
61                int          n5d,
62                int          n3d,
63                vrna_param_t *p);
64
65
66
67
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81
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83
84
85 int
86 vrna_eval_ext_stem(vrna_fold_compound_t *fc,
87                   int                    i,
88                   int                    j);
89
90
91
92
93 int
94 vrna_E_ext_loop_5(vrna_fold_compound_t *fc);
95
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```

94
95 int
96 vrna_E_ext_loop_3(vrna_fold_compound_t *fc,
97                  int i);
98
99
100 /* End basic interface */
101 typedef struct vrna_mx_pf_aux_el_s *vrna_mx_pf_aux_el_t;
102
103 FLT_OR_DBL
104 vrna_exp_E_ext_stem(unsigned int type,
105                   int n5d,
106                   int n3d,
107                   vrna_exp_param_t *p);
108
109
110 vrna_mx_pf_aux_el_t
111 vrna_exp_E_ext_fast_init(vrna_fold_compound_t *fc);
112
113 void
114 vrna_exp_E_ext_fast_rotate(vrna_mx_pf_aux_el_t aux_mx);
115
116 void
117 vrna_exp_E_ext_fast_free(vrna_mx_pf_aux_el_t aux_mx);
118
119 FLT_OR_DBL
120 vrna_exp_E_ext_fast(vrna_fold_compound_t *fc,
121                   int i,
122                   int j,
123                   vrna_mx_pf_aux_el_t aux_mx);
124
125 void
126 vrna_exp_E_ext_fast_update(vrna_fold_compound_t *fc,
127                          int j,
128                          vrna_mx_pf_aux_el_t aux_mx);
129
130 /* End partition function interface */
131 int
132 vrna_BT_ext_loop_f5(vrna_fold_compound_t *fc,
133                   int *k,
134                   int *i,
135                   int *j,
136                   vrna_bp_stack_t *bp_stack,
137                   int *stack_count);
138
139 int
140 vrna_BT_ext_loop_f3(vrna_fold_compound_t *fc,
141                   int *k,
142                   int maxdist,
143                   int *i,
144                   int *j,
145                   vrna_bp_stack_t *bp_stack,
146                   int *stack_count);
147
148 int
149 vrna_BT_ext_loop_f3_pp(vrna_fold_compound_t *fc,
150                      int *i,
151                      int maxdist);
152
153 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
154
155 DEPRECATED(int E_Stem(int type,
156                    int sil,
157                    int sjl,
158                    int extLoop,
159                    vrna_param_t *P),
160           "This function is obsolete. Use vrna_E_ext_stem() or E_MLstem() instead");
161
162 DEPRECATED(int E_ExtLoop(int type,
163                       int sil,
164                       int sjl,
165                       vrna_param_t *P),
166           "Use vrna_E_ext_stem() instead");
167
168 DEPRECATED(FLT_OR_DBL exp_E_ExtLoop(int type,
169                                     int sil,

```

```

292                                     int          sj1,
293                                     vrna_exp_param_t *P),
294     "Use vrna_exp_E_ext_stem() instead");
295
296
305 DEPRECATED (FLT_OR_DBL exp_E_Stem(int          type,
306                                     int          si1,
307                                     int          sj1,
308                                     int          extLoop,
309                                     vrna_exp_param_t *P),
310     "This function is obsolete");
311
312
313 #endif
314
320 #endif

```

## 18.117 ViennaRNA/loops/hairpin.h File Reference

Energy evaluation of hairpin loops for MFE and partition function calculations.

Include dependency graph for hairpin.h: This graph shows which files directly or indirectly include this file:

### Functions

- int [vrna\\_BT\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int en, [vrna\\_bp\\_stack\\_t](#) \*bp\_stack, int \*stack\_↔ count)  
*Backtrack a hairpin loop closed by (i, j).*

#### Basic free energy interface

- int [vrna\\_E\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of a hairpin loop and consider hard constraints if they apply.*
- int [vrna\\_E\\_ext\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate the free energy of an exterior hairpin loop and consider possible hard constraints.*
- int [vrna\\_eval\\_ext\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate free energy of an exterior hairpin loop.*
- int [vrna\\_eval\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*Evaluate free energy of a hairpin loop.*
- PRIVATE int [E\\_Hairpin](#) (int size, int type, int si1, int sj1, const char \*string, [vrna\\_param\\_t](#) \*P)  
*Compute the Energy of a hairpin-loop.*

#### Boltzmann weight (partition function) interface

- PRIVATE [FLT\\_OR\\_DBL exp\\_E\\_Hairpin](#) (int u, int type, short si1, short sj1, const char \*string, [vrna\\_exp\\_param\\_t](#) \*P)  
*Compute Boltzmann weight  $e^{-\Delta G/kT}$  of a hairpin loop.*
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_hp\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)  
*High-Level function for hairpin loop energy evaluation (partition function variant)*

### 18.117.1 Detailed Description

Energy evaluation of hairpin loops for MFE and partition function calculations.

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## 18.118 hairpin.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_HAIRPIN_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_HAIRPIN_H
3
4 #include <math.h>
5 #include <string.h>
6 #include <ViennaRNA/utils/basic.h>
7 #include <ViennaRNA/datastructures/basic.h>
8 #include <ViennaRNA/fold_compound.h>

```

```

9 #include <ViennaRNA/params/basic.h>
10
11 #ifdef VRNA_WARN_DEPRECATED
12 # if defined(DEPRECATED)
13 #   undef DEPRECATED
14 # endif
15 # if defined(__clang__)
16 #   define DEPRECATED(func, msg) func __attribute__ ((deprecated("", msg)))
17 # elif defined(__GNUC__)
18 #   define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
19 # else
20 #   define DEPRECATED(func, msg) func
21 # endif
22 #else
23 # define DEPRECATED(func, msg) func
24 #endif
25
26 #ifdef __GNUC__
27 # define INLINE inline
28 #else
29 # define INLINE
30 #endif
31
32 int
33 vrna_E_hp_loop(vrna_fold_compound_t *fc,
34               int i,
35               int j);
36
37 int
38 vrna_E_ext_hp_loop(vrna_fold_compound_t *fc,
39                   int i,
40                   int j);
41
42 int
43 vrna_eval_ext_hp_loop(vrna_fold_compound_t *fc,
44                      int i,
45                      int j);
46
47 int
48 vrna_eval_hp_loop(vrna_fold_compound_t *fc,
49                  int i,
50                  int j);
51
52 PRIVATE INLINE int
53 E_Hairpin(int size,
54           int type,
55           int sil,
56           int sjl,
57           const char *string,
58           vrna_param_t *P)
59 {
60     int energy;
61
62     if (size <= 30)
63         energy = P->hairpin[size];
64     else
65         energy = P->hairpin[30] + (int) (P->lxc * log((size) / 30.));
66
67     if (size < 3)
68         return energy; /* should only be the case when folding alignments */
69
70     if ((string) && (P->model_details.special_hp)) {
71         if (size == 4) {
72             /* check for tetraloop bonus */
73             char tl[7] = {
74                 0
75             }, *ts;
76             memcpy(tl, string, sizeof(char) * 6);
77             tl[6] = '\0';
78             if ((ts = strstr(P->Tetraloops, tl)))
79                 return P->Tetraloop_E[(ts - P->Tetraloops) / 7];
80         } else if (size == 6) {
81             char tl[9] = {
82                 0
83             }, *ts;
84             memcpy(tl, string, sizeof(char) * 8);
85             tl[8] = '\0';
86             if ((ts = strstr(P->Hexaloops, tl)))
87                 return P->Hexaloop_E[(ts - P->Hexaloops) / 9];
88         } else if (size == 3) {
89             char tl[6] = {
90                 0
91             }, *ts;
92         }
93     }
94 }

```

```

188     memcpy(tl, string, sizeof(char) * 5);
189     tl[5] = '\0';
190     if ((ts = strstr(P->Triloops, tl)))
191         return P->Triloop_E[(ts - P->Triloops) / 6];
192
193     return energy + (type > 2 ? P->TerminalAU : 0);
194 }
195 }
196
197 energy += P->mismatchH[type][sil][sjl];
198
199 return energy;
200 }
201
202
203 /* End basic interface */
204 PRIVATE INLINE FLT_OR_DBL
205 exp_E_Hairpin(int u,
206               int type,
207               short sil,
208               short sjl,
209               const char *string,
210               vrna_exp_param_t *P)
211 {
212     double q, kT;
213
214     kT = P->kT; /* kT in cal/mol */
215
216     if (u <= 30)
217         q = P->exphairpin[u];
218     else
219         q = P->exphairpin[30] * exp(-(P->lxc * log(u / 30.)) * 10. / kT);
220
221     if (u < 3)
222         return (FLT_OR_DBL)q; /* should only be the case when folding alignments */
223
224     if ((string) && (P->model_details.special_hp)) {
225         if (u == 4) {
226             char tl[7] = {
227                 0,
228                 }, *ts;
229             memcpy(tl, string, sizeof(char) * 6);
230             tl[6] = '\0';
231             if ((ts = strstr(P->Tetraloops, tl))) {
232                 if (type != 7)
233                     return (FLT_OR_DBL) (P->exptetra[(ts - P->Tetraloops) / 7]);
234                 else
235                     q *= P->exptetra[(ts - P->Tetraloops) / 7];
236             }
237         } else if (u == 6) {
238             char tl[9] = {
239                 0,
240                 }, *ts;
241             memcpy(tl, string, sizeof(char) * 8);
242             tl[8] = '\0';
243             if ((ts = strstr(P->Hexaloops, tl)))
244                 return (FLT_OR_DBL) (P->expheh[(ts - P->Hexaloops) / 9]);
245         } else if (u == 3) {
246             char tl[6] = {
247                 0,
248                 }, *ts;
249             memcpy(tl, string, sizeof(char) * 5);
250             tl[5] = '\0';
251             if ((ts = strstr(P->Triloops, tl)))
252                 return (FLT_OR_DBL) (P->exptri[(ts - P->Triloops) / 6]);
253
254             if (type > 2)
255                 return (FLT_OR_DBL) (q * P->expTermAU);
256             else
257                 return (FLT_OR_DBL)q;
258         }
259     }
260
261     q *= P->expmismatchH[type][sil][sjl];
262
263     return (FLT_OR_DBL)q;
264 }
265
266
267 FLT_OR_DBL
268 vrna_exp_E_hp_loop(vrna_fold_compound_t *fc,
269                   int i,
270                   int j);
271
272
273 /* End partition function interface */
274 int

```



```

331 vrna_BT_hp_loop(vrna_fold_compound_t *fc,
332                int i,
333                int j,
334                int en,
335                vrna_bp_stack_t *bp_stack,
336                int *stack_count);
337
338
343 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
344
354 #endif
355
356 #endif

```

## 18.119 ViennaRNA/loops/internal.h File Reference

Energy evaluation of interior loops for MFE and partition function calculations.

Include dependency graph for internal.h: This graph shows which files directly or indirectly include this file:

### Functions

- `int vrna_BT_stack(vrna_fold_compound_t *fc, int *i, int *j, int *en, vrna_bp_stack_t *bp_stack, int *stack_count)`  
Backtrack a stacked pair closed by  $(i, j)$ .
- `int vrna_BT_int_loop(vrna_fold_compound_t *fc, int *i, int *j, int en, vrna_bp_stack_t *bp_stack, int *stack_count)`  
Backtrack an interior loop closed by  $(i, j)$ .
- `PRIVATE int E_IntLoop(int n1, int n2, int type, int type_2, int si1, int sj1, int sp1, int sq1, vrna_param_t *P)`
- `PRIVATE FLT_OR_DBL exp_E_IntLoop(int u1, int u2, int type, int type2, short si1, short sj1, short sp1, short sq1, vrna_exp_param_t *P)`

#### Basic free energy interface

- `int vrna_E_int_loop(vrna_fold_compound_t *fc, int i, int j)`
- `int vrna_eval_int_loop(vrna_fold_compound_t *fc, int i, int j, int k, int l)`  
Evaluate the free energy contribution of an interior loop with delimiting base pairs  $(i, j)$  and  $(k, l)$ .
- `int vrna_E_ext_int_loop(vrna_fold_compound_t *fc, int i, int j, int *ip, int *iq)`
- `int vrna_E_stack(vrna_fold_compound_t *fc, int i, int j)`

#### Boltzmann weight (partition function) interface

- `FLT_OR_DBL vrna_exp_E_int_loop(vrna_fold_compound_t *fc, int i, int j)`
- `FLT_OR_DBL vrna_exp_E_interior_loop(vrna_fold_compound_t *fc, int i, int j, int k, int l)`

### 18.119.1 Detailed Description

Energy evaluation of interior loops for MFE and partition function calculations.

, ,

## 18.120 internal.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_INTERNAL_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_INTERNAL_H
3
4 #include <math.h>
5
6 #include <ViennaRNA/utils/basic.h>
7 #include <ViennaRNA/params/default.h>
8 #include <ViennaRNA/datastructures/basic.h>
9 #include <ViennaRNA/fold_compound.h>
10 #include <ViennaRNA/params/basic.h>
11 #include <ViennaRNA/constraints/hard.h>
12 #include <ViennaRNA/constraints/soft.h>
13
14 #ifdef VRNA_WARN_DEPRECATED

```

```

15 # if defined(DEPRECATED)
16 #     undef DEPRECATED
17 # endif
18 # if defined(__clang__)
19 #     define DEPRECATED(func, msg) func __attribute__ ((deprecated("", msg)))
20 # elif defined(__GNUC__)
21 #     define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
22 # else
23 #     define DEPRECATED(func, msg) func
24 # endif
25 #else
26 # define DEPRECATED(func, msg) func
27 #endif
28
29 #ifdef __GNUC__
30 # define INLINE inline
31 #else
32 # define INLINE
33 #endif
34
35 int
36 vrna_E_int_loop(vrna_fold_compound_t *fc,
37                 int i,
38                 int j);
39
40 int
41 vrna_eval_int_loop(vrna_fold_compound_t *fc,
42                    int i,
43                    int j,
44                    int k,
45                    int l);
46
47 int
48 vrna_E_ext_int_loop(vrna_fold_compound_t *fc,
49                     int i,
50                     int j,
51                     int *ip,
52                     int *iq);
53
54 int
55 vrna_E_stack(vrna_fold_compound_t *fc,
56               int i,
57               int j);
58
59 /* End basic interface */
60 /* j < i indicates circular folding, i.e. collect contributions for exterior int loops */
61 FLT_OR_DBL
62 vrna_exp_E_int_loop(vrna_fold_compound_t *fc,
63                     int i,
64                     int j);
65
66 FLT_OR_DBL
67 vrna_exp_E_interior_loop(vrna_fold_compound_t *fc,
68                           int i,
69                           int j,
70                           int k,
71                           int l);
72
73 /* End partition function interface */
74 int
75 vrna_BT_stack(vrna_fold_compound_t *fc,
76               int *i,
77               int *j,
78               int *en,
79               vrna_bp_stack_t *bp_stack,
80               int *stack_count);
81
82 int
83 vrna_BT_int_loop(vrna_fold_compound_t *fc,
84                  int *i,
85                  int *j,
86                  int *en,
87                  vrna_bp_stack_t *bp_stack,
88                  int *stack_count);
89
90 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
91 #ifdef ON_SAME_STRAND
92 #undef ON_SAME_STRAND
93 #endif
94 #endif

```

```

167
168 #define ON_SAME_STRAND(I, J, C)  (((I) >= (C)) || ((J) < (C)))
169
214 PRIVATE INLINE int E_IntLoop(int          n1,
215                               int          n2,
216                               int          type,
217                               int          type_2,
218                               int          si1,
219                               int          sj1,
220                               int          sp1,
221                               int          sq1,
222                               vrna_param_t *P);
223
224
244 PRIVATE INLINE FLT_OR_DBL exp_E_IntLoop(int          u1,
245   int          u2,
246   int          type,
247   int          type2,
248   short         si1,
249   short         sj1,
250   short         sp1,
251   short         sq1,
252   vrna_exp_param_t *P);
253
254
255 PRIVATE INLINE int E_IntLoop_Co(int          type,
256                                 int          type_2,
257                                 int          i,
258                                 int          j,
259                                 int          p,
260                                 int          q,
261                                 int          cutpoint,
262                                 short         si1,
263                                 short         sj1,
264                                 short         sp1,
265                                 short         sq1,
266                                 int          dangles,
267                                 vrna_param_t *P);
268
269
270 /*
271  * ugly but fast interior loop evaluation
272  *
273  * Avoid including this function in your own code. It only serves
274  * as a fast inline block internally re-used throughout the RNAlib. It
275  * evaluates the free energy of interior loops in single sequences or sequence
276  * hybrids. Soft constraints are also applied if available.
277  *
278  * NOTE: do not include into doxygen reference manual!
279  */
280 PRIVATE INLINE int
281 ubf_eval_int_loop(int          i,
282                   int          j,
283                   int          p,
284                   int          q,
285                   int          il,
286                   int          jl,
287                   int          pl,
288                   int          ql,
289                   short         si,
290                   short         sj,
291                   short         sp,
292                   short         sq,
293                   unsigned char type,
294                   unsigned char type_2,
295                   int          *rtype,
296                   int          ij,
297                   int          cp,
298                   vrna_param_t *P,
299                   vrna_sc_t     *sc)
300 {
301     int energy, u1, u2;
302
303     u1 = p1 - i;
304     u2 = j1 - q;
305
306     if ((cp < 0) || (ON_SAME_STRAND(i, p, cp) && ON_SAME_STRAND(q, j, cp))) {
307         /* regular interior loop */
308         energy = E_IntLoop(u1, u2, type, type_2, si, sj, sp, sq, P);
309     } else {
310         /* interior loop like cofold structure */
311         short Si, Sj;
312         Si = ON_SAME_STRAND(i, il, cp) ? si : -1;
313         Sj = ON_SAME_STRAND(jl, j, cp) ? sj : -1;
314         energy = E_IntLoop_Co(rtype[type], rtype[type_2],
315                               i, j, p, q,
316                               cp,

```

```

317             Si, Sj,
318             sp, sq,
319             P->model_details.dangles,
320             P);
321     }
322
323     /* add soft constraints */
324     if (sc) {
325         if (sc->energy_up)
326             energy += sc->energy_up[i1][u1]
327                     + sc->energy_up[q1][u2];
328
329         if (sc->energy_bp)
330             energy += sc->energy_bp[ij];
331
332         if (sc->energy_stack)
333             if (u1 + u2 == 0) {
334                 int a = sc->energy_stack[i]
335                         + sc->energy_stack[p]
336                         + sc->energy_stack[q]
337                         + sc->energy_stack[j];
338                 energy += a;
339             }
340
341         if (sc->f)
342             energy += sc->f(i, j, p, q, VRNA_DECOMP_PAIR_IL, sc->data);
343     }
344
345     return energy;
346 }
347
348 PRIVATE INLINE int
349 ubf_eval_int_loop2(int i,
350                    int j,
351                    int p,
352                    int q,
353                    int i1,
354                    int j1,
355                    int p1,
356                    int q1,
357                    short si,
358                    short sj,
359                    short sp,
360                    short sq,
361                    unsigned char type,
362                    unsigned char type_2,
363                    int rtype,
364                    int ij,
365                    unsigned int *sn,
366                    unsigned int *ss,
367                    vrna_param_t *P,
368                    vrna_sc_t *sc)
369 {
370     int energy, u1, u2;
371
372     u1 = p1 - i;
373     u2 = j1 - q;
374
375     if ((sn[i] == sn[p]) && (sn[q] == sn[j])) {
376         /* regular interior loop */
377         energy = E_IntLoop(u1, u2, type, type_2, si, sj, sp, sq, P);
378     } else {
379         /* interior loop like cofold structure */
380         short Si, Sj;
381         Si = (sn[i1] == sn[i]) ? si : -1;
382         Sj = (sn[j] == sn[j1]) ? sj : -1;
383         energy = E_IntLoop_Co(rtype[type], rtype[type_2],
384                               i, j, p, q,
385                               ss[l],
386                               Si, Sj,
387                               sp, sq,
388                               P->model_details.dangles,
389                               P);
390     }
391 }
392
393     /* add soft constraints */
394     if (sc) {
395         if (sc->energy_up)
396             energy += sc->energy_up[i1][u1]
397                     + sc->energy_up[q1][u2];
398
399         if (sc->energy_bp)
400             energy += sc->energy_bp[ij];
401
402         if (sc->energy_stack)
403             if (u1 + u2 == 0) {

```

```

404         int a = sc->energy_stack[i]
405             + sc->energy_stack[p]
406             + sc->energy_stack[q]
407             + sc->energy_stack[j];
408         energy += a;
409     }
410
411     if (sc->f)
412         energy += sc->f(i, j, p, q, VRNA_DECOMP_PAIR_IL, sc->data);
413 }
414
415 return energy;
416 }
417
418
419 /*
420  * ugly but fast exterior interior loop evaluation
421  *
422  * Avoid including this function in your own code. It only serves
423  * as a fast inline block internally re-used throughout the RNAlib. It
424  * evaluates the free energy of interior loops in single sequences or sequence
425  * hybrids. Soft constraints are also applied if available.
426  *
427  * NOTE: do not include into doxygen reference manual!
428  */
429 PRIVATE INLINE int
430 ubf_eval_ext_int_loop(int i,
431                       int j,
432                       int p,
433                       int q,
434                       int il,
435                       int jl,
436                       int pl,
437                       int ql,
438                       short si,
439                       short sj,
440                       short sp,
441                       short sq,
442                       unsigned char type,
443                       unsigned char type_2,
444                       int length,
445                       vrna_param_t *P,
446                       vrna_sc_t *sc)
447 {
448     int energy, u1, u2, u3;
449
450     u1 = il;
451     u2 = pl - j;
452     u3 = length - q;
453
454     energy = E_IntLoop(u2, u1 + u3, type, type_2, si, sj, sp, sq, P);
455
456     /* add soft constraints */
457     if (sc) {
458         if (sc->energy_up) {
459             energy += sc->energy_up[jl][u2]
460                 + ((u3 > 0) ? sc->energy_up[ql][u3] : 0)
461                 + ((u1 > 0) ? sc->energy_up[l][u1] : 0);
462         }
463
464         if (sc->energy_stack)
465             if (u1 + u2 + u3 == 0)
466                 energy += sc->energy_stack[i]
467                     + sc->energy_stack[p]
468                     + sc->energy_stack[q]
469                     + sc->energy_stack[j];
470
471         if (sc->f)
472             energy += sc->f(i, j, p, q, VRNA_DECOMP_PAIR_IL, sc->data);
473     }
474
475     return energy;
476 }
477
478
479 PRIVATE INLINE int
480 E_IntLoop(int n1,
481           int n2,
482           int type,
483           int type_2,
484           int sil,
485           int sjl,
486           int spl,
487           int sql,
488           vrna_param_t *P)
489 {
490     /* compute energy of degree 2 loop (stack bulge or interior) */

```

```

491 int nl, ns, u, energy;
492
493 if (nl > n2) {
494     nl = n1;
495     ns = n2;
496 } else {
497     nl = n2;
498     ns = n1;
499 }
500
501 if (nl == 0)
502     return P->stack[type][type_2]; /* stack */
503
504 if (ns == 0) {
505     /* bulge */
506     energy = (nl <= MAXLOOP) ? P->bulge[nl] :
507         (P->bulge[30] + (int)(P->lxc * log(nl / 30.)));
508     if (nl == 1) {
509         energy += P->stack[type][type_2];
510     } else {
511         if (type > 2)
512             energy += P->TerminalAU;
513
514         if (type_2 > 2)
515             energy += P->TerminalAU;
516     }
517
518     return energy;
519 } else {
520     /* interior loop */
521     if (ns == 1) {
522         if (nl == 1) /* 1x1 loop */
523             return P->int11[type][type_2][sil][sjl];
524
525         if (nl == 2) {
526             /* 2x1 loop */
527             if (nl == 1)
528                 energy = P->int21[type][type_2][sil][sq1][sjl];
529             else
530                 energy = P->int21[type_2][type][sq1][sil][spl];
531
532             return energy;
533         } else {
534             /* 1xn loop */
535             energy =
536                 (nl + 1 <=
537                  MAXLOOP) ? (P->internal_loop[nl + 1]) : (P->internal_loop[30] +
538                     (int)(P->lxc * log((nl + 1) / 30.)));
539             energy += MIN2(MAX_NINIO, (nl - ns) * P->ninio[2]);
540             energy += P->mismatchlnI[type][sil][sjl] + P->mismatchlnI[type_2][sq1][spl];
541             return energy;
542         }
543     } else if (ns == 2) {
544         if (nl == 2) {
545             /* 2x2 loop */
546             return P->int22[type][type_2][sil][spl][sq1][sjl];
547         } else if (nl == 3) {
548             /* 2x3 loop */
549             energy = P->internal_loop[5] + P->ninio[2];
550             energy += P->mismatch23I[type][sil][sjl] + P->mismatch23I[type_2][sq1][spl];
551             return energy;
552         }
553     }
554
555     {
556         /* generic interior loop (no else here!) */
557         u = nl + ns;
558         energy =
559             (u <=
560              MAXLOOP) ? (P->internal_loop[u]) : (P->internal_loop[30] + (int)(P->lxc * log((u) / 30.)));
561
562         energy += MIN2(MAX_NINIO, (nl - ns) * P->ninio[2]);
563
564         energy += P->mismatchI[type][sil][sjl] + P->mismatchI[type_2][sq1][spl];
565     }
566 }
567
568 return energy;
569 }
570
571
572 PRIVATE INLINE FLT_OR_DBL
573 exp_E_IntLoop(int u1,
574               int u2,
575               int type,
576               int type2,
577               short sil,

```

```

578         short          sj1,
579         short          spl,
580         short          sql,
581         vrna_exp_param_t *P)
582 {
583     int    ul, us, no_close = 0;
584     double z          = 0.;
585     int    noGUclosure = P->model_details.noGUclosure;
586
587     if ((noGUclosure) && ((type2 == 3) || (type2 == 4) || (type == 3) || (type == 4)))
588         no_close = 1;
589
590     if (ul > u2) {
591         ul = u1;
592         us = u2;
593     } else {
594         ul = u2;
595         us = u1;
596     }
597
598     if (ul == 0) {
599         /* stack */
600         z = P->expstack[type][type2];
601     } else if (!no_close) {
602         if (us == 0) {
603             /* bulge */
604             z = P->expbulge[ul];
605             if (ul == 1) {
606                 z *= P->expstack[type][type2];
607             } else {
608                 if (type > 2)
609                     z *= P->expTermAU;
610
611                 if (type2 > 2)
612                     z *= P->expTermAU;
613             }
614
615             return (FLT_OR_DBL)z;
616         } else if (us == 1) {
617             if (ul == 1) /* 1x1 loop */
618                 return (FLT_OR_DBL) (P->expint11[type][type2][sil][sj1]);
619
620             if (ul == 2) {
621                 /* 2x1 loop */
622                 if (ul == 1)
623                     return (FLT_OR_DBL) (P->expint21[type][type2][sil][sql][sj1]);
624                 else
625                     return (FLT_OR_DBL) (P->expint21[type2][type][sql][sil][spl]);
626             } else {
627                 /* 1xn loop */
628                 z = P->expinternal[ul + us] * P->expmismatchlnI[type][sil][sj1] *
629                     P->expmismatchlnI[type2][sql][spl];
630                 return (FLT_OR_DBL) (z * P->expninio[2][ul - us]);
631             }
632         } else if (us == 2) {
633             if (ul == 2) {
634                 /* 2x2 loop */
635                 return (FLT_OR_DBL) (P->expint22[type][type2][sil][spl][sql][sj1]);
636             } else if (ul == 3) {
637                 /* 2x3 loop */
638                 z = P->expinternal[5] * P->expmismatch23I[type][sil][sj1] *
639                     P->expmismatch23I[type2][sql][spl];
640                 return (FLT_OR_DBL) (z * P->expninio[2][1]);
641             }
642         }
643
644         /* generic interior loop (no else here!)*/
645         z = P->expinternal[ul + us] * P->expmismatchI[type][sil][sj1] *
646             P->expmismatchI[type2][sql][spl];
647         return (FLT_OR_DBL) (z * P->expninio[2][ul - us]);
648     }
649
650     return (FLT_OR_DBL)z;
651 }
652
653
654 PRIVATE INLINE int
655 E_IntLoop_Co(int          type,
656             int          type_2,
657             int          i,
658             int          j,
659             int          p,
660             int          q,
661             int          cutpoint,
662             short        sil,
663             short        sj1,
664             short        spl,

```

```

665         short      sql,
666         int         dangles,
667         vrna_param_t *P)
668 {
669     int e, energy, ci, cj, cp, cq, d3, d5, d5_2, d3_2, tmm, tmm_2;
670
671     energy = 0;
672     if (type > 2)
673         energy += P->TerminalAU;
674
675     if (type_2 > 2)
676         energy += P->TerminalAU;
677
678     if (!dangles)
679         return energy;
680
681     ci = ON_SAME_STRAND(i, i + 1, cutpoint);
682     cj = ON_SAME_STRAND(j - 1, j, cutpoint);
683     cp = ON_SAME_STRAND(p - 1, p, cutpoint);
684     cq = ON_SAME_STRAND(q, q + 1, cutpoint);
685
686     d3 = ci ? P->dangle3[type][s1] : 0;
687     d5 = cj ? P->dangle5[type][s1] : 0;
688     d5_2 = cp ? P->dangle5[type_2][s1] : 0;
689     d3_2 = cq ? P->dangle3[type_2][s1] : 0;
690
691     tmm = (cj && ci) ? P->mismatchExt[type][s1][s1] : d5 + d3;
692     tmm_2 = (cp && cq) ? P->mismatchExt[type_2][s1][s1] : d5_2 + d3_2;
693
694     if (dangles == 2)
695         return energy + tmm + tmm_2;
696
697     /* now we may have non-double dangles only */
698     if (p - i > 2) {
699         if (j - q > 2) {
700             /* all degrees of freedom */
701             e = MIN2(tmm, d5);
702             e = MIN2(e, d3);
703             energy += e;
704             e = MIN2(tmm_2, d5_2);
705             e = MIN2(e, d3_2);
706             energy += e;
707         } else if (j - q == 2) {
708             /* all degrees of freedom in 5' part between i and p */
709             e = MIN2(tmm + d5_2, d3 + d5_2);
710             e = MIN2(e, d5 + d5_2);
711             e = MIN2(e, d3 + tmm_2);
712             e = MIN2(e, d3 + d3_2);
713             e = MIN2(e, tmm_2); /* no dangles on enclosing pair */
714             e = MIN2(e, d5_2); /* no dangles on enclosing pair */
715             e = MIN2(e, d3_2); /* no dangles on enclosing pair */
716             energy += e;
717         } else {
718             /* no unpaired base between q and j */
719             energy += d3 + d5_2;
720         }
721     } else if (p - i == 2) {
722         if (j - q > 2) {
723             /* all degrees of freedom in 3' part between q and j */
724             e = MIN2(tmm + d3_2, d5 + d3_2);
725             e = MIN2(e, d5 + d3_2);
726             e = MIN2(e, d3 + d3_2);
727             e = MIN2(e, d5 + tmm_2);
728             e = MIN2(e, tmm_2);
729             e = MIN2(e, d5_2);
730             e = MIN2(e, d3_2);
731             energy += e;
732         } else if (j - q == 2) {
733             /* one possible dangling base between either side */
734             e = MIN2(tmm, tmm_2);
735             e = MIN2(e, d3);
736             e = MIN2(e, d5);
737             e = MIN2(e, d5_2);
738             e = MIN2(e, d3_2);
739             e = MIN2(e, d3 + d3_2);
740             e = MIN2(e, d5 + d5_2);
741             energy += e;
742         } else {
743             /* one unpaired base between i and p */
744             energy += MIN2(d3, d5_2);
745         }
746     } else {
747         /* no unpaired base between i and p */
748         if (j - q > 2) {
749             /* all degrees of freedom in 3' part between q and j */
750             energy += d5 + d3_2;
751         } else if (j - q == 2) {

```



```

752     /* one unpaired base between q and j */
753     energy += MIN2(d5, d3_2);
754 }
755 }
756
757 return energy;
758 }
759
760
765 #endif
766
767 #endif

```

## 18.121 ViennaRNA/loops/multibranch.h File Reference

Energy evaluation of multibranch loops for MFE and partition function calculations.

Include dependency graph for multibranch.h: This graph shows which files directly or indirectly include this file:

### Functions

- int [vrna\\_BT\\_mb\\_loop](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int \*i, int \*j, int \*k, int en, int \*component1, int \*component2)

*Backtrack the decomposition of a multi branch loop closed by (i, j).*

#### Basic free energy interface

- int [vrna\\_E\\_mb\\_loop\\_stack](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j)
- *Evaluate energy of a multi branch helices stacking onto closing pair (i,j)*
- int [vrna\\_E\\_mb\\_loop\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int \*dmli1, int \*dmli2)
- int [E\\_ml\\_rightmost\\_stem](#) (int i, int j, [vrna\\_fold\\_compound\\_t](#) \*fc)
- int [vrna\\_E\\_ml\\_stems\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, int \*fmi, int \*dmli)

#### Boltzmann weight (partition function) interface

- typedef struct [vrna\\_mx\\_pf\\_aux\\_ml\\_s](#) \* [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#)
- *Auxiliary helper arrays for fast exterior loop computations.*
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_mb\\_loop\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- [vrna\\_mx\\_pf\\_aux\\_ml\\_t vrna\\_exp\\_E\\_ml\\_fast\\_init](#) ([vrna\\_fold\\_compound\\_t](#) \*fc)
- void [vrna\\_exp\\_E\\_ml\\_fast\\_rotate](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- void [vrna\\_exp\\_E\\_ml\\_fast\\_free](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- const [FLT\\_OR\\_DBL](#) \* [vrna\\_exp\\_E\\_ml\\_fast\\_qqm](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- const [FLT\\_OR\\_DBL](#) \* [vrna\\_exp\\_E\\_ml\\_fast\\_qqm1](#) ([vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)
- [FLT\\_OR\\_DBL vrna\\_exp\\_E\\_ml\\_fast](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int i, int j, [vrna\\_mx\\_pf\\_aux\\_ml\\_t](#) aux\_mx)

### 18.121.1 Detailed Description

Energy evaluation of multibranch loops for MFE and partition function calculations.

, ,

## 18.122 multibranch.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_MULTIBRANCH_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_MULTIBRANCH_H
3
4 #include <ViennaRNA/utils/basic.h>
5 #include <ViennaRNA/datastructures/basic.h>
6 #include <ViennaRNA/fold_compound.h>
7 #include <ViennaRNA/params/basic.h>
8
9 #ifdef VRNA_WARN_DEPRECATED
10 # if defined(DEPRECATED)
11 #   undef DEPRECATED

```

```

12 # endif
13 # if defined(__clang__)
14 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
15 # elif defined(__GNUC__)
16 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
17 # else
18 #   define DEPRECATED(func, msg) func
19 # endif
20 #else
21 # define DEPRECATED(func, msg) func
22 #endif
23
24 #ifdef __GNUC__
25 # define INLINE inline
26 #else
27 # define INLINE
28 #endif
29
30 int
31 vrna_E_mb_loop_stack(vrna_fold_compound_t *fc,
32                     int i,
33                     int j);
34
35 int
36 vrna_E_mb_loop_fast(vrna_fold_compound_t *fc,
37                    int i,
38                    int j,
39                    int *dmli1,
40                    int *dmli2);
41
42 int
43 E_ml_rightmost_stem(int i,
44                    int j,
45                    vrna_fold_compound_t *fc);
46
47 int
48 vrna_E_ml_stems_fast(vrna_fold_compound_t *fc,
49                     int i,
50                     int j,
51                     int *fmi,
52                     int *dmli);
53
54 /* End basic interface */
55 typedef struct vrna_mx_pf_aux_ml_s *vrna_mx_pf_aux_ml_t;
56
57 FLT_OR_DBL
58 vrna_exp_E_mb_loop_fast(vrna_fold_compound_t *fc,
59                        int i,
60                        int j,
61                        vrna_mx_pf_aux_ml_t aux_mx);
62
63 vrna_mx_pf_aux_ml_t
64 vrna_exp_E_ml_fast_init(vrna_fold_compound_t *fc);
65
66 void
67 vrna_exp_E_ml_fast_rotate(vrna_mx_pf_aux_ml_t aux_mx);
68
69 void
70 vrna_exp_E_ml_fast_free(vrna_mx_pf_aux_ml_t aux_mx);
71
72 const FLT_OR_DBL *
73 vrna_exp_E_ml_fast_qqm(vrna_mx_pf_aux_ml_t aux_mx);
74
75 const FLT_OR_DBL *
76 vrna_exp_E_ml_fast_qqml(vrna_mx_pf_aux_ml_t aux_mx);
77
78 FLT_OR_DBL
79 vrna_exp_E_ml_fast(vrna_fold_compound_t *fc,
80                   int i,
81                   int j,
82                   vrna_mx_pf_aux_ml_t aux_mx);
83
84 /* End partition function interface */
85 int
86 vrna_BT_mb_loop(vrna_fold_compound_t *fc,

```

```

165             int                *i,
166             int                *j,
167             int                *k,
168             int                en,
169             int                *component1,
170             int                *component2);
171
172
173 int
174 vrna_BT_mb_loop_split(vrna_fold_compound_t *fc,
175                      int                *i,
176                      int                *j,
177                      int                *k,
178                      int                *l,
179                      int                *component1,
180                      int                *component2,
181                      vrna_bp_stack_t   *bp_stack,
182                      int                *stack_count);
183
184
185 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
186
187 PRIVATE INLINE int
188 E_MLstem(int        type,
189          int        sil,
190          int        sjl,
191          vrna_param_t *P)
192 {
193     int energy = 0;
194
195     if (sil >= 0 && sjl >= 0)
196         energy += P->mismatchM[type][sil][sjl];
197     else if (sil >= 0)
198         energy += P->dangle5[type][sil];
199     else if (sjl >= 0)
200         energy += P->dangle3[type][sjl];
201
202     if (type > 2)
203         energy += P->TerminalAU;
204
205     energy += P->MLintern[type];
206
207     return energy;
208 }
209
210 PRIVATE INLINE FLT_OR_DBL
211 exp_E_MLstem(int        type,
212              int        sil,
213              int        sjl,
214              vrna_exp_param_t *P)
215 {
216     double energy = 1.0;
217
218     if (sil >= 0 && sjl >= 0)
219         energy = P->expmismatchM[type][sil][sjl];
220     else if (sil >= 0)
221         energy = P->expdangle5[type][sil];
222     else if (sjl >= 0)
223         energy = P->expdangle3[type][sjl];
224
225     if (type > 2)
226         energy *= P->expTermAU;
227
228     energy *= P->expMLintern[type];
229     return (FLT_OR_DBL)energy;
230 }
231
232 #endif
233
234 #endif

```

## 18.123 ViennaRNA/LPfold.h File Reference

Partition function and equilibrium probability implementation for the sliding window algorithm.  
Include dependency graph for LPfold.h:

### Functions

- void [update\\_pf\\_paramsLP](#) (int length)

- `vrna_ep_t * pfl_fold` (char \*sequence, int winSize, int pairSize, float cutoffb, double \*\*pU, `vrna_ep_t **dpp2`, FILE \*pUfp, FILE \*spup)  
*Compute partition functions for locally stable secondary structures.*
- `vrna_ep_t * pfl_fold_par` (char \*sequence, int winSize, int pairSize, float cutoffb, double \*\*pU, `vrna_ep_t **dpp2`, FILE \*pUfp, FILE \*spup, `vrna_exp_param_t *parameters`)  
*Compute partition functions for locally stable secondary structures.*
- void `putoutpU_prob` (double \*\*pU, int length, int ulength, FILE \*fp, int energies)  
*Writes the unpaired probabilities (pU) or opening energies into a file.*
- void `putoutpU_prob_bin` (double \*\*pU, int length, int ulength, FILE \*fp, int energies)  
*Writes the unpaired probabilities (pU) or opening energies into a binary file.*
- void `init_pf_foldLP` (int length)

### 18.123.1 Detailed Description

Partition function and equilibrium probability implementation for the sliding window algorithm.

This file contains the implementation for sliding window partition function and equilibrium probabilities. It also provides the unpaired probability implementation from Bernhart et al. 2011 [4]

### 18.123.2 Function Documentation

#### 18.123.2.1 `init_pf_foldLP()`

```
void init_pf_foldLP (
    int length )
```

Dunno if this function was ever used by external programs linking to RNAlib, but it was declared PUBLIC before. Anyway, never use this function as it will be removed soon and does nothing at all

## 18.124 LPfold.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LPFOLD_H
2 #define VIENNA_RNA_PACKAGE_LPFOLD_H
3
4 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
5
6 #include <stdio.h>
7
8 #include <ViennaRNA/datastructures/basic.h>
9 #include <ViennaRNA/params/basic.h>
10 #include <ViennaRNA/part_func_window.h>
11
12 #ifdef VRNA_WARN_DEPRECATED
13 # if defined(__clang__)
14 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
15 # elif defined(__GNUC__)
16 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
17 # else
18 #   define DEPRECATED(func, msg) func
19 # endif
20 #else
21 # define DEPRECATED(func, msg) func
22 #endif
23
24 DEPRECATED(void update_pf_paramsLP(int length),
25 "This function is obsolete");
26
27 DEPRECATED(void update_pf_paramsLP_par(int length,
28   vrna_exp_param_t *parameters),
29 "Use the new API with vrna_folc_compound_t instead");
30
31 DEPRECATED(vrna_ep_t *pfl_fold(char *sequence,
32                                 int winSize,
33                                 int pairSize,
34                                 float cutoffb,
35                                 double **pU,
```

```

98             vrna_ep_t      **dpp2,
99             FILE           *pUfp,
100             FILE           *spup),
101 "Use vrna_pfl_fold(), vrna_pfl_fold_cb(), vrna_pfl_fold_up(), or vrna_pfl_fold_up_cb() instead");
102
103
104 DEPRECATED(vrna_ep_t *pfl_fold_par(char          *sequence,
105                                     int           winSize,
106                                     int           pairSize,
107                                     float         cutoffb,
108                                     double        **pU,
109                                     vrna_ep_t     **dpp2,
110                                     FILE          *pUfp,
111                                     FILE          *spup,
112                                     vrna_exp_param_t *parameters),
113 "Use the new API and vrna_probs_window() instead");
114
115
116 DEPRECATED(void putoutpU_prob_par(double **pU,
117                                     int    length,
118                                     int    ulength,
119                                     FILE    *fp,
120                                     int     energies,
121                                     vrna_exp_param_t *parameters),
122 "");
123
124
125 DEPRECATED(void putoutpU_prob(double **pU,
126                               int    length,
127                               int    ulength,
128                               FILE    *fp,
129                               int     energies),
130 "");
131
132
133 DEPRECATED(void putoutpU_prob_bin_par(double **pU,
134                                       int    length,
135                                       int    ulength,
136                                       FILE    *fp,
137                                       int     energies,
138                                       vrna_exp_param_t *parameters),
139 "");
140
141
142 DEPRECATED(void putoutpU_prob_bin(double **pU,
143                                   int    length,
144                                   int    ulength,
145                                   FILE    *fp,
146                                   int     energies),
147 "");
148
149
150 DEPRECATED(void init_pf_foldLP(int length),
151 "This function is obsolete");
152
153 #endif
154 #endif

```

## 18.125 ViennaRNA/MEA.h File Reference

Computes a MEA (maximum expected accuracy) structure.

Include dependency graph for MEA.h:

### Functions

- char \* [vrna\\_MEA](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, double gamma, float \*mea)  
*Compute a MEA (maximum expected accuracy) structure.*
- char \* [vrna\\_MEA\\_from\\_plist](#) ([vrna\\_ep\\_t](#) \*plist, const char \*sequence, double gamma, [vrna\\_md\\_t](#) \*md, float \*mea)  
*Compute a MEA (maximum expected accuracy) structure from a list of probabilities.*
- float [MEA](#) ([plist](#) \*p, char \*structure, double gamma)  
*Computes a MEA (maximum expected accuracy) structure.*

### 18.125.1 Detailed Description

Computes a MEA (maximum expected accuracy) structure.

## 18.126 MEA.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_MEA_H
2 #define VIENNA_RNA_PACKAGE_MEA_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5 #include <ViennaRNA/params/basic.h>
6
35 char *
36 vrna_MEA(vrna_fold_compound_t *fc,
37          double gamma,
38          float *mea);
39
40
70 char *
71 vrna_MEA_from_plist(vrna_ep_t *plist,
72                    const char *sequence,
73                    double gamma,
74                    vrna_md_t *md,
75                    float *mea);
76
77
78 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
79
80 #ifdef VRNA_WARN_DEPRECATED
81 # if defined(__clang__)
82 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
83 # elif defined(__GNUC__)
84 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
85 # else
86 #  define DEPRECATED(func, msg) func
87 # endif
88 #else
89 # define DEPRECATED(func, msg) func
90 #endif
91
92
108 DEPRECATED(float
109            MEA(plist *p,
110               char *structure,
111               double gamma),
112            "Use vrna_MEA() or vrna_MEA_from_plist() instead!");
113
114
115 DEPRECATED(float
116            MEA_seq(plist *p,
117                   const char *sequence,
118                   char *structure,
119                   double gamma,
120                   vrna_exp_param_t *pf),
121            "Use vrna_MEA() or vrna_MEA_from_plist() instead!");
122
123
124 #endif
125
126 #endif

```

## 18.127 ViennaRNA/mfe.h File Reference

Compute Minimum Free energy (MFE) and backtrace corresponding secondary structures from RNA sequence data.

Include dependency graph for mfe.h: This graph shows which files directly or indirectly include this file:

### Functions

- float [vrna\\_backtrack5](#) (vrna\_fold\_compound\_t \*fc, unsigned int length, char \*structure)  
*Backtrack an MFE (sub)structure.*

#### Basic global MFE prediction interface

- float [vrna\\_mfe](#) (vrna\_fold\_compound\_t \*vc, char \*structure)

Compute minimum free energy and an appropriate secondary structure of an RNA sequence, or RNA sequence alignment.

- float `vrna_mfe_dimer` (`vrna_fold_compound_t` \*vc, char \*structure)

Compute the minimum free energy of two interacting RNA molecules.

### Simplified global MFE prediction using sequence(s) or multiple sequence alignment(s)

- float `vrna_fold` (const char \*sequence, char \*structure)  
Compute Minimum Free Energy (MFE), and a corresponding secondary structure for an RNA sequence.
- float `vrna_circfold` (const char \*sequence, char \*structure)  
Compute Minimum Free Energy (MFE), and a corresponding secondary structure for a circular RNA sequence.
- float `vrna_alifold` (const char \*\*sequences, char \*structure)  
Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for an RNA sequence alignment using a comparative method.
- float `vrna_circalifold` (const char \*\*sequences, char \*structure)  
Compute Minimum Free Energy (MFE), and a corresponding consensus secondary structure for a sequence alignment of circular RNAs using a comparative method.
- float `vrna_cofold` (const char \*sequence, char \*structure)  
Compute Minimum Free Energy (MFE), and a corresponding secondary structure for two dimerized RNA sequences.

## 18.127.1 Detailed Description

Compute Minimum Free energy (MFE) and backtrace corresponding secondary structures from RNA sequence data.

This file includes (almost) all function declarations within the RNAlib that are related to MFE folding...

## 18.128 mfe.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_MFE_H
2 #define VIENNA_RNA_PACKAGE_MFE_H
3
4 #include <stdio.h>
5 #include <ViennaRNA/datastructures/basic.h>
6 #include <ViennaRNA/fold_compound.h>
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(__clang__)
10 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
11 # elif defined(__GNUC__)
12 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
13 # else
14 #  define DEPRECATED(func, msg) func
15 # endif
16 #else
17 # define DEPRECATED(func, msg) func
18 #endif
19
20
21 float
22 vrna_mfe(vrna_fold_compound_t *vc,
23         char *structure);
24
25 DEPRECATED(float
26             vrna_mfe_dimer(vrna_fold_compound_t *vc,
27                             char *structure),
28             "Use vrna_mfe() instead");
29
30 float
31 vrna_fold(const char *sequence,
32           char *structure);
33
34 float
35 vrna_circfold(const char *sequence,
36              char *structure);
37
38
39
```

```

206 float
207 vrna_alifold(const char **sequences,
208             char      *structure);
209
210
211 float
212 vrna_circalifold(const char **sequences,
213                 char      *structure);
214
215 DEPRECATED(float
216            vrna_cofold(const char *sequence,
217                      char      *structure),
218            "Use vrna_fold() instead");
219
220 int
221 vrna_backtrack_from_intervals(vrna_fold_compound_t *vc,
222                             vrna_bp_stack_t      *bp_stack,
223                             sect                 bt_stack[],
224                             int                  s);
225
226 float
227 vrna_backtrack5(vrna_fold_compound_t *fc,
228                unsigned int          length,
229                char                  *structure);
230
231 int
232 vrna_backtrack_window(vrna_fold_compound_t *fc,
233                      const char            *lfold_filename,
234                      long                  file_pos,
235                      char                  **structure,
236                      double                mfe);
237 #endif

```

## 18.129 ViennaRNA/mfe\_window.h File Reference

Compute local Minimum Free Energy (MFE) using a sliding window approach and backtrace corresponding secondary structures.

Include dependency graph for mfe\_window.h: This graph shows which files directly or indirectly include this file:

### Typedefs

- typedef void() [vrna\\_mfe\\_window\\_callback](#)(int start, int end, const char \*structure, float en, void \*data)  
*The default callback for sliding window MFE structure predictions.*

### Functions

#### Basic local (sliding window) MFE prediction interface

- float [vrna\\_mfe\\_window](#) (vrna\_fold\_compound\_t \*vc, FILE \*file)  
*Local MFE prediction using a sliding window approach.*
- float [vrna\\_mfe\\_window\\_cb](#) (vrna\_fold\_compound\_t \*vc, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)
- float [vrna\\_mfe\\_window\\_zscore](#) (vrna\_fold\_compound\_t \*vc, double min\_z, FILE \*file)  
*Local MFE prediction using a sliding window approach (with z-score cut-off)*
- float [vrna\\_mfe\\_window\\_zscore\\_cb](#) (vrna\_fold\_compound\_t \*vc, double min\_z, [vrna\\_mfe\\_window\\_zscore\\_callback](#) \*cb, void \*data)

#### Simplified local MFE prediction using sequence(s) or multiple sequence alignment(s)

- float [vrna\\_Lfold](#) (const char \*string, int window\_size, FILE \*file)  
*Local MFE prediction using a sliding window approach (simplified interface)*
- float [vrna\\_Lfold\\_cb](#) (const char \*string, int window\_size, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)
- float [vrna\\_Lfoldz](#) (const char \*string, int window\_size, double min\_z, FILE \*file)  
*Local MFE prediction using a sliding window approach with z-score cut-off (simplified interface)*
- float [vrna\\_Lfoldz\\_cb](#) (const char \*string, int window\_size, double min\_z, [vrna\\_mfe\\_window\\_zscore\\_callback](#) \*cb, void \*data)
- float [vrna\\_alifold](#) (const char \*\*alignment, int maxdist, FILE \*fp)
- float [vrna\\_alifold\\_cb](#) (const char \*\*alignment, int maxdist, [vrna\\_mfe\\_window\\_callback](#) \*cb, void \*data)



### 18.129.1 Detailed Description

Compute local Minimum Free Energy (MFE) using a sliding window approach and backtrace corresponding secondary structures.

This file includes the interface to all functions related to predicting locally stable secondary structures.

## 18.130 mfe\_window.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_MFE_WINDOW_H
2 #define VIENNA_RNA_PACKAGE_MFE_WINDOW_H
3
4 #include <stdio.h>
5 #include <ViennaRNA/fold_compound.h>
6
7 #ifdef VRNA_WITH_SVM
8 #include <ViennaRNA/zscore.h>
9 #endif
10
11 typedef void (vrna_mfe_window_callback)(int start,
12 int end,
13 const char *structure,
14 float en,
15 void *data);
16
17 #ifdef VRNA_WITH_SVM
18 typedef void (vrna_mfe_window_zscore_callback)(int start,
19 int end,
20 const char *structure,
21 float en,
22 float zscore,
23 void *data);
24 #endif
25
26 float
27 vrna_mfe_window(vrna_fold_compound_t *vc,
28 FILE *file);
29
30 float
31 vrna_mfe_window_cb(vrna_fold_compound_t *vc,
32 vrna_mfe_window_callback *cb,
33 void *data);
34
35 #ifdef VRNA_WITH_SVM
36 float
37 vrna_mfe_window_zscore(vrna_fold_compound_t *vc,
38 double min_z,
39 FILE *file);
40
41 float
42 vrna_mfe_window_zscore_cb(vrna_fold_compound_t *vc,
43 double min_z,
44 vrna_mfe_window_zscore_callback *cb,
45 void *data);
46 #endif
47
48 /* End basic local MFE interface */
49 float
50 vrna_Lfold(const char *string,
51 int window_size,
52 FILE *file);
53
54 float
55 vrna_Lfold_cb(const char *string,
56 int window_size,
57 vrna_mfe_window_callback *cb,
58 void *data);
59
60 #ifdef VRNA_WITH_SVM
61 float
62 vrna_Lfoldz(const char *string,
63 int window_size,
64 double min_z,

```

```

232         FILE          *file);
233
234
235 float
236 vrna_Lfoldz_cb(const char          *string,
237               int                  window_size,
238               double               min_z,
239               vrna_mfe_window_zscore_callback *cb,
240               void                  *data);
241
242
243 #endif
244
245 float vrna_alilfold(const char **alignment,
246                   int          maxdist,
247                   FILE          *fp);
248
249
250 float vrna_alilfold_cb(const char          **alignment,
251                       int                  maxdist,
252                       vrna_mfe_window_callback *cb,
253                       void                  *data);
254
255
256 /* End simplified local MFE interface */
257 /* End group mfe_fold_window */
263 #endif

```

## 18.131 ViennaRNA/mm.h File Reference

Several Maximum Matching implementations.

Include dependency graph for mm.h:

### Functions

- int [vrna\\_maximum\\_matching](#) (vrna\_fold\_compound\_t \*fc)
- int [vrna\\_maximum\\_matching\\_simple](#) (const char \*sequence)

#### 18.131.1 Detailed Description

Several Maximum Matching implementations.

This file contains the declarations for several maximum matching implementations

#### 18.131.2 Function Documentation

##### 18.131.2.1 vrna\_maximum\_matching()

```
int vrna_maximum_matching (
    vrna_fold_compound_t * fc )
```

**SWIG Wrapper Notes** This function is attached as method **maximum\_matching()** to objects of type `fold_compound` (i.e. [vrna\\_fold\\_compound\\_t](#)).

##### 18.131.2.2 vrna\_maximum\_matching\_simple()

```
int vrna_maximum_matching_simple (
    const char * sequence )
```

**SWIG Wrapper Notes** This function is available as global function **maximum\_matching()**.

## 18.132 mm.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_MM_H
2 #define VIENNA_RNA_PACKAGE_MM_H
3
13 #include <ViennaRNA/fold_compound.h>
14
15 int
16 vrna_maximum_matching(vrna_fold_compound_t *fc);
17
18
19 int
20 vrna_maximum_matching_simple(const char *sequence);
21
22
23 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
24
25 unsigned int
26 maximumMatching(const char *string);
27
28
29 unsigned int *
30 maximumMatchingConstraint(const char *string,
31                           short *ptable);
32
33
34 unsigned int *
35 maximumMatching2Constraint(const char *string,
36                           short *ptable,
37                           short *ptable2);
38
39
40 #endif
41
42 #endif
```

## 18.133 ViennaRNA/model.h File Reference

The model details data structure and its corresponding modifiers.

This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_md\\_s](#)

*The data structure that contains the complete model details used throughout the calculations. [More...](#)*

### Macros

- #define [VRNA\\_MODEL\\_DEFAULT\\_TEMPERATURE](#) 37.0  
*Default temperature for structure prediction and free energy evaluation in °C*
- #define [VRNA\\_MODEL\\_DEFAULT\\_PF\\_SCALE](#) -1  
*Default scaling factor for partition function computations.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_BETA\\_SCALE](#) 1.  
*Default scaling factor for absolute thermodynamic temperature in Boltzmann factors.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_DANGLES](#) 2  
*Default dangling end model.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_SPECIAL\\_HP](#) 1  
*Default model behavior for lookup of special tri-, tetra-, and hexa-loops.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_NO\\_LP](#) 0  
*Default model behavior for so-called 'lonely pairs'.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU](#) 0  
*Default model behavior for G-U base pairs.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_NO\\_GU\\_CLOSURE](#) 0  
*Default model behavior for G-U base pairs closing a loop.*
- #define [VRNA\\_MODEL\\_DEFAULT\\_CIRC](#) 0

- *Default model behavior to treat a molecule as a circular RNA (DNA)*
- `#define VRNA_MODEL_DEFAULT_GQUAD 0`
- *Default model behavior regarding the treatment of G-Quadruplexes.*
- `#define VRNA_MODEL_DEFAULT_UNIQ_ML 0`
- *Default behavior of the model regarding unique multi-branch loop decomposition.*
- `#define VRNA_MODEL_DEFAULT_ENERGY_SET 0`
- *Default model behavior on which energy set to use.*
- `#define VRNA_MODEL_DEFAULT_BACKTRACK 1`
- *Default model behavior with regards to backtracking of structures.*
- `#define VRNA_MODEL_DEFAULT_BACKTRACK_TYPE 'F'`
- *Default model behavior on what type of backtracking to perform.*
- `#define VRNA_MODEL_DEFAULT_COMPUTE_BPP 1`
- *Default model behavior with regards to computing base pair probabilities.*
- `#define VRNA_MODEL_DEFAULT_MAX_BP_SPAN -1`
- *Default model behavior for the allowed maximum base pair span.*
- `#define VRNA_MODEL_DEFAULT_WINDOW_SIZE -1`
- *Default model behavior for the sliding window approach.*
- `#define VRNA_MODEL_DEFAULT_LOG_ML 0`
- *Default model behavior on how to evaluate the energy contribution of multi-branch loops.*
- `#define VRNA_MODEL_DEFAULT_ALI_OLD_EN 0`
- *Default model behavior for consensus structure energy evaluation.*
- `#define VRNA_MODEL_DEFAULT_ALI_RIBO 0`
- *Default model behavior for consensus structure co-variance contribution assessment.*
- `#define VRNA_MODEL_DEFAULT_ALI_CV_FACT 1.`
- *Default model behavior for weighting the co-variance score in consensus structure prediction.*
- `#define VRNA_MODEL_DEFAULT_ALI_NC_FACT 1.`
- *Default model behavior for weighting the nucleotide conservation? in consensus structure prediction.*
- `#define MAXALPHA 20`
- *Maximal length of alphabet.*

## Typedefs

- `typedef struct vrna_md_s vrna_md_t`
- *Typename for the model details data structure `vrna_md_s`.*

## Functions

- `void vrna_md_set_default (vrna_md_t *md)`
- *Apply default model details to a provided `vrna_md_t` data structure.*
- `void vrna_md_update (vrna_md_t *md)`
- *Update the model details data structure.*
- `vrna_md_t * vrna_md_copy (vrna_md_t *md_to, const vrna_md_t *md_from)`
- *Copy/Clone a `vrna_md_t` model.*
- `char * vrna_md_option_string (vrna_md_t *md)`
- *Get a corresponding cmdline parameter string of the options in a `vrna_md_t`.*
- `void vrna_md_defaults_reset (vrna_md_t *md_p)`
- *Reset the global default model details to a specific set of parameters, or their initial values.*
- `void vrna_md_defaults_temperature (double T)`
- *Set default temperature for energy evaluation of loops.*
- `double vrna_md_defaults_temperature_get (void)`
- *Get default temperature for energy evaluation of loops.*
- `void vrna_md_defaults_betaScale (double b)`

- Set default scaling factor of thermodynamic temperature in Boltzmann factors.*

  - double [vrna\\_md\\_defaults\\_betaScale\\_get](#) (void)

*Get default scaling factor of thermodynamic temperature in Boltzmann factors.*
- void [vrna\\_md\\_defaults\\_dangles](#) (int d)

*Set default dangle model for structure prediction.*

  - int [vrna\\_md\\_defaults\\_dangles\\_get](#) (void)

*Get default dangle model for structure prediction.*
- void [vrna\\_md\\_defaults\\_special\\_hp](#) (int flag)

*Set default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.*

  - int [vrna\\_md\\_defaults\\_special\\_hp\\_get](#) (void)

*Get default behavior for lookup of tabulated free energies for special hairpin loops, such as Tri-, Tetra-, or Hexa-loops.*
- void [vrna\\_md\\_defaults\\_noLP](#) (int flag)

*Set default behavior for prediction of canonical secondary structures.*

  - int [vrna\\_md\\_defaults\\_noLP\\_get](#) (void)

*Get default behavior for prediction of canonical secondary structures.*
- void [vrna\\_md\\_defaults\\_noGU](#) (int flag)

*Set default behavior for treatment of G-U wobble pairs.*

  - int [vrna\\_md\\_defaults\\_noGU\\_get](#) (void)

*Get default behavior for treatment of G-U wobble pairs.*
- void [vrna\\_md\\_defaults\\_noGUclosure](#) (int flag)

*Set default behavior for G-U pairs as closing pair for loops.*

  - int [vrna\\_md\\_defaults\\_noGUclosure\\_get](#) (void)

*Get default behavior for G-U pairs as closing pair for loops.*
- void [vrna\\_md\\_defaults\\_logML](#) (int flag)

*Set default behavior recomputing free energies of multi-branch loops using a logarithmic model.*

  - int [vrna\\_md\\_defaults\\_logML\\_get](#) (void)

*Get default behavior recomputing free energies of multi-branch loops using a logarithmic model.*
- void [vrna\\_md\\_defaults\\_circ](#) (int flag)

*Set default behavior whether input sequences are circularized.*

  - int [vrna\\_md\\_defaults\\_circ\\_get](#) (void)

*Get default behavior whether input sequences are circularized.*
- void [vrna\\_md\\_defaults\\_gquad](#) (int flag)

*Set default behavior for treatment of G-Quadruplexes.*

  - int [vrna\\_md\\_defaults\\_gquad\\_get](#) (void)

*Get default behavior for treatment of G-Quadruplexes.*
- void [vrna\\_md\\_defaults\\_uniq\\_ML](#) (int flag)

*Set default behavior for creating additional matrix for unique multi-branch loop prediction.*

  - int [vrna\\_md\\_defaults\\_uniq\\_ML\\_get](#) (void)

*Get default behavior for creating additional matrix for unique multi-branch loop prediction.*
- void [vrna\\_md\\_defaults\\_energy\\_set](#) (int e)

*Set default energy set.*

  - int [vrna\\_md\\_defaults\\_energy\\_set\\_get](#) (void)

*Get default energy set.*
- void [vrna\\_md\\_defaults\\_backtrack](#) (int flag)

*Set default behavior for whether to backtrack secondary structures.*

  - int [vrna\\_md\\_defaults\\_backtrack\\_get](#) (void)

*Get default behavior for whether to backtrack secondary structures.*
- void [vrna\\_md\\_defaults\\_backtrack\\_type](#) (char t)

*Set default backtrack type, i.e. which DP matrix is used.*

  - char [vrna\\_md\\_defaults\\_backtrack\\_type\\_get](#) (void)

*Get default backtrack type, i.e. which DP matrix is used.*

- void `vrna_md_defaults_compute_bpp` (int flag)  
*Set the default behavior for whether to compute base pair probabilities after partition function computation.*
- int `vrna_md_defaults_compute_bpp_get` (void)  
*Get the default behavior for whether to compute base pair probabilities after partition function computation.*
- void `vrna_md_defaults_max_bp_span` (int span)  
*Set default maximal base pair span.*
- int `vrna_md_defaults_max_bp_span_get` (void)  
*Get default maximal base pair span.*
- void `vrna_md_defaults_min_loop_size` (int size)  
*Set default minimal loop size.*
- int `vrna_md_defaults_min_loop_size_get` (void)  
*Get default minimal loop size.*
- void `vrna_md_defaults_window_size` (int size)  
*Set default window size for sliding window structure prediction approaches.*
- int `vrna_md_defaults_window_size_get` (void)  
*Get default window size for sliding window structure prediction approaches.*
- void `vrna_md_defaults_oldAliEn` (int flag)  
*Set default behavior for whether to use old energy model for comparative structure prediction.*
- int `vrna_md_defaults_oldAliEn_get` (void)  
*Get default behavior for whether to use old energy model for comparative structure prediction.*
- void `vrna_md_defaults_ribo` (int flag)  
*Set default behavior for whether to use Ribosum Scoring in comparative structure prediction.*
- int `vrna_md_defaults_ribo_get` (void)  
*Get default behavior for whether to use Ribosum Scoring in comparative structure prediction.*
- void `vrna_md_defaults_cv_fact` (double factor)  
*Set the default co-variance scaling factor used in comparative structure prediction.*
- double `vrna_md_defaults_cv_fact_get` (void)  
*Get the default co-variance scaling factor used in comparative structure prediction.*
- void `vrna_md_defaults_nc_fact` (double factor)
- double `vrna_md_defaults_nc_fact_get` (void)
- void `vrna_md_defaults_sfact` (double factor)  
*Set the default scaling factor used to avoid under-/overflows in partition function computation.*
- double `vrna_md_defaults_sfact_get` (void)  
*Get the default scaling factor used to avoid under-/overflows in partition function computation.*
- void `set_model_details` (`vrna_md_t` \*md)  
*Set default model details.*

## Variables

- double `temperature`  
*Rescale energy parameters to a temperature in degC.*
- double `pf_scale`  
*A scaling factor used by `pf_fold()` to avoid overflows.*
- int `dangles`  
*Switch the energy model for dangling end contributions (0, 1, 2, 3)*
- int `tetra_loop`  
*Include special stabilizing energies for some tri-, tetra- and hexa-loops;*
- int `noLonelyPairs`  
*Global switch to avoid/allow helices of length 1.*
- int `noGU`  
*Global switch to forbid/allow GU base pairs at all.*

- int **no\_closingGU**  
*GU allowed only inside stacks if set to 1.*
- int **circ**  
*backward compatibility variable.. this does not effect anything*
- int **gquad**  
*Allow G-quadruplex formation.*
- int **uniq\_ML**  
*do ML decomposition uniquely (for subopt)*
- int **energy\_set**  
*0 = BP; 1=any with GC; 2=any with AU-parameter*
- int **do\_backtrack**  
*do backtracking, i.e. compute secondary structures or base pair probabilities*
- char **backtrack\_type**  
*A backtrack array marker for [inverse\\_fold\(\)](#)*
- char \* **nonstandards**  
*contains allowed non standard base pairs*
- int **max\_bp\_span**  
*Maximum allowed base pair span.*
- int **oldAliEn**  
*use old alifold energies (with gaps)*
- int **ribo**  
*use ribosum matrices*
- int **logML**  
*if nonzero use logarithmic ML energy in energy\_of\_struct*

### 18.133.1 Detailed Description

The model details data structure and its corresponding modifiers.

## 18.134 model.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_MODEL_H
2 #define VIENNA_RNA_PACKAGE_MODEL_H
3
17 #ifndef NBASES
18 #define NBASES 8
19 #endif
20
22 typedef struct vrna_md_s vrna_md_t;
23
30 #define VRNA_MODEL_DEFAULT_TEMPERATURE 37.0
31
36 #define VRNA_MODEL_DEFAULT_PF_SCALE -1
37
42 #define VRNA_MODEL_DEFAULT_BETA_SCALE 1.
43
47 #define VRNA_MODEL_DEFAULT_DANGLES 2
48
53 #define VRNA_MODEL_DEFAULT_SPECIAL_HP 1
54
59 #define VRNA_MODEL_DEFAULT_NO_LP 0
60
65 #define VRNA_MODEL_DEFAULT_NO_GU 0
66
71 #define VRNA_MODEL_DEFAULT_NO_GU_CLOSURE 0
72
77 #define VRNA_MODEL_DEFAULT_CIRC 0
78
83 #define VRNA_MODEL_DEFAULT_GQUAD 0
84
89 #define VRNA_MODEL_DEFAULT_UNIQ_ML 0
90
95 #define VRNA_MODEL_DEFAULT_ENERGY_SET 0

```

```

96
101 #define VRNA_MODEL_DEFAULT_BACKTRACK      1
102
107 #define VRNA_MODEL_DEFAULT_BACKTRACK_TYPE 'F'
108
113 #define VRNA_MODEL_DEFAULT_COMPUTE_BPP     1
114
119 #define VRNA_MODEL_DEFAULT_MAX_BP_SPAN     -1
120
125 #define VRNA_MODEL_DEFAULT_WINDOW_SIZE     -1
126
131 #define VRNA_MODEL_DEFAULT_LOG_ML          0
132
137 #define VRNA_MODEL_DEFAULT_ALI_OLD_EN      0
138
143 #define VRNA_MODEL_DEFAULT_ALI_RIBO        0
144
149 #define VRNA_MODEL_DEFAULT_ALI_CV_FACT     1.
150
154 #define VRNA_MODEL_DEFAULT_ALI_NC_FACT     1.
155
156
157 #define VRNA_MODEL_DEFAULT_PF_SMOOTH        1
158
159
160 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
161
162 #ifndef MAXALPHA
166 #define MAXALPHA                20
167 #endif
168
169 #endif
170
180 struct vrna_md_s {
181     double temperature;
182     double betaScale;
183     int    pf_smooth;
184     int    dangles;
208     int    special_hp;
209     int    noLP;
210     int    noGU;
211     int    noGUclosure;
212     int    logML;
213     int    circ;
214     int    gquad;
215     int    uniq_ML;
216     int    energy_set;
217     int    backtrack;
218     char   backtrack_type;
219     int    compute_bpp;
220     char   nonstandards[64];
221     int    max_bp_span;
223     int    min_loop_size;
227     int    window_size;
228     int    oldAliEn;
229     int    ribo;
230     double cv_fact;
231     double nc_fact;
232     double sfact;
233     int    rtype[8];
234     short  alias[MAXALPHA + 1];
235     int    pair[MAXALPHA + 1][MAXALPHA + 1];
236     float  pair_dist[7][7];
237 };
238
239
248 void
249 vrna_md_set_default(vrna_md_t *md);
250
251
264 void
265 vrna_md_update(vrna_md_t *md);
266
267
278 vrna_md_t *
279 vrna_md_copy(vrna_md_t      *md_to,
280              const vrna_md_t *md_from);
281
282
288 char *
289 vrna_md_option_string(vrna_md_t *md);
290
291
292 void
293 vrna_md_set_nonstandards(vrna_md_t *md,
294                          const char *ns_bases);
295

```



```
296
314 void
315 vrna_md_defaults_reset(vrna_md_t *md_p);
316
317
323 void
324 vrna_md_defaults_temperature(double T);
325
326
332 double
333 vrna_md_defaults_temperature_get(void);
334
335
343 void
344 vrna_md_defaults_betaScale(double b);
345
346
353 double
354 vrna_md_defaults_betaScale_get(void);
355
356
357 void
358 vrna_md_defaults_pf_smooth(int s);
359
360
361 int
362 vrna_md_defaults_pf_smooth_get(void);
363
364
370 void
371 vrna_md_defaults_dangles(int d);
372
373
379 int
380 vrna_md_defaults_dangles_get(void);
381
382
388 void
389 vrna_md_defaults_special_hp(int flag);
390
391
397 int
398 vrna_md_defaults_special_hp_get(void);
399
400
406 void
407 vrna_md_defaults_noLP(int flag);
408
409
415 int
416 vrna_md_defaults_noLP_get(void);
417
418
424 void
425 vrna_md_defaults_noGU(int flag);
426
427
433 int
434 vrna_md_defaults_noGU_get(void);
435
436
442 void
443 vrna_md_defaults_noGUclosure(int flag);
444
445
451 int
452 vrna_md_defaults_noGUclosure_get(void);
453
454
460 void
461 vrna_md_defaults_logML(int flag);
462
463
469 int
470 vrna_md_defaults_logML_get(void);
471
472
478 void
479 vrna_md_defaults_circ(int flag);
480
481
487 int
488 vrna_md_defaults_circ_get(void);
489
490
496 void
497 vrna_md_defaults_gquad(int flag);
```

```
498
499
505 int
506 vrna_md_defaults_gquad_get(void);
507
508
515 void
516 vrna_md_defaults_uniq_ML(int flag);
517
518
524 int
525 vrna_md_defaults_uniq_ML_get(void);
526
527
533 void
534 vrna_md_defaults_energy_set(int e);
535
536
542 int
543 vrna_md_defaults_energy_set_get(void);
544
545
551 void
552 vrna_md_defaults_backtrack(int flag);
553
554
560 int
561 vrna_md_defaults_backtrack_get(void);
562
563
569 void
570 vrna_md_defaults_backtrack_type(char t);
571
572
578 char
579 vrna_md_defaults_backtrack_type_get(void);
580
581
587 void
588 vrna_md_defaults_compute_bpp(int flag);
589
590
596 int
597 vrna_md_defaults_compute_bpp_get(void);
598
599
605 void
606 vrna_md_defaults_max_bp_span(int span);
607
608
614 int
615 vrna_md_defaults_max_bp_span_get(void);
616
617
623 void
624 vrna_md_defaults_min_loop_size(int size);
625
626
632 int
633 vrna_md_defaults_min_loop_size_get(void);
634
635
641 void
642 vrna_md_defaults_window_size(int size);
643
644
650 int
651 vrna_md_defaults_window_size_get(void);
652
653
661 void
662 vrna_md_defaults_oldAliEn(int flag);
663
664
670 int
671 vrna_md_defaults_oldAliEn_get(void);
672
673
679 void
680 vrna_md_defaults_ribo(int flag);
681
682
688 int
689 vrna_md_defaults_ribo_get(void);
690
691
697 void
```

```

698 vrna_md_defaults_cv_fact(double factor);
699
700
706 double
707 vrna_md_defaults_cv_fact_get(void);
708
709
715 void
716 vrna_md_defaults_nc_fact(double factor);
717
718
724 double
725 vrna_md_defaults_nc_fact_get(void);
726
727
733 void
734 vrna_md_defaults_sfact(double factor);
735
736
742 double
743 vrna_md_defaults_sfact_get(void);
744
745
746 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
747
748 #define model_detailsT      vrna_md_t      /* restore compatibility of struct rename */
749
750 /* BEGIN deprecated global variables: */
751
761 extern double temperature;
762
774 extern double pf_scale;
775
797 extern int dangles;
798
804 extern int tetra_loop;
805
813 extern int noLonelyPairs;
814
818 extern int noGU;
819
823 extern int no_closingGU;
824
828 extern int circ;
829
833 extern int gquad;
834
838 extern int uniq_ML;
839
847 extern int energy_set;
848
855 extern int do_backtrack;
856
864 extern char backtrack_type;
865
873 extern char *nonstandards;
874
880 extern int max_bp_span;
881
885 extern int oldAliEn;
886
890 extern int ribo;
891
892 extern double cv_fact;
893
894 extern double nc_fact;
895
897 extern int logML;
898
899 /* END deprecated global variables: */
900
914 void
915 set_model_details(vrna_md_t *md);
916
917
918 char *
919 option_string(void);
920
921
922 #endif
927 #endif

```

## 18.135 move\_set.h

```
1 #ifndef __MOVE_SET_H
```

```

2 #define __MOVE_SET_H
3
4 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
5
6
7
8
9 typedef struct _struct_en{
10     int energy; /* energy in 10kcal/mol*/
11     short *structure; /* structure in energy_of_move format*/
12 } struct_en;
13
14 /* prints structure*/
15 void print_stren(FILE *out, struct_en *str);
16 void print_str(FILE *out, short *str);
17
18 /* copying functions*/
19 void copy_arr(short *dest, short *src); /*just copy*/
20 short *allocopy(short *src); /*copy and make space*/
21
22 enum MOVE_TYPE {GRADIENT, FIRST, ADAPTIVE};
23
24 /* walking methods (verbose_lvl 0-2, shifts = use shift moves? noLP = no lone pairs? (not compatible with
    shifts))
25     input:     seq - sequence
26                ptable - structure encoded with make_pair_table() from pair_mat.h
27                s, sl - sequence encoded with encode_sequence from pair_mat.h
28     methods:  deepest - lowest energy structure is used
29                first - first found lower energy structure is used
30                rand - random lower energy structure is used
31     returns local minima structure in ptable and its energy in 10kcal/mol as output */
32
33 int move_gradient( char *seq,
34                   short *ptable,
35                   short *s,
36                   short *sl,
37                   int verbosity_level,
38                   int shifts,
39                   int noLP);
40 int move_first( char *seq,
41                short *ptable,
42                short *s,
43                short *sl,
44                int verbosity_level,
45                int shifts,
46                int noLP);
47 int move_adaptive( char *seq,
48                  short *ptable,
49                  short *s,
50                  short *sl,
51                  int verbosity_level);
52
53 /* standardized method that encapsulates above "_pt" methods
54     input:  seq - sequence
55            struc - structure in dot-bracket notation
56            type - type of move selection according to MOVE_TYPE enum
57     return: energy of LM
58            structure of LM in struc in bracket-dot notation
59 */
60 int move_standard(char *seq,
61                  char *struc,
62                  enum MOVE_TYPE type,
63                  int verbosity_level,
64                  int shifts,
65                  int noLP);
66
67
68 /* browse_neighbours and perform funct function on each of them (used mainly for user specified flooding)
69     input:  seq - sequence
70            ptable - structure encoded with make_pair_table() from pair_mat.h
71            s, sl - sequence encoded with encode_sequence from pair_mat.h
72            funct - function (structure from neighbourhood, structure from input) toperform on every
73                  structure in neighbourhood (if the function returns non-zero, the iteration through neighbourhood
74                  stops.)
75     returns energy of the structure funct sets as second argument*/
76 int browse_neighs_pt( char *seq,
77                      short *ptable,
78                      short *s,
79                      short *sl,
80                      int verbosity_level,
81                      int shifts,
82                      int noLP,
83                      int (*funct) (struct_en*, struct_en*));
84
85 int browse_neighs( char *seq,
86                   char *struc,
87                   int verbosity_level,
88                   int shifts,
89                   int noLP,
90                   int (*funct) (struct_en*, struct_en*));

```

```
89
90 #endif
91
92 #endif
93
94
```

## 18.136 ViennaRNA/multibranch\_loops.h File Reference

Use [ViennaRNA/loops/multibranch.h](#) instead.

Include dependency graph for multibranch\_loops.h:

### 18.136.1 Detailed Description

Use [ViennaRNA/loops/multibranch.h](#) instead.

**Deprecated** Use [ViennaRNA/loops/multibranch.h](#) instead

## 18.137 multibranch\_loops.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_LOOPS_MULTIBRANCH_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_LOOPS_MULTIBRANCH_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #       warning "Including deprecated header file <ViennaRNA/multibranch_loops.h>! Use
13           <ViennaRNA/loops/multibranch.h> instead!"
14 #   endif
15 #   include <ViennaRNA/loops/multibranch.h>
16 #   endif
17 #endif
```

## 18.138 ViennaRNA/naview.h File Reference

Use ViennaRNA/plotting/naview/naview.h instead.

### 18.138.1 Detailed Description

Use ViennaRNA/plotting/naview/naview.h instead.

**Deprecated** Use ViennaRNA/plotting/naview/naview.h instead

## 18.139 naview.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_NAVIEW_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_NAVIEW_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #       warning "Including deprecated header file <ViennaRNA/naview.h>! Use <ViennaRNA/plotting/naview.h>
13           instead!"
14 #   endif
15 #   include <ViennaRNA/plotting/naview/naview.h>
16 #   else
17 #       warning "Naview Layout algorithm is not available in this version!"
18 #   endif
19 #endif
20
21 #endif
```

## 18.140 ViennaRNA/landscape/neighbor.h File Reference

Methods to compute the neighbors of an RNA secondary structure.

Include dependency graph for neighbor.h: This graph shows which files directly or indirectly include this file:

### Macros

- `#define VRNA_NEIGHBOR_CHANGE 1`  
*State indicator for a neighbor that has been changed.*
- `#define VRNA_NEIGHBOR_INVALID 2`  
*State indicator for a neighbor that has been invalidated.*
- `#define VRNA_NEIGHBOR_NEW 3`  
*State indicator for a neighbor that has become newly available.*

### Typedefs

- `typedef void() vrna_callback_move_update(vrna_fold_compound_t *fc, vrna_move_t neighbor, unsigned int state, void *data)`  
*Prototype of the neighborhood update callback.*

### Functions

- `void vrna_loopidx_update (int *loopidx, const short *pt, int length, const vrna_move_t *m)`  
*Alters the loopIndices array that was constructed with vrna\_loopidx\_from\_ptable().*
- `vrna_move_t * vrna_neighbors (vrna_fold_compound_t *vc, const short *pt, unsigned int options)`  
*Generate neighbors of a secondary structure.*
- `vrna_move_t * vrna_neighbors_successive (const vrna_fold_compound_t *vc, const vrna_move_t *curr↔_move, const short *prev_pt, const vrna_move_t *prev_neighbors, int size_prev_neighbors, int *size↔_neighbors, unsigned int options)`  
*Generate neighbors of a secondary structure (the fast way)*
- `int vrna_move_neighbor_diff_cb (vrna_fold_compound_t *fc, short *ptable, vrna_move_t move, vrna_callback_move_update *cb, void *data, unsigned int options)`  
*Apply a move to a secondary structure and indicate which neighbors have changed consequentially.*
- `vrna_move_t * vrna_move_neighbor_diff (vrna_fold_compound_t *fc, short *ptable, vrna_move_t move, vrna_move_t **invalid_moves, unsigned int options)`  
*Apply a move to a secondary structure and indicate which neighbors have changed consequentially.*

### 18.140.1 Detailed Description

Methods to compute the neighbors of an RNA secondary structure.

## 18.141 neighbor.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_NEIGHBOR_H
2 #define VIENNA_RNA_PACKAGE_NEIGHBOR_H
3
111 #include <ViennaRNA/fold_compound.h>
112 #include <ViennaRNA/landscape/move.h>
113
124 typedef void (vrna_callback_move_update) (vrna_fold_compound_t *fc,
125   vrna_move_t neighbor,
126   unsigned int state,
127   void *data);
128
129
135 #define VRNA_NEIGHBOR_CHANGE 1
136
137
143 #define VRNA_NEIGHBOR_INVALID 2
144

```

```

145
151 #define VRNA_NEIGHBOR_NEW      3
152
153
154
155 void
156 vrna_loopidx_update(int          *loopidx,
157                     const short  *pt,
158                     int          length,
159                     const vrna_move_t *m);
160
161
162
163 vrna_move_t *
164 vrna_neighbors(vrna_fold_compound_t *vc,
165               const short  *pt,
166               unsigned int  options);
167
168
169
170 vrna_move_t *
171 vrna_neighbors_successive(const vrna_fold_compound_t *vc,
172                          const vrna_move_t          *curr_move,
173                          const short                *prev_pt,
174                          const vrna_move_t          *prev_neighbors,
175                          int                        size_prev_neighbors,
176                          int                        size_neighbors,
177                          unsigned int                options);
178
179
180
181 int
182 vrna_move_neighbor_diff_cb(vrna_fold_compound_t *fc,
183                           short                *ptable,
184                           vrna_move_t          move,
185                           vrna_callback_move_update *cb,
186                           void                  *data,
187                           unsigned int          options);
188
189
190
191 vrna_move_t *
192 vrna_move_neighbor_diff(vrna_fold_compound_t *fc,
193                        short                *ptable,
194                        vrna_move_t          move,
195                        vrna_move_t          **invalid_moves,
196                        unsigned int          options);
197
198
199
200 #endif /* VIENNA_RNA_PACKAGE_NEIGHBOR_H */

```

## 18.142 ViennaRNA/neighbor.h File Reference

Use [ViennaRNA/landscape/neighbor.h](#) instead.

Include dependency graph for neighbor.h:

### 18.142.1 Detailed Description

Use [ViennaRNA/landscape/neighbor.h](#) instead.

**Deprecated** Use [ViennaRNA/landscape/neighbor.h](#) instead

## 18.143 neighbor.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_NEIGHBOR_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_NEIGHBOR_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/neighbor.h>! Use <ViennaRNA/landscape/neighbor.h>
    instead!"
13 # endif
14 #include <ViennaRNA/landscape/neighbor.h>
15 #include <ViennaRNA/landscape/move.h>
16 #endif
17
18 #endif

```

## 18.144 pair\_mat.h

```

1  #ifndef VIENNA_RNA_PACKAGE_PAIR_MAT_H
2  #define VIENNA_RNA_PACKAGE_PAIR_MAT_H
3
4  #include <ctype.h>
5  #include <ViennaRNA/utils/basic.h>
6  #include <ViennaRNA/fold_vars.h>
7
8  #define NBASES 8
9  /*@nonnull@*/
10
11 #ifndef INLINE
12 #  ifdef __GNUC__
13 #    define INLINE inline
14 #  else
15 #    define INLINE
16 #  endif
17 #endif
18
19 static const char Law_and_Order[] = "_ACGUTXKI";
20 static int BP_pair[NBASES][NBASES] =
21 /* _ A C G U X K I */
22 { { 0, 0, 0, 0, 0, 0, 0, 0 },
23   { 0, 0, 0, 0, 5, 0, 0, 5 },
24   { 0, 0, 0, 1, 0, 0, 0, 0 },
25   { 0, 0, 2, 0, 3, 0, 0, 0 },
26   { 0, 6, 0, 4, 0, 0, 0, 6 },
27   { 0, 0, 0, 0, 0, 0, 2, 0 },
28   { 0, 0, 0, 0, 0, 1, 0, 0 },
29   { 0, 6, 0, 0, 5, 0, 0, 0 } };
30
31 #define MAXALPHA 20 /* maximal length of alphabet */
32
33 static short alias[MAXALPHA + 1];
34 static int pair[MAXALPHA + 1][MAXALPHA + 1];
35 /* rtype[pair[i][j]]:=pair[j][i] */
36 static int rtype[8] = {
37   0, 2, 1, 4, 3, 6, 5, 7
38 };
39
40 #ifdef _OPENMP
41 #pragma omp threadprivate(Law_and_Order, BP_pair, alias, pair, rtype)
42 #endif
43
44 /* for backward compatibility */
45 #define ENCODE(c) encode_char(c)
46
47 static INLINE int
48 encode_char(char c)
49 {
50   /* return numerical representation of base used e.g. in pair[][] */
51   int code;
52
53   c = toupper(c);
54
55   if (energy_set > 0) {
56     code = (int)(c - 'A') + 1;
57   } else {
58     const char *pos;
59     pos = strchr(Law_and_Order, c);
60     if (pos == NULL)
61       code = 0;
62     else
63       code = (int)(pos - Law_and_Order);
64
65     if (code > 5)
66       code = 0;
67
68     if (code > 4)
69       code--; /* make T and U equivalent */
70   }
71
72   return code;
73 }
74
75 /*@+boolint +charint@*/
76 /*@nonnull@*/
77 extern char *nonstandards;
78
79
80 static INLINE void
81 make_pair_matrix(void)
82 {
83   int i, j;
84
85   if (energy_set == 0) {

```



```

86     for (i = 0; i < 5; i++)
87         alias[i] = (short)i;
88     alias[5] = 3; /* X <-> G */
89     alias[6] = 2; /* K <-> C */
90     alias[7] = 0; /* I <-> default base '@' */
91     for (i = 0; i < NBASES; i++)
92         for (j = 0; j < NBASES; j++)
93             pair[i][j] = BP_pair[i][j];
94     if (noGU)
95         pair[3][4] = pair[4][3] = 0;
96
97     if (nonstandards != NULL) {
98         /* allow nonstandard bp's */
99         for (i = 0; i < (int)strlen(nonstandards); i += 2)
100             pair[encode_char(nonstandards[i])]
101                 [encode_char(nonstandards[i + 1])] = 7;
102     }
103
104     for (i = 0; i < NBASES; i++)
105         for (j = 0; j < NBASES; j++)
106             rtype[pair[i][j]] = pair[j][i];
107 } else {
108     for (i = 0; i <= MAXALPHA; i++)
109         for (j = 0; j <= MAXALPHA; j++)
110             pair[i][j] = 0;
111     if (energy_set == 1) {
112         for (i = 1; i < MAXALPHA; ) {
113             alias[i++] = 3; /* A <-> G */
114             alias[i++] = 2; /* B <-> C */
115         }
116         for (i = 1; i < MAXALPHA; i++) {
117             pair[i][i + 1] = 2; /* AB <-> GC */
118             i++;
119             pair[i][i - 1] = 1; /* BA <-> CG */
120         }
121     } else if (energy_set == 2) {
122         for (i = 1; i < MAXALPHA; ) {
123             alias[i++] = 1; /* A <-> A */
124             alias[i++] = 4; /* B <-> U */
125         }
126         for (i = 1; i < MAXALPHA; i++) {
127             pair[i][i + 1] = 5; /* AB <-> AU */
128             i++;
129             pair[i][i - 1] = 6; /* BA <-> UA */
130         }
131     } else if (energy_set == 3) {
132         for (i = 1; i < MAXALPHA - 2; ) {
133             alias[i++] = 3; /* A <-> G */
134             alias[i++] = 2; /* B <-> C */
135             alias[i++] = 1; /* C <-> A */
136             alias[i++] = 4; /* D <-> U */
137         }
138         for (i = 1; i < MAXALPHA - 2; i++) {
139             pair[i][i + 1] = 2; /* AB <-> GC */
140             i++;
141             pair[i][i - 1] = 1; /* BA <-> CG */
142             i++;
143             pair[i][i + 1] = 5; /* CD <-> AU */
144             i++;
145             pair[i][i - 1] = 6; /* DC <-> UA */
146         }
147     } else {
148         vrna_message_error("What energy_set are YOU using??");
149     }
150
151     for (i = 0; i <= MAXALPHA; i++)
152         for (j = 0; j <= MAXALPHA; j++)
153             rtype[pair[i][j]] = pair[j][i];
154 }
155 }
156
157 static INLINE short *
158 encode_sequence(const char *sequence,
159                 short how)
160 {
161     {
162         unsigned int i, l = (unsigned int)strlen(sequence);
163         short *S = (short *)vrna_alloc(sizeof(short) * (l + 2));
164
165         switch (how) {
166             /* standard encoding as always used for S */
167             case 0:
168                 for (i = 1; i <= l; i++) /* make numerical encoding of sequence */
169                     S[i] = (short)encode_char(sequence[i - 1]);
170                 S[l + 1] = S[1];
171                 S[0] = (short)1;
172                 break;

```

```

173      /* encoding for mismatches of nostandard bases (normally used for S1) */
174      case 1:
175          for (i = 1; i <= 1; i++)
176              S[i] = alias[(short)encode_char(sequence[i - 1])];
177              S[1 + 1] = S[1];
178              S[0] = S[1];
179              break;
180      }
181
182      return S;
183  }
184
185
186 #endif /* VIENNA_RNA_PACKAGE_PAIR_MAT_H */

```

## 18.145 ViennaRNA/params.h File Reference

Use [ViennaRNA/params/basic.h](#) instead.

Include dependency graph for params.h:

### 18.145.1 Detailed Description

Use [ViennaRNA/params/basic.h](#) instead.

**Deprecated** Use [ViennaRNA/params/basic.h](#) instead

## 18.146 params.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/params.h>! Use <ViennaRNA/params/basic.h> instead!"
13 #   endif
14 #include <ViennaRNA/params/basic.h>
15 #endif
16
17 #endif

```

## 18.147 ViennaRNA/params/1.8.4\_epars.h File Reference

Free energy parameters for parameter file conversion.

### 18.147.1 Detailed Description

Free energy parameters for parameter file conversion.

This file contains the free energy parameters used in ViennaRNAPackage 1.8.4. They are summarized in:

D.H.Mathews, J. Sabina, M. Zuker, D.H. Turner "Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure" JMB, 288, pp 911-940, 1999

Enthalpies taken from:

A. Walter, D Turner, J Kim, M Lyttle, P M"uller, D Mathews, M Zuker "Coaxial stckaing of helices enhances binding of oligoribonucleotides.." PNAS, 91, pp 9218-9222, 1994 D.H. Turner, N. Sugimoto, and S.M. Freier. "RNA Structure Prediction", Ann. Rev. Biophys. Biophys. Chem. 17, 167-192, 1988. John A.Jaeger, Douglas H.Turner, and Michael Zuker. "Improved predictions of secondary structures for RNA", PNAS, 86, 7706-7710, October 1989. L. He, R. Kierzek, J. SantaLucia, A.E. Walter, D.H. Turner "Nearest-Neughbor Parameters for GU Mismatches...." ↔ Biochemistry 1991, 30 11124-11132 A.E. Peritz, R. Kierzek, N. Sugimoto, D.H. Turner "Thermodynamic Study of Internal Loops in Oligoribonucleotides..." Biochemistry 1991, 30, 6428-6435

## 18.148 1.8.4\_epars.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_OLD_EPARS__

```

```

2 #define VIENNA_RNA_PACKAGE_OLD_EPARS__
39 #define K0 273.15
40 #ifndef INF
41 #undef INF
42 #endif
43 #define INF 1000000
44 #define NBPAIRS 7
45 #define NST 0 /* Energy for nonstandard stacked pairs */
46 #define DEF -50 /* Default terminal mismatch, used for I */
47 /* and any non_pairing bases */
48 #define NSM 0 /* terminal mismatch for non standard pairs */
49
50 PRIVATE double Tmeasure_184 = 37 + K0; /* temperature of param measurements */
51 PRIVATE double lxc37_184 = 107.856; /* parameter for logarithmic loop
52 energy extrapolation */
53
54 PRIVATE int stack37_184[NBPAIRS+1][NBPAIRS+1] =
55 /*
56 { { INF, INF, INF, INF, INF, INF, INF, INF},
57 { INF, -240, -330, -210, -140, -210, -210, NST},
58 { INF, -330, -340, -250, -150, -220, -240, NST},
59 { INF, -210, -250, 130, -50, -140, -130, NST},
60 { INF, -140, -150, -50, 30, -60, -100, NST},
61 { INF, -210, -220, -140, -60, -110, -90, NST},
62 { INF, -210, -240, -130, -100, -90, -130, NST},
63 { INF, NST, NST, NST, NST, NST, NST, NST}};
64
65 /* enthalpies (0.01*kcal/mol at 37 C) for stacked pairs */
66 /* different from mfold-2.3, which uses values from mfold-2.2 */
67 PRIVATE int enthalpies_184[NBPAIRS+1][NBPAIRS+1] =
68 /*
69 { { INF, INF, INF, INF, INF, INF, INF, INF},
70 { INF, -1060, -1340, -1210, -560, -1050, -1040, NST},
71 { INF, -1340, -1490, -1260, -830, -1140, -1240, NST},
72 { INF, -1210, -1260, -1460, -1350, -880, -1280, NST},
73 { INF, -560, -830, -1350, -930, -320, -700, NST},
74 { INF, -1050, -1140, -880, -320, -940, -680, NST},
75 { INF, -1040, -1240, -1280, -700, -680, -770, NST},
76 { INF, NST, NST, NST, NST, NST, NST, NST}};
77
78
79 /* old values are here just for comparison */
80 PRIVATE int oldhairpin37_184[31] = { /* from ViennaRNA 1.3 */
81 INF, INF, INF, 410, 490, 440, 470, 500, 510, 520, 531,
82 542, 551, 560, 568, 575, 582, 589, 595, 601, 606,
83 611, 616, 621, 626, 630, 634, 638, 642, 646, 650};
84
85 PRIVATE int hairpin37_184[31] = {
86 INF, INF, INF, 570, 560, 560, 540, 590, 560, 640, 650,
87 660, 670, 678, 686, 694, 701, 707, 713, 719, 725,
88 730, 735, 740, 744, 749, 753, 757, 761, 765, 769};
89
90 PRIVATE int oldbulge37_184[31] = {
91 INF, 390, 310, 350, 420, 480, 500, 516, 531, 543, 555,
92 565, 574, 583, 591, 598, 605, 612, 618, 624, 630,
93 635, 640, 645, 649, 654, 658, 662, 666, 670, 673};
94
95 PRIVATE int bulge37_184[31] = {
96 INF, 380, 280, 320, 360, 400, 440, 459, 470, 480, 490,
97 500, 510, 519, 527, 534, 541, 548, 554, 560, 565,
98 571, 576, 580, 585, 589, 594, 598, 602, 605, 609};
99
100 PRIVATE int oldinternal_loop37_184[31] = {
101 INF, INF, 410, 510, 490, 530, 570, 587, 601, 614, 625,
102 635, 645, 653, 661, 669, 676, 682, 688, 694, 700,
103 705, 710, 715, 720, 724, 728, 732, 736, 740, 744};
104
105 PRIVATE int internal_loop37_184[31] = {
106 INF, INF, 410, 510, 170, 180, 200, 220, 230, 240, 250,
107 260, 270, 278, 286, 294, 301, 307, 313, 319, 325,
108 330, 335, 340, 345, 349, 353, 357, 361, 365, 369};
109
110 /* terminal mismatches */
111 /* mismatch free energies for interior loops at 37C */
112 PRIVATE int mismatchI37_184[NBPAIRS+1][5][5] =
113 { /* @@ */
114 {{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0}},
115 { /* CG */
116 { 0, 0, 0, 0, 0}, /* @@ @A @C @G @U */
117 { 0, 0, 0, -110, 0}, /* A@ AA AC AG AU */
118 { 0, 0, 0, 0, 0}, /* C@ CA CC CG CU */
119 { 0, -110, 0, 0, 0}, /* G@ GA GC GG GU */
120 { 0, 0, 0, 0, -70}}, /* U@ UA UC UG UU */
121 { /* GC */
122 { 0, 0, 0, 0, 0}, /* @@ @A @C @G @U */
123 { 0, 0, 0, -110, 0}, /* A@ AA AC AG AU */
124 { 0, 0, 0, 0, 0}, /* C@ CA CC CG CU */

```

```

125 { 0, -110, 0, 0, 0}, /* G@ GA GC GG GU */
126 { 0, 0, 0, 0, -70}, /* U@ UA UC UG UU */
127 { /* GU */
128 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
129 { 0, 70, 70, -40, 70}, /* A@ AA AC AG AU */
130 { 0, 70, 70, 70, 70}, /* C@ CA CC CG CU */
131 { 0, -40, 70, 70, 70}, /* G@ GA GC GG GU */
132 { 0, 70, 70, 70, 0}, /* U@ UA UC UG UU */
133 { /* UG */
134 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
135 { 0, 70, 70, -40, 70}, /* A@ AA AC AG AU */
136 { 0, 70, 70, 70, 70}, /* C@ CA CC CG CU */
137 { 0, -40, 70, 70, 70}, /* G@ GA GC GG GU */
138 { 0, 70, 70, 70, 0}, /* U@ UA UC UG UU */
139 { /* AU */
140 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
141 { 0, 70, 70, -40, 70}, /* A@ AA AC AG AU */
142 { 0, 70, 70, 70, 70}, /* C@ CA CC CG CU */
143 { 0, -40, 70, 70, 70}, /* G@ GA GC GG GU */
144 { 0, 70, 70, 70, 0}, /* U@ UA UC UG UU */
145 { /* UA */
146 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
147 { 0, 70, 70, -40, 70}, /* A@ AA AC AG AU */
148 { 0, 70, 70, 70, 70}, /* C@ CA CC CG CU */
149 { 0, -40, 70, 70, 70}, /* G@ GA GC GG GU */
150 { 0, 70, 70, 70, 0}, /* U@ UA UC UG UU */
151 { /* @@ */
152 { 90, 90, 90, 90, 90}, { 90, 90, 90, 90, -20}, { 90, 90, 90, 90, 90},
153 { 90, -20, 90, 90, 90}, { 90, 90, 90, 90, 20}}
154 };
155
156 /* mismatch free energies for hairpins at 37C */
157 PRIVATE int mismatchH37_184[NBPAIRS+1][5][5] =
158 { /* @@ */
159 {{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0}},
160 { /* CG */
161 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
162 {-90, -150, -150, -140, -180}, /* A@ AA AC AG AU */
163 {-90, -100, -90, -290, -80}, /* C@ CA CC CG CU */
164 {-90, -220, -200, -160, -110}, /* G@ GA GC GG GU */
165 {-90, -170, -140, -180, -200}, /* U@ UA UC UG UU */
166 { /* GC */
167 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
168 {-70, -110, -150, -130, -210}, /* A@ AA AC AG AU */
169 {-70, -110, -70, -240, -50}, /* C@ CA CC CG CU */
170 {-70, -240, -290, -140, -120}, /* G@ GA GC GG GU */
171 {-70, -190, -100, -220, -150}, /* U@ UA UC UG UU */
172 { /* GU */
173 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
174 { 0, 20, -50, -30, -30}, /* A@ AA AC AG AU */
175 { 0, -10, -20, -150, -20}, /* C@ CA CC CG CU */
176 { 0, -90, -110, -30, 0}, /* G@ GA GC GG GU */
177 { 0, -30, -30, -40, -110}, /* U@ UA UC UG UU */
178 { /* UG */
179 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
180 { 0, -50, -30, -60, -50}, /* A@ AA AC AG AU */
181 { 0, -20, -10, -170, 0}, /* C@ CA CC CG CU */
182 { 0, -80, -120, -30, -70}, /* G@ GA GC GG GU */
183 { 0, -60, -10, -60, -80}, /* U@ UA UC UG UU */
184 { /* AU */
185 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
186 { 0, -30, -50, -30, -30}, /* A@ AA AC AG AU */
187 { 0, -10, -20, -150, -20}, /* C@ CA CC CG CU */
188 { 0, -110, -120, -20, 20}, /* G@ GA GC GG GU */
189 { 0, -30, -30, -60, -110}, /* U@ UA UC UG UU */
190 { /* UA */
191 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
192 { 0, -50, -30, -60, -50}, /* A@ AA AC AG AU */
193 { 0, -20, -10, -120, -0}, /* C@ CA CC CG CU */
194 { 0, -140, -120, -70, -20}, /* G@ GA GC GG GU */
195 { 0, -30, -10, -50, -80}, /* U@ UA UC UG UU */
196 { /* @@ */
197 { 0, 0, 0, 0, 0}, { 0, 0, 0, 0, 0}, { 0, 0, 0, 0, 0},
198 { 0, 0, 0, 0, 0}, { 0, 0, 0, 0, 0}}
199 };
200
201 /* mismatch energies in multiloops */
202 PRIVATE int mismatchM37_184[NBPAIRS+1][5][5];
203
204 /* these are probably junk */
205 /* mismatch enthalpies for temperature scaling */
206 PRIVATE int mism_H_184[NBPAIRS+1][5][5] =
207 { /* no pair */
208 {{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0},{0,0,0,0,0}},
209 { /* CG */
210 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
211 { DEF, -1030, -950, -1030, -1030}, /* A@ AA AC AG AU */

```

```

212 { DEF, -520, -450, -520, -670}, /* C@ CA CC CG CU */
213 { DEF, -940, -940, -940, -940}, /* G@ GA GC GG GU */
214 { DEF, -810, -740, -810, -860}}, /* U@ UA UC UG UU */
215 { /* GC */
216 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
217 { DEF, -520, -880, -560, -880}, /* A@ AA AC AG AU */
218 { DEF, -720, -310, -310, -390}, /* C@ CA CC CG CU */
219 { DEF, -710, -740, -620, -740}, /* G@ GA GC GG GU */
220 { DEF, -500, -500, -500, -570}}, /* U@ UA UC UG UU */
221 { /* GU */
222 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
223 { DEF, -430, -600, -600, -600}, /* A@ AA AC AG AU */
224 { DEF, -260, -240, -240, -240}, /* C@ CA CC CG CU */
225 { DEF, -340, -690, -690, -690}, /* G@ GA GC GG GU */
226 { DEF, -330, -330, -330, -330}}, /* U@ UA UC UG UU */
227 { /* UG */
228 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
229 { DEF, -720, -790, -960, -810}, /* A@ AA AC AG AU */
230 { DEF, -480, -480, -360, -480}, /* C@ CA CC CG CU */
231 { DEF, -660, -810, -920, -810}, /* G@ GA GC GG GU */
232 { DEF, -550, -440, -550, -360}}, /* U@ UA UC UG UU */
233 { /* AU */
234 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
235 { DEF, -430, -600, -600, -600}, /* A@ AA AC AG AU */
236 { DEF, -260, -240, -240, -240}, /* C@ CA CC CG CU */
237 { DEF, -340, -690, -690, -690}, /* G@ GA GC GG GU */
238 { DEF, -330, -330, -330, -330}}, /* U@ UA UC UG UU */
239 { /* UA */
240 { 0, 0, 0, 0, 0}, /* @A @C @G @U */
241 { DEF, -400, -630, -890, -590}, /* A@ AA AC AG AU */
242 { DEF, -430, -510, -200, -180}, /* C@ CA CC CG CU */
243 { DEF, -380, -680, -890, -680}, /* G@ GA GC GG GU */
244 { DEF, -280, -140, -280, -140}}, /* U@ UA UC UG UU */
245 { /* nonstandard pair */
246 {DEF,DEF,DEF,DEF,DEF},{DEF,DEF,DEF,DEF,DEF},{DEF,DEF,DEF,DEF,DEF},
247 {DEF,DEF,DEF,DEF,DEF},{DEF,DEF,DEF,DEF,DEF}}
248 };
249
250 /* 5' dangling ends (unpaired base stacks on first paired base) */
251 PRIVATE int dangle5_37_184[NBPAIRS+1][5]=
252 { /* @ A C G U */
253 { INF, INF, INF, INF, INF}, /* no pair */
254 { INF, -50, -30, -20, -10}, /* CG (stacks on C) */
255 { INF, -20, -30, -0, -0}, /* GC (stacks on G) */
256 { INF, -30, -30, -40, -20}, /* GU */
257 { INF, -30, -10, -20, -20}, /* UG */
258 { INF, -30, -30, -40, -20}, /* AU */
259 { INF, -30, -10, -20, -20}, /* UA */
260 { 0, 0, 0, 0, 0} /* @ */
261 };
262
263 /* 3' dangling ends (unpaired base stacks on second paired base */
264 PRIVATE int dangle3_37_184[NBPAIRS+1][5]=
265 { /* @ A C G U */
266 { INF, INF, INF, INF, INF}, /* no pair */
267 { INF, -110, -40, -130, -60}, /* CG (stacks on G) */
268 { INF, -170, -80, -170, -120}, /* GC */
269 { INF, -70, -10, -70, -10}, /* GU */
270 { INF, -80, -50, -80, -60}, /* UG */
271 { INF, -70, -10, -70, -10}, /* AU */
272 { INF, -80, -50, -80, -60}, /* UA */
273 { 0, 0, 0, 0, 0} /* @ */
274 };
275
276 /* enthalpies for temperature scaling */
277 PRIVATE int dangle3_H_184[NBPAIRS+1][5] =
278 { /* @ A C G U */
279 { INF, INF, INF, INF, INF}, /* no pair */
280 { 0, -740, -280, -640, -360},
281 { 0, -900, -410, -860, -750},
282 { 0, -740, -240, -720, -490},
283 { 0, -490, -90, -550, -230},
284 { 0, -570, -70, -580, -220},
285 { 0, -490, -90, -550, -230},
286 { 0, 0, 0, 0, 0}
287 };
288
289 PRIVATE int dangle5_H_184[NBPAIRS+1][5] =
290 { /* @ A C G U */
291 { INF, INF, INF, INF, INF}, /* no pair */
292 { 0, -240, 330, 80, -140},
293 { 0, -160, 70, -460, -40},
294 { 0, 160, 220, 70, 310},
295 { 0, -150, 510, 10, 100},
296 { 0, 160, 220, 70, 310},
297 { 0, -50, 690, -60, -60},
298 { 0, 0, 0, 0, 0}

```

```

299 };
300
301
302 /* constants for linearly destabilizing contributions for multi-loops
303    F = ML_closing + ML_intern*k + ML_BASE*u */
304 /* old versions erroneously used ML_intern*(k-1) */
305 PRIVATE int ML_BASE37_184 = 0;
306 PRIVATE int ML_closing37_184 = 340;
307 PRIVATE int ML_intern37_184 = 40;
308
309 /* Ninio-correction for asymmetric internal loops with branches n1 and n2 */
310 /*    ninio_energy = min{max_ninio, |n1-n2|*F_ninio[min{4.0, n1, n2}] } */
311 PRIVATE int MAX_NINIO_184 = 300; /* maximum correction */
312 PRIVATE int F_ninio37_184[5] = { 0, 40, 50, 20, 10 }; /* only F[2] used */
313
314 /* stabilizing contribution due to special hairpins of size 4 (tetraloops) */
315
316 PRIVATE char Tetraloops_184[1400] = /* place for up to 200 tetra loops */
317 "GGGGAC "
318 "GGUGAC "
319 "CGAAAG "
320 "GGAGAC "
321 "CGCAAG "
322 "GGAAAC "
323 "CGGAAG "
324 "CUUCGG "
325 "CGUGAG "
326 "CGAAGG "
327 "CUACGG "
328 "GGCAAC "
329 "CGCGAG "
330 "UGAGAG "
331 "CGAGAG "
332 "AGAAAU "
333 "CGUAAG "
334 "CUAACG "
335 "UGAAAG "
336 "GGAAGC "
337 "GGGAAC "
338 "UGAAAA "
339 "AGCAAU "
340 "AGUAAU "
341 "CGGGAG "
342 "AGUGAU "
343 "GGCGAC "
344 "GGGAGC "
345 "GUGAAC "
346 "UGGAAA "
347 ;
348
349 PRIVATE int TETRA_ENERGY37_184[200] = {
350 -300, -300, -300, -300, -300, -300, -300, -300, -300, -300, -250, -250, -250,
351 -250, -250, -200, -200, -200, -200, -200, -200, -150, -150, -150, -150, -150,
352 -150, -150, -150, -150, -150, -150};
353
354 PRIVATE int TETRA_ENTH37_184 = -400;
355
356 PRIVATE char Triloops_184[241] = "";
357
358 PRIVATE int Triloop_E37_184[40];
359
360 /* penalty for AU (or GU) terminating helix) */
361 /* mismatches already contain these */
362 PRIVATE int TerminalAU_184 = 50;
363
364 /* penalty for forming a bi-molecular duplex */
365 PRIVATE int DuplexInit_184 = 410;
366
367 #endif

```

## 18.149 ViennaRNA/params/1.8.4\_intloops.h File Reference

Free energy parameters for interior loop contributions needed by the parameter file conversion functions.

### 18.149.1 Detailed Description

Free energy parameters for interior loop contributions needed by the parameter file conversion functions.

## 18.150 1.8.4\_intloops.h

[Go to the documentation of this file.](#)

```

1
2 PRIVATE int int11_37_184[NBPAIRS+1][NBPAIRS+1][5][5] =
3 { /* noPair */ {{0}}},
4 { /* noPair */ {{0}}},
5 /* CG..CG */
6 {{ 110, 110, 110, 110, 110},
7 { 110, 110, 40, 40, 40},
8 { 110, 40, 40, 40, 40},
9 { 110, 40, 40, -140, 40},
10 { 110, 40, 40, 40, 40}
11 },
12 /* CG..GC */
13 {{ 110, 110, 110, 110, 110},
14 { 110, 40, -40, 40, 40},
15 { 110, 30, 50, 40, 50},
16 { 110, -10, 40, -170, 40},
17 { 110, 40, 0, 40, -30}
18 },
19 /* CG..GU */
20 {{ 110, 110, 110, 110, 110},
21 { 110, 110, 110, 110, 110},
22 { 110, 110, 110, 110, 110},
23 { 110, 110, 110, -100, 110},
24 { 110, 110, 110, 110, 110}
25 },
26 /* CG..UG */
27 {{ 110, 110, 110, 110, 110},
28 { 110, 110, 110, 110, 110},
29 { 110, 110, 110, 110, 110},
30 { 110, 110, 110, -100, 110},
31 { 110, 110, 110, 110, 110}
32 },
33 /* CG..AU */
34 {{ 110, 110, 110, 110, 110},
35 { 110, 110, 110, 110, 110},
36 { 110, 110, 110, 110, 110},
37 { 110, 110, 110, -100, 110},
38 { 110, 110, 110, 110, 110}
39 },
40 /* CG..UA */
41 {{ 110, 110, 110, 110, 110},
42 { 110, 110, 110, 110, 110},
43 { 110, 110, 110, 110, 110},
44 { 110, 110, 110, -100, 110},
45 { 110, 110, 110, 110, 110}
46 },
47 /* CG..?? */
48 {{ 110, 110, 110, 110, 110},
49 { 110, 110, 110, 110, 110},
50 { 110, 110, 110, 110, 110},
51 { 110, 110, 110, 110, 110},
52 { 110, 110, 110, 110, 110}
53 },
54 { /* noPair */ {{0}}},
55 /* GC..CG */
56 {{ 110, 110, 110, 110, 110},
57 { 110, 40, 30, -10, 40},
58 { 110, -40, 50, 40, 0},
59 { 110, 40, 40, -170, 40},
60 { 110, 40, 50, 40, -30}
61 },
62 /* GC..GC */
63 {{ 110, 110, 110, 110, 110},
64 { 110, 80, 40, 40, 40},
65 { 110, 40, 40, 40, 40},
66 { 110, 40, 40, -210, 40},
67 { 110, 40, 40, 40, -70}
68 },
69 /* GC..GU */
70 {{ 110, 110, 110, 110, 110},
71 { 110, 110, 110, 110, 110},
72 { 110, 110, 110, 110, 110},
73 { 110, 110, 110, -100, 110},
74 { 110, 110, 110, 110, 110}
75 },
76 /* GC..UG */
77 {{ 110, 110, 110, 110, 110},
78 { 110, 110, 110, 110, 110},
79 { 110, 110, 110, 110, 110},
80 { 110, 110, 110, -100, 110},
81 { 110, 110, 110, 110, 110}
82 },
83

```

```

89 /* GC..AU */
90 {{ 110, 110, 110, 110, 110},
91 { 110, 110, 110, 110, 110},
92 { 110, 110, 110, 110, 110},
93 { 110, 110, 110, -100, 110},
94 { 110, 110, 110, 110, 100}
95 },
96 /* GC..UA */
97 {{ 110, 110, 110, 110, 110},
98 { 110, 110, 110, 110, 110},
99 { 110, 110, 110, 110, 110},
100 { 110, 110, 110, -100, 110},
101 { 110, 110, 110, 110, 110}
102 },
103 /* GC..?? */
104 {{ 110, 110, 110, 110, 110},
105 { 110, 110, 110, 110, 110},
106 { 110, 110, 110, 110, 110},
107 { 110, 110, 110, 110, 110},
108 { 110, 110, 110, 110, 110}
109 }
110 },
111 { /* noPair */ {{0}},
112 /* GU..CG */
113 {{ 110, 110, 110, 110, 110},
114 { 110, 110, 110, 110, 110},
115 { 110, 110, 110, 110, 110},
116 { 110, 110, 110, -100, 110},
117 { 110, 110, 110, 110, 110}
118 },
119 /* GU..GC */
120 {{ 110, 110, 110, 110, 110},
121 { 110, 110, 110, 110, 110},
122 { 110, 110, 110, 110, 110},
123 { 110, 110, 110, -100, 110},
124 { 110, 110, 110, 110, 110}
125 },
126 /* GU..GU */
127 {{ 170, 170, 170, 170, 170},
128 { 170, 170, 170, 170, 170},
129 { 170, 170, 170, 170, 170},
130 { 170, 170, 170, -40, 170},
131 { 170, 170, 170, 170, 170}
132 },
133 /* GU..UG */
134 {{ 170, 170, 170, 170, 170},
135 { 170, 170, 170, 170, 170},
136 { 170, 170, 170, 170, 170},
137 { 170, 170, 170, -40, 170},
138 { 170, 170, 170, 170, 170}
139 },
140 /* GU..AU */
141 {{ 170, 170, 170, 170, 170},
142 { 170, 170, 170, 170, 170},
143 { 170, 170, 170, 170, 170},
144 { 170, 170, 170, -40, 170},
145 { 170, 170, 170, 170, 170}
146 },
147 /* GU..UA */
148 {{ 170, 170, 170, 170, 170},
149 { 170, 170, 170, 170, 170},
150 { 170, 170, 170, 170, 170},
151 { 170, 170, 170, -40, 170},
152 { 170, 170, 170, 170, 170}
153 },
154 /* GU..?? */
155 {{ 170, 170, 170, 170, 170},
156 { 170, 170, 170, 170, 170},
157 { 170, 170, 170, 170, 170},
158 { 170, 170, 170, 170, 170},
159 { 170, 170, 170, 170, 170}
160 }
161 },
162 { /* noPair */ {{0}},
163 /* UG..CG */
164 {{ 110, 110, 110, 110, 110},
165 { 110, 110, 110, 110, 110},
166 { 110, 110, 110, 110, 110},
167 { 110, 110, 110, -100, 110},
168 { 110, 110, 110, 110, 110}
169 },
170 /* UG..GC */
171 {{ 110, 110, 110, 110, 110},
172 { 110, 110, 110, 110, 110},
173 { 110, 110, 110, 110, 110},
174 { 110, 110, 110, -100, 110},
175 { 110, 110, 110, 110, 110}

```



```

176 },
177 /* UG..GU */
178 {{ 170, 170, 170, 170, 170},
179 { 170, 170, 170, 170, 170},
180 { 170, 170, 170, 170, 170},
181 { 170, 170, 170, -40, 170},
182 { 170, 170, 170, 170, 170}
183 },
184 /* UG..UG */
185 {{ 170, 170, 170, 170, 170},
186 { 170, 170, 170, 170, 170},
187 { 170, 170, 170, 170, 170},
188 { 170, 170, 170, -40, 170},
189 { 170, 170, 170, 170, 170}
190 },
191 /* UG..AU */
192 {{ 170, 170, 170, 170, 170},
193 { 170, 170, 170, 170, 170},
194 { 170, 170, 170, 170, 170},
195 { 170, 170, 170, -40, 170},
196 { 170, 170, 170, 170, 170}
197 },
198 /* UG..UA */
199 {{ 170, 170, 170, 170, 170},
200 { 170, 170, 170, 170, 170},
201 { 170, 170, 170, 170, 170},
202 { 170, 170, 170, -40, 170},
203 { 170, 170, 170, 170, 170}
204 },
205 /* UG..?? */
206 {{ 170, 170, 170, 170, 170},
207 { 170, 170, 170, 170, 170},
208 { 170, 170, 170, 170, 170},
209 { 170, 170, 170, 170, 170},
210 { 170, 170, 170, 170, 170}
211 }
212 },
213 { /* noPair */ {{0}},
214 /* AU..CG */
215 {{ 110, 110, 110, 110, 110},
216 { 110, 110, 110, 110, 110},
217 { 110, 110, 110, 110, 110},
218 { 110, 110, 110, -100, 110},
219 { 110, 110, 110, 110, 110}
220 },
221 /* AU..GC */
222 {{ 110, 110, 110, 110, 110},
223 { 110, 110, 110, 110, 110},
224 { 110, 110, 110, 110, 110},
225 { 110, 110, 110, -100, 110},
226 { 110, 110, 110, 110, 100}
227 },
228 /* AU..GU */
229 {{ 170, 170, 170, 170, 170},
230 { 170, 170, 170, 170, 170},
231 { 170, 170, 170, 170, 170},
232 { 170, 170, 170, -40, 170},
233 { 170, 170, 170, 170, 170}
234 },
235 /* AU..UG */
236 {{ 170, 170, 170, 170, 170},
237 { 170, 170, 170, 170, 170},
238 { 170, 170, 170, 170, 170},
239 { 170, 170, 170, -40, 170},
240 { 170, 170, 170, 170, 170}
241 },
242 /* AU..AU */
243 {{ 170, 170, 170, 170, 170},
244 { 170, 170, 170, 170, 170},
245 { 170, 170, 170, 170, 170},
246 { 170, 170, 170, -40, 170},
247 { 170, 170, 170, 170, 120}
248 },
249 /* AU..UA */
250 {{ 170, 170, 170, 170, 170},
251 { 170, 170, 170, 170, 170},
252 { 170, 170, 170, 170, 170},
253 { 170, 170, 170, -40, 170},
254 { 170, 170, 170, 170, 150}
255 },
256 /* AU..?? */
257 {{ 170, 170, 170, 170, 170},
258 { 170, 170, 170, 170, 170},
259 { 170, 170, 170, 170, 170},
260 { 170, 170, 170, 170, 170},
261 { 170, 170, 170, 170, 170}
262 }

```

```

263 },
264 { /* noPair */ {{0}},
265 /* UA..CG */
266 {{ 110, 110, 110, 110, 110}},
267 { 110, 110, 110, 110, 110},
268 { 110, 110, 110, 110, 110},
269 { 110, 110, 110, -100, 110},
270 { 110, 110, 110, 110, 110}
271 },
272 /* UA..GC */
273 {{ 110, 110, 110, 110, 110}},
274 { 110, 110, 110, 110, 110},
275 { 110, 110, 110, 110, 110},
276 { 110, 110, 110, -100, 110},
277 { 110, 110, 110, 110, 110}
278 },
279 /* UA..GU */
280 {{ 170, 170, 170, 170, 170}},
281 { 170, 170, 170, 170, 170},
282 { 170, 170, 170, 170, 170},
283 { 170, 170, 170, -40, 170},
284 { 170, 170, 170, 170, 170}
285 },
286 /* UA..UG */
287 {{ 170, 170, 170, 170, 170}},
288 { 170, 170, 170, 170, 170},
289 { 170, 170, 170, 170, 170},
290 { 170, 170, 170, -40, 170},
291 { 170, 170, 170, 170, 170}
292 },
293 /* UA..AU */
294 {{ 170, 170, 170, 170, 170}},
295 { 170, 170, 170, 170, 170},
296 { 170, 170, 170, 170, 170},
297 { 170, 170, 170, -40, 170},
298 { 170, 170, 170, 170, 150}
299 },
300 /* UA..UA */
301 {{ 170, 170, 170, 170, 170}},
302 { 170, 170, 170, 170, 170},
303 { 170, 170, 170, 170, 170},
304 { 170, 170, 170, -40, 170},
305 { 170, 170, 170, 170, 180}
306 },
307 /* UA..?? */
308 {{ 170, 170, 170, 170, 170}},
309 { 170, 170, 170, 170, 170},
310 { 170, 170, 170, 170, 170},
311 { 170, 170, 170, 170, 170},
312 { 170, 170, 170, 170, 170}
313 }
314 },
315 { /* noPair */ {{0}},
316 /* ??..CG */
317 {{ 110, 110, 110, 110, 110}},
318 { 110, 110, 110, 110, 110},
319 { 110, 110, 110, 110, 110},
320 { 110, 110, 110, 110, 110},
321 { 110, 110, 110, 110, 110}
322 },
323 /* ??..GC */
324 {{ 110, 110, 110, 110, 110}},
325 { 110, 110, 110, 110, 110},
326 { 110, 110, 110, 110, 110},
327 { 110, 110, 110, 110, 110},
328 { 110, 110, 110, 110, 110}
329 },
330 /* ??..GU */
331 {{ 170, 170, 170, 170, 170}},
332 { 170, 170, 170, 170, 170},
333 { 170, 170, 170, 170, 170},
334 { 170, 170, 170, 170, 170},
335 { 170, 170, 170, 170, 170}
336 },
337 /* ??..UG */
338 {{ 170, 170, 170, 170, 170}},
339 { 170, 170, 170, 170, 170},
340 { 170, 170, 170, 170, 170},
341 { 170, 170, 170, 170, 170},
342 { 170, 170, 170, 170, 170}
343 },
344 /* ??..AU */
345 {{ 170, 170, 170, 170, 170}},
346 { 170, 170, 170, 170, 170},
347 { 170, 170, 170, 170, 170},
348 { 170, 170, 170, 170, 170},
349 { 170, 170, 170, 170, 170}

```

```

350 },
351 /* ??..UA */
352 {{ 170, 170, 170, 170, 170},
353 { 170, 170, 170, 170, 170},
354 { 170, 170, 170, 170, 170},
355 { 170, 170, 170, 170, 170},
356 { 170, 170, 170, 170, 170}
357 },
358 /* ??..?? */
359 {{ 170, 170, 170, 170, 170},
360 { 170, 170, 170, 170, 170},
361 { 170, 170, 170, 170, 170},
362 { 170, 170, 170, 170, 170},
363 { 170, 170, 170, 170, 170}
364 }
365 }
366 };
367
368 PRIVATE int int11_H_184[NBPAIRS+1][NBPAIRS+1][5][5] =
369 /* GC..GC */
370 { /* noPair */ {{0}},
371 { /* noPair */ {{0}},
372 { { 0, 0, 0, 0, 0},
373 { 0, 0, 0, 0, 0},
374 { 0, 0, 0, 0, 0},
375 { 0, 0, 0, 0, 0},
376 { 0, 0, 0, 0, 0}},
377 /* GC..CG */
378 { { 0, 0, 0, 0, 0},
379 { 0, 0, 0, 0, 0},
380 { 0, 0, 0, 0, 0},
381 { 0, 0, 0, 0, 0},
382 { 0, 0, 0, 0, 0}},
383 /* GC..GU */
384 { { 0, 0, 0, 0, 0},
385 { 0, 0, 0, 0, 0},
386 { 0, 0, 0, 0, 0},
387 { 0, 0, 0, 0, 0},
388 { 0, 0, 0, 0, 0}},
389 /* GC..UG */
390 { { 0, 0, 0, 0, 0},
391 { 0, 0, 0, 0, 0},
392 { 0, 0, 0, 0, 0},
393 { 0, 0, 0, 0, 0},
394 { 0, 0, 0, 0, 0}},
395 /* GC..AU */
396 { { 0, 0, 0, 0, 0},
397 { 0, 0, 0, 0, 0},
398 { 0, 0, 0, 0, 0},
399 { 0, 0, 0, 0, 0},
400 { 0, 0, 0, 0, 0}},
401 /* GC..UA */
402 { { 0, 0, 0, 0, 0},
403 { 0, 0, 0, 0, 0},
404 { 0, 0, 0, 0, 0},
405 { 0, 0, 0, 0, 0},
406 { 0, 0, 0, 0, 0}},
407 /* GC.. @ */
408 { { 0, 0, 0, 0, 0},
409 { 0, 0, 0, 0, 0},
410 { 0, 0, 0, 0, 0},
411 { 0, 0, 0, 0, 0},
412 { 0, 0, 0, 0, 0}},
413 /* CG..GC */
414 { /* noPair */ {{0}},
415 { { 0, 0, 0, 0, 0},
416 { 0, 0, 0, 0, 0},
417 { 0, 0, 0, 0, 0},
418 { 0, 0, 0, 0, 0},
419 { 0, 0, 0, 0, 0}},
420 /* CG..CG */
421 { { 0, 0, 0, 0, 0},
422 { 0, 0, 0, 0, 0},
423 { 0, 0, 0, 0, 0},
424 { 0, 0, 0, 0, 0},
425 { 0, 0, 0, 0, 0}},
426 /* CG..GU */
427 { { 0, 0, 0, 0, 0},
428 { 0, 0, 0, 0, 0},
429 { 0, 0, 0, 0, 0},
430 { 0, 0, 0, 0, 0},
431 { 0, 0, 0, 0, 0}},
432 /* CG..UG */
433 { { 0, 0, 0, 0, 0},
434 { 0, 0, 0, 0, 0},
435 { 0, 0, 0, 0, 0},
436 { 0, 0, 0, 0, 0},

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437 { 0, 0, 0, 0, 0},
438 /* CG..AU */
439 { { 0, 0, 0, 0, 0},
440 { 0, 0, 0, 0, 0},
441 { 0, 0, 0, 0, 0},
442 { 0, 0, 0, 0, 0},
443 { 0, 0, 0, 0, 0}},
444 /* CG..UA */
445 { { 0, 0, 0, 0, 0},
446 { 0, 0, 0, 0, 0},
447 { 0, 0, 0, 0, 0},
448 { 0, 0, 0, 0, 0},
449 { 0, 0, 0, 0, 0}},
450 /* CG.. @ */
451 { { 0, 0, 0, 0, 0},
452 { 0, 0, 0, 0, 0},
453 { 0, 0, 0, 0, 0},
454 { 0, 0, 0, 0, 0},
455 { 0, 0, 0, 0, 0}},
456 /* GU..GC */
457 { /* noPair */ {{0}},
458 { { 0, 0, 0, 0, 0},
459 { 0, 0, 0, 0, 0},
460 { 0, 0, 0, 0, 0},
461 { 0, 0, 0, 0, 0},
462 { 0, 0, 0, 0, 0}},
463 /* GU..CG */
464 { { 0, 0, 0, 0, 0},
465 { 0, 0, 0, 0, 0},
466 { 0, 0, 0, 0, 0},
467 { 0, 0, 0, 0, 0},
468 { 0, 0, 0, 0, 0}},
469 /* GU..GU */
470 { { 0, 0, 0, 0, 0},
471 { 0, 0, 0, 0, 0},
472 { 0, 0, 0, 0, 0},
473 { 0, 0, 0, 0, 0},
474 { 0, 0, 0, 0, 0}},
475 /* GU..UG */
476 { { 0, 0, 0, 0, 0},
477 { 0, 0, 0, 0, 0},
478 { 0, 0, 0, 0, 0},
479 { 0, 0, 0, 0, 0},
480 { 0, 0, 0, 0, 0}},
481 /* GU..AU */
482 { { 0, 0, 0, 0, 0},
483 { 0, 0, 0, 0, 0},
484 { 0, 0, 0, 0, 0},
485 { 0, 0, 0, 0, 0},
486 { 0, 0, 0, 0, 0}},
487 /* GU..UA */
488 { { 0, 0, 0, 0, 0},
489 { 0, 0, 0, 0, 0},
490 { 0, 0, 0, 0, 0},
491 { 0, 0, 0, 0, 0},
492 { 0, 0, 0, 0, 0}},
493 /* GU.. @ */
494 { { 0, 0, 0, 0, 0},
495 { 0, 0, 0, 0, 0},
496 { 0, 0, 0, 0, 0},
497 { 0, 0, 0, 0, 0},
498 { 0, 0, 0, 0, 0}},
499 /* UG..GC */
500 { /* noPair */ {{0}},
501 { { 0, 0, 0, 0, 0},
502 { 0, 0, 0, 0, 0},
503 { 0, 0, 0, 0, 0},
504 { 0, 0, 0, 0, 0},
505 { 0, 0, 0, 0, 0}},
506 /* UG..CG */
507 { { 0, 0, 0, 0, 0},
508 { 0, 0, 0, 0, 0},
509 { 0, 0, 0, 0, 0},
510 { 0, 0, 0, 0, 0},
511 { 0, 0, 0, 0, 0}},
512 /* UG..GU */
513 { { 0, 0, 0, 0, 0},
514 { 0, 0, 0, 0, 0},
515 { 0, 0, 0, 0, 0},
516 { 0, 0, 0, 0, 0},
517 { 0, 0, 0, 0, 0}},
518 /* UG..UG */
519 { { 0, 0, 0, 0, 0},
520 { 0, 0, 0, 0, 0},
521 { 0, 0, 0, 0, 0},
522 { 0, 0, 0, 0, 0},
523 { 0, 0, 0, 0, 0}},

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524  /* UG..AU */
525 { { 0, 0, 0, 0, 0, 0 },
526 { 0, 0, 0, 0, 0, 0 },
527 { 0, 0, 0, 0, 0, 0 },
528 { 0, 0, 0, 0, 0, 0 },
529 { 0, 0, 0, 0, 0, 0 }},
530  /* UG..UA */
531 { { 0, 0, 0, 0, 0, 0 },
532 { 0, 0, 0, 0, 0, 0 },
533 { 0, 0, 0, 0, 0, 0 },
534 { 0, 0, 0, 0, 0, 0 },
535 { 0, 0, 0, 0, 0, 0 }},
536  /* UG.. @ */
537 { { 0, 0, 0, 0, 0, 0 },
538 { 0, 0, 0, 0, 0, 0 },
539 { 0, 0, 0, 0, 0, 0 },
540 { 0, 0, 0, 0, 0, 0 },
541 { 0, 0, 0, 0, 0, 0 }},
542  /* AU..GC */
543 { /* noPair */ { {0}},
544 { { 0, 0, 0, 0, 0, 0 },
545 { 0, 0, 0, 0, 0, 0 },
546 { 0, 0, 0, 0, 0, 0 },
547 { 0, 0, 0, 0, 0, 0 },
548 { 0, 0, 0, 0, 0, 0 }},
549  /* AU..CG */
550 { { 0, 0, 0, 0, 0, 0 },
551 { 0, 0, 0, 0, 0, 0 },
552 { 0, 0, 0, 0, 0, 0 },
553 { 0, 0, 0, 0, 0, 0 },
554 { 0, 0, 0, 0, 0, 0 }},
555  /* AU..GU */
556 { { 0, 0, 0, 0, 0, 0 },
557 { 0, 0, 0, 0, 0, 0 },
558 { 0, 0, 0, 0, 0, 0 },
559 { 0, 0, 0, 0, 0, 0 },
560 { 0, 0, 0, 0, 0, 0 }},
561  /* AU..UG */
562 { { 0, 0, 0, 0, 0, 0 },
563 { 0, 0, 0, 0, 0, 0 },
564 { 0, 0, 0, 0, 0, 0 },
565 { 0, 0, 0, 0, 0, 0 },
566 { 0, 0, 0, 0, 0, 0 }},
567  /* AU..AU */
568 { { 0, 0, 0, 0, 0, 0 },
569 { 0, 0, 0, 0, 0, 0 },
570 { 0, 0, 0, 0, 0, 0 },
571 { 0, 0, 0, 0, 0, 0 },
572 { 0, 0, 0, 0, 0, 0 }},
573  /* AU..UA */
574 { { 0, 0, 0, 0, 0, 0 },
575 { 0, 0, 0, 0, 0, 0 },
576 { 0, 0, 0, 0, 0, 0 },
577 { 0, 0, 0, 0, 0, 0 },
578 { 0, 0, 0, 0, 0, 0 }},
579  /* AU.. @ */
580 { { 0, 0, 0, 0, 0, 0 },
581 { 0, 0, 0, 0, 0, 0 },
582 { 0, 0, 0, 0, 0, 0 },
583 { 0, 0, 0, 0, 0, 0 },
584 { 0, 0, 0, 0, 0, 0 }},
585  /* UA..GC */
586 { /* noPair */ { {0}},
587 { { 0, 0, 0, 0, 0, 0 },
588 { 0, 0, 0, 0, 0, 0 },
589 { 0, 0, 0, 0, 0, 0 },
590 { 0, 0, 0, 0, 0, 0 },
591 { 0, 0, 0, 0, 0, 0 }},
592  /* UA..CG */
593 { { 0, 0, 0, 0, 0, 0 },
594 { 0, 0, 0, 0, 0, 0 },
595 { 0, 0, 0, 0, 0, 0 },
596 { 0, 0, 0, 0, 0, 0 },
597 { 0, 0, 0, 0, 0, 0 }},
598  /* UA..GU */
599 { { 0, 0, 0, 0, 0, 0 },
600 { 0, 0, 0, 0, 0, 0 },
601 { 0, 0, 0, 0, 0, 0 },
602 { 0, 0, 0, 0, 0, 0 },
603 { 0, 0, 0, 0, 0, 0 }},
604  /* UA..UG */
605 { { 0, 0, 0, 0, 0, 0 },
606 { 0, 0, 0, 0, 0, 0 },
607 { 0, 0, 0, 0, 0, 0 },
608 { 0, 0, 0, 0, 0, 0 },
609 { 0, 0, 0, 0, 0, 0 }},
610  /* UA..AU */

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```

611 { { 0, 0, 0, 0, 0},
612 { 0, 0, 0, 0, 0},
613 { 0, 0, 0, 0, 0},
614 { 0, 0, 0, 0, 0},
615 { 0, 0, 0, 0, 0}},
616 /* UA..UA */
617 { { 0, 0, 0, 0, 0},
618 { 0, 0, 0, 0, 0},
619 { 0, 0, 0, 0, 0},
620 { 0, 0, 0, 0, 0},
621 { 0, 0, 0, 0, 0}},
622 /* UA.. @ */
623 { { 0, 0, 0, 0, 0},
624 { 0, 0, 0, 0, 0},
625 { 0, 0, 0, 0, 0},
626 { 0, 0, 0, 0, 0},
627 { 0, 0, 0, 0, 0}},
628 /* @..GC */
629 { /* noPair */ {{0}},
630 { { 0, 0, 0, 0, 0},
631 { 0, 0, 0, 0, 0},
632 { 0, 0, 0, 0, 0},
633 { 0, 0, 0, 0, 0},
634 { 0, 0, 0, 0, 0}},
635 /* @..CG */
636 { { 0, 0, 0, 0, 0},
637 { 0, 0, 0, 0, 0},
638 { 0, 0, 0, 0, 0},
639 { 0, 0, 0, 0, 0},
640 { 0, 0, 0, 0, 0}},
641 /* @..GU */
642 { { 0, 0, 0, 0, 0},
643 { 0, 0, 0, 0, 0},
644 { 0, 0, 0, 0, 0},
645 { 0, 0, 0, 0, 0},
646 { 0, 0, 0, 0, 0}},
647 /* @..UG */
648 { { 0, 0, 0, 0, 0},
649 { 0, 0, 0, 0, 0},
650 { 0, 0, 0, 0, 0},
651 { 0, 0, 0, 0, 0},
652 { 0, 0, 0, 0, 0}},
653 /* @..AU */
654 { { 0, 0, 0, 0, 0},
655 { 0, 0, 0, 0, 0},
656 { 0, 0, 0, 0, 0},
657 { 0, 0, 0, 0, 0},
658 { 0, 0, 0, 0, 0}},
659 /* @..UA */
660 { { 0, 0, 0, 0, 0},
661 { 0, 0, 0, 0, 0},
662 { 0, 0, 0, 0, 0},
663 { 0, 0, 0, 0, 0},
664 { 0, 0, 0, 0, 0}},
665 /* @.. @ */
666 { { 0, 0, 0, 0, 0},
667 { 0, 0, 0, 0, 0},
668 { 0, 0, 0, 0, 0},
669 { 0, 0, 0, 0, 0},
670 { 0, 0, 0, 0, 0}}};
671
672 PRIVATE int int21_37_184[NBPAIRS+1][NBPAIRS+1][5][5][5] =
673 { /* noPair */ {{{0}}},
674 { /* noPair */ {{{0}}},
675 {
676 /* CG.@..GC */
677 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
678 /* CG.A..GC */
679 {{ 550, 550, 550, 550, 550},{ 550, 240, 220, 160, 400},{ 550, 210, 170, 160, 400},{ 550, 100, 60, 40,
400},{ 550, 400, 400, 400, 400}},
680 /* CG.C..GC */
681 {{ 550, 550, 550, 550, 550},{ 550, 230, 220, 400, 220},{ 550, 220, 250, 400, 220},{ 550, 400, 400, 400,
400},{ 550, 250, 190, 400, 220}},
682 /* CG.G..GC */
683 {{ 550, 550, 550, 550, 550},{ 550, 170, 400, 80, 400},{ 550, 400, 400, 400, 400},{ 550, 80, 400, 220,
400},{ 550, 400, 400, 400, 400}},
684 /* CG.U..GC */
685 {{ 550, 550, 550, 550, 550},{ 550, 400, 400, 400, 400},{ 550, 400, 220, 400, 130},{ 550, 400, 400, 400,
400},{ 550, 400, 170, 400, 120}}
686 },
687 {
688 /* CG.@..CG */
689 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
690 /* CG.A..CG */
691 {{ 550, 550, 550, 550, 550},{ 550, 230, 220, 110, 400},{ 550, 210, 170, 160, 400},{ 550, 80, 60, 40,

```

```

        400},{ 550, 400, 400, 400, 400}},
692 /* CG.C..CG */
693 {{ 550, 550, 550, 550, 550},{ 550, 230, 220, 400, 220},{ 550, 220, 250, 400, 220},{ 550, 400, 400, 400,
        400},{ 550, 250, 190, 400, 220}},
694 /* CG.G..CG */
695 {{ 550, 550, 550, 550, 550},{ 550, 170, 400, 80, 400},{ 550, 400, 400, 400, 400},{ 550, 80, 400, 220,
        400},{ 550, 400, 400, 400, 400}},
696 /* CG.U..CG */
697 {{ 550, 550, 550, 550, 550},{ 550, 400, 400, 400, 400},{ 550, 400, 220, 400, 150},{ 550, 400, 400, 400,
        400},{ 550, 400, 170, 400, 120}}
698 },
699 {
700 /* CG.@..UG */
701 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
702 /* CG.A..UG */
703 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
        480},{ 550, 480, 480, 480, 480}},
704 /* CG.C..UG */
705 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
        480},{ 550, 330, 270, 480, 300}},
706 /* CG.G..UG */
707 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
        480},{ 550, 480, 480, 480, 480}},
708 /* CG.U..UG */
709 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
        480},{ 550, 480, 250, 480, 200}}
710 },
711 {
712 /* CG.@..GU */
713 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
714 /* CG.A..GU */
715 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
        480},{ 550, 480, 480, 480, 480}},
716 /* CG.C..GU */
717 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
        480},{ 550, 330, 270, 480, 300}},
718 /* CG.G..GU */
719 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
        480},{ 550, 480, 480, 480, 480}},
720 /* CG.U..GU */
721 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
        480},{ 550, 480, 250, 480, 200}}
722 },
723 {
724 /* CG.@..UA */
725 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
726 /* CG.A..UA */
727 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
        480},{ 550, 480, 480, 480, 480}},
728 /* CG.C..UA */
729 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
        480},{ 550, 330, 270, 480, 300}},
730 /* CG.G..UA */
731 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
        480},{ 550, 480, 480, 480, 480}},
732 /* CG.U..UA */
733 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
        480},{ 550, 480, 250, 480, 200}}
734 },
735 {
736 /* CG.@..AU */
737 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
738 /* CG.A..AU */
739 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
        480},{ 550, 480, 480, 480, 480}},
740 /* CG.C..AU */
741 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
        480},{ 550, 330, 270, 480, 300}},
742 /* CG.G..AU */
743 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
        480},{ 550, 480, 480, 480, 480}},
744 /* CG.U..AU */
745 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
        480},{ 550, 480, 250, 480, 200}}
746 },
747 {
748 /* CG.@..?? */
749 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
750 /* CG.A..?? */
751 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
752 /* CG.C..?? */

```

```
753 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
754 /* CG.G.?? */
755 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
756 /* CG.U.?? */
757 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}}
758 }
759 },
760 { /* noPair */ {{0}}},
761 {
762 /* GC.@.GC */
763 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
764 /* GC.A.GC */
765 {{ 550, 550, 550, 550, 550},{ 550, 250, 220, 210, 400},{ 550, 210, 170, 160, 400},{ 550, 120, 60, 40,
400},{ 550, 400, 400, 400, 400}},
766 /* GC.C.GC */
767 {{ 550, 550, 550, 550, 550},{ 550, 230, 220, 400, 220},{ 550, 220, 250, 400, 220},{ 550, 400, 400, 400,
400},{ 550, 250, 190, 400, 220}},
768 /* GC.G.GC */
769 {{ 550, 550, 550, 550, 550},{ 550, 170, 400, 80, 400},{ 550, 400, 400, 400, 400},{ 550, 80, 400, 220,
400},{ 550, 400, 400, 400, 400}},
770 /* GC.U.GC */
771 {{ 550, 550, 550, 550, 550},{ 550, 400, 400, 400, 400},{ 550, 400, 220, 400, 120},{ 550, 400, 400, 400,
400},{ 550, 400, 170, 400, 120}}
772 },
773 {
774 /* GC.@.CG */
775 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
776 /* GC.A.CG */
777 {{ 550, 550, 550, 550, 550},{ 550, 240, 220, 160, 400},{ 550, 210, 170, 160, 400},{ 550, 100, 60, 40,
400},{ 550, 400, 400, 400, 400}},
778 /* GC.C.CG */
779 {{ 550, 550, 550, 550, 550},{ 550, 230, 220, 400, 220},{ 550, 220, 250, 400, 220},{ 550, 400, 400, 400,
400},{ 550, 250, 190, 400, 220}},
780 /* GC.G.CG */
781 {{ 550, 550, 550, 550, 550},{ 550, 170, 400, 80, 400},{ 550, 400, 400, 400, 400},{ 550, 80, 400, 220,
400},{ 550, 400, 400, 400, 400}},
782 /* GC.U.CG */
783 {{ 550, 550, 550, 550, 550},{ 550, 400, 400, 400, 400},{ 550, 400, 220, 400, 130},{ 550, 400, 400, 400,
400},{ 550, 400, 170, 400, 120}}
784 },
785 {
786 /* GC.@.UG */
787 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
788 /* GC.A.UG */
789 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
790 /* GC.C.UG */
791 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
480},{ 550, 330, 270, 480, 300}},
792 /* GC.G.UG */
793 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
480},{ 550, 480, 480, 480, 480}},
794 /* GC.U.UG */
795 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
480},{ 550, 480, 250, 480, 200}}
796 },
797 {
798 /* GC.@.GU */
799 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
800 /* GC.A.GU */
801 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
802 /* GC.C.GU */
803 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
480},{ 550, 330, 270, 480, 300}},
804 /* GC.G.GU */
805 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
480},{ 550, 480, 480, 480, 480}},
806 /* GC.U.GU */
807 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
480},{ 550, 480, 250, 480, 200}}
808 },
809 {
810 /* GC.@.UA */
811 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
812 /* GC.A.UA */
813 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
814 /* GC.C.UA */
```



```
815 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
816 /* GC.G..UA */
817 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
818 /* GC.U..UA */
819 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
480},{ 550, 480, 250, 480, 200}}
820 },
821 {
822 /* GC.@..AU */
823 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
824 /* GC.A..AU */
825 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
826 /* GC.C..AU */
827 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
480},{ 550, 330, 270, 480, 300}},
828 /* GC.G..AU */
829 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
480},{ 550, 480, 480, 480, 480}},
830 /* GC.U..AU */
831 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
480},{ 550, 480, 250, 480, 200}}
832 },
833 {
834 /* GC.@.?? */
835 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
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836 /* GC.A.?? */
837 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
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838 /* GC.C.?? */
839 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
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840 /* GC.G.?? */
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842 /* GC.U.?? */
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844 }
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848 /* GU.@..GC */
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850 /* GU.A..GC */
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852 /* GU.C..GC */
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854 /* GU.G..GC */
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856 /* GU.U..GC */
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860 /* GU.@..CG */
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862 /* GU.A..CG */
863 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
864 /* GU.C..CG */
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866 /* GU.G..CG */
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868 /* GU.U..CG */
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872 /* GU.@..UG */
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874 /* GU.A..UG */
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876 /* GU.C..UG */
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877 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
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878 /* GU.G..UG */
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880 /* GU.U..UG */
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884 /* GU.@..GU */
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886 /* GU.A..GU */
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888 /* GU.C..GU */
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890 /* GU.G..GU */
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892 /* GU.U..GU */
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895 {
896 /* GU.@..UA */
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898 /* GU.A..UA */
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900 /* GU.C..UA */
901 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
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902 /* GU.G..UA */
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904 /* GU.U..UA */
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907 {
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910 /* GU.A..AU */
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912 /* GU.C..AU */
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914 /* GU.G..AU */
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916 /* GU.U..AU */
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919 {
920 /* GU.@..?? */
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922 /* GU.A..?? */
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924 /* GU.C..?? */
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926 /* GU.G..?? */
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928 /* GU.U..?? */
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931 },
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933 {
934 /* UG.@..GC */
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936 /* UG.A..GC */
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938 /* UG.C..GC */

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940 /* UG.G..GC */
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942 /* UG.U..GC */
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945 {
946 /* UG.@..CG */
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948 /* UG.A..CG */
949 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
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950 /* UG.C..CG */
951 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
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952 /* UG.G..CG */
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954 /* UG.U..CG */
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957 {
958 /* UG.@..UG */
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966 /* UG.U..UG */
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970 /* UG.@..GU */
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974 /* UG.C..GU */
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976 /* UG.G..GU */
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978 /* UG.U..GU */
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982 /* UG.@..UA */
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984 /* UG.A..UA */
985 {{ 550, 550, 550, 550, 550},{ 550, 390, 370, 310, 550},{ 550, 360, 320, 310, 550},{ 550, 250, 210, 190,
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986 /* UG.C..UA */
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990 /* UG.U..UA */
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1000 /* UG.G..AU */
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1014 /* UG.U...?? */
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1026 /* AU.G..GC */
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1034 /* AU.A..CG */
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1038 /* AU.G..CG */
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1070 /* AU.A..UA */
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1080 /* AU.@..AU */
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1096 /* AU.C..?? */
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1098 /* AU.G..?? */
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1106 /* UA.@..GC */
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1108 /* UA.A..GC */
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1110 /* UA.C..GC */
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1112 /* UA.G..GC */
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1114 /* UA.U..GC */
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1117 {
1118 /* UA.@..CG */
1119 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1120 /* UA.A..CG */
1121 {{ 550, 550, 550, 550, 550},{ 550, 320, 300, 240, 480},{ 550, 290, 250, 240, 480},{ 550, 180, 140, 120,
480},{ 550, 480, 480, 480, 480}},
1122 /* UA.C..CG */
1123 {{ 550, 550, 550, 550, 550},{ 550, 310, 300, 480, 300},{ 550, 300, 330, 480, 300},{ 550, 480, 480, 480,
480},{ 550, 330, 270, 480, 300}},

```

```
1124 /* UA.G..CG */
1125 {{ 550, 550, 550, 550, 550},{ 550, 250, 480, 160, 480},{ 550, 480, 480, 480, 480},{ 550, 160, 480, 300,
480},{ 550, 480, 480, 480, 480}},
1126 /* UA.U..CG */
1127 {{ 550, 550, 550, 550, 550},{ 550, 480, 480, 480, 480},{ 550, 480, 300, 480, 210},{ 550, 480, 480, 480,
480},{ 550, 480, 250, 480, 200}}
1128 },
1129 {
1130 /* UA.@..UG */
1131 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1132 /* UA.A..UG */
1133 {{ 550, 550, 550, 550, 550},{ 550, 390, 370, 310, 550},{ 550, 360, 320, 310, 550},{ 550, 250, 210, 190,
550},{ 550, 550, 550, 550, 550}},
1134 /* UA.C..UG */
1135 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
550},{ 550, 400, 340, 550, 370}},
1136 /* UA.G..UG */
1137 {{ 550, 550, 550, 550, 550},{ 550, 320, 550, 230, 550},{ 550, 550, 550, 550, 550},{ 550, 230, 550, 370,
550},{ 550, 550, 550, 550, 550}},
1138 /* UA.U..UG */
1139 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 370, 550, 280},{ 550, 550, 550, 550,
550},{ 550, 550, 320, 550, 270}}
1140 },
1141 {
1142 /* UA.@..GU */
1143 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1144 /* UA.A..GU */
1145 {{ 550, 550, 550, 550, 550},{ 550, 390, 370, 310, 550},{ 550, 360, 320, 310, 550},{ 550, 250, 210, 190,
550},{ 550, 550, 550, 550, 550}},
1146 /* UA.C..GU */
1147 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
550},{ 550, 400, 340, 550, 370}},
1148 /* UA.G..GU */
1149 {{ 550, 550, 550, 550, 550},{ 550, 320, 550, 230, 550},{ 550, 550, 550, 550, 550},{ 550, 230, 550, 370,
550},{ 550, 550, 550, 550, 550}},
1150 /* UA.U..GU */
1151 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 370, 550, 280},{ 550, 550, 550, 550,
550},{ 550, 550, 320, 550, 270}}
1152 },
1153 {
1154 /* UA.@..UA */
1155 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1156 /* UA.A..UA */
1157 {{ 550, 550, 550, 550, 550},{ 550, 390, 370, 310, 550},{ 550, 360, 320, 310, 550},{ 550, 250, 210, 190,
550},{ 550, 550, 550, 550, 550}},
1158 /* UA.C..UA */
1159 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
550},{ 550, 400, 340, 550, 370}},
1160 /* UA.G..UA */
1161 {{ 550, 550, 550, 550, 550},{ 550, 320, 550, 230, 550},{ 550, 550, 550, 550, 550},{ 550, 230, 550, 370,
550},{ 550, 550, 550, 550, 550}},
1162 /* UA.U..UA */
1163 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 370, 550, 280},{ 550, 550, 550, 550,
550},{ 550, 550, 320, 550, 270}}
1164 },
1165 {
1166 /* UA.@..AU */
1167 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1168 /* UA.A..AU */
1169 {{ 550, 550, 550, 550, 550},{ 550, 390, 370, 310, 550},{ 550, 360, 320, 310, 550},{ 550, 250, 210, 190,
550},{ 550, 550, 550, 550, 550}},
1170 /* UA.C..AU */
1171 {{ 550, 550, 550, 550, 550},{ 550, 380, 370, 550, 370},{ 550, 370, 400, 550, 370},{ 550, 550, 550, 550,
550},{ 550, 400, 340, 550, 370}},
1172 /* UA.G..AU */
1173 {{ 550, 550, 550, 550, 550},{ 550, 320, 550, 230, 550},{ 550, 550, 550, 550, 550},{ 550, 230, 550, 370,
550},{ 550, 550, 550, 550, 550}},
1174 /* UA.U..AU */
1175 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 370, 550, 280},{ 550, 550, 550, 550,
550},{ 550, 550, 320, 550, 270}}
1176 },
1177 {
1178 /* UA.@..?? */
1179 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1180 /* UA.A..?? */
1181 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1182 /* UA.C..?? */
1183 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550},{ 550, 550, 550, 550, 550}},
1184 /* UA.G..?? */
1185 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
550}}
```

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        550},{ 550, 550, 550, 550, 550}},
1248 /* ??..U..AU */
1249 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550},{ 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1250 },
1251 {
1252 /* ??..@..AU */
1253 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1254 /* ??..A..AU */
1255 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1256 /* ??..C..AU */
1257 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1258 /* ??..G..AU */
1259 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1260 /* ??..U..AU */
1261 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1262 },
1263 {
1264 /* ??..@..?? */
1265 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1266 /* ??..A..?? */
1267 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1268 /* ??..C..?? */
1269 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1270 /* ??..G..?? */
1271 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1272 /* ??..U..?? */
1273 {{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550, 550},{ 550, 550, 550, 550,
        550},{ 550, 550, 550, 550, 550}},
1274 },
1275 },
1276 };
1277
1278 PRIVATE int int21_H_184[NBPAIRS+1][NBPAIRS+1][5][5][5] =
1279 { /* noPair */ {{{{0}}}},
1280 { /* noPair */ {{{{0}}}},
1281 {
1282 /* CG.@..CG */
1283 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
        DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1284 /* CG.A..CG */
1285 {{ DEF, -1029, -949, -1029, -1029},{ -1079, -2058, -1978, -2058, -2058},{ -569, -1548, -1468, -1548, -1548},{
        -989, -1968, -1888, -1968, -1968},{ -859, -1838, -1758, -1838, -1838}},
1286 /* CG.C..CG */
1287 {{ DEF, -519, -449, -519, -669},{ -999, -1468, -1398, -1468, -1618},{ -499, -968, -898, -968, -1118},{
        -989, -1458, -1388, -1458, -1608},{ -789, -1258, -1188, -1258, -1408}},
1288 /* CG.G..CG */
1289 {{ DEF, -939, -939, -939, -939},{ -1079, -1968, -1968, -1968, -1968},{ -569, -1458, -1458, -1458, -1458},{
        -989, -1878, -1878, -1878, -1878},{ -859, -1748, -1748, -1748, -1748}},
1290 /* CG.U..CG */
1291 {{ DEF, -809, -739, -809, -859},{ -1079, -1838, -1768, -1838, -1888},{ -719, -1478, -1408, -1478, -1528},{
        -989, -1748, -1678, -1748, -1798},{ -909, -1668, -1598, -1668, -1718}},
1292 },
1293 {
1294 /* CG.@..GC */
1295 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
        DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1296 /* CG.A..GC */
1297 {{ DEF, -1029, -949, -1029, -1029},{ -569, -1548, -1468, -1548, -1548},{ -769, -1748, -1668, -1748, -1748},{
        -759, -1738, -1658, -1738, -1738},{ -549, -1528, -1448, -1528, -1528}},
1298 /* CG.C..GC */
1299 {{ DEF, -519, -449, -519, -669},{ -929, -1398, -1328, -1398, -1548},{ -359, -828, -758, -828, -978},{
        -789, -1258, -1188, -1258, -1408},{ -549, -1018, -948, -1018, -1168}},
1300 /* CG.G..GC */
1301 {{ DEF, -939, -939, -939, -939},{ -609, -1498, -1498, -1498, -1498},{ -359, -1248, -1248, -1248, -1248},{
        -669, -1558, -1558, -1558, -1558},{ -549, -1438, -1438, -1438, -1438}},
1302 /* CG.U..GC */
1303 {{ DEF, -809, -739, -809, -859},{ -929, -1688, -1618, -1688, -1738},{ -439, -1198, -1128, -1198, -1248},{
        -789, -1548, -1478, -1548, -1598},{ -619, -1378, -1308, -1378, -1428}},
1304 },
1305 {
1306 /* CG.@..GU */
1307 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
        DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1308 /* CG.A..GU */
1309 {{ DEF, -1029, -949, -1029, -1029},{ -479, -1458, -1378, -1458, -1458},{ -309, -1288, -1208, -1288, -1288},{
        -389, -1368, -1288, -1368, -1368},{ -379, -1358, -1278, -1358, -1358}},
1310 /* CG.C..GU */

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1311 {{ DEF, -519, -449, -519, -669},{ -649,-1118,-1048,-1118,-1268},{ -289, -758, -688, -758, -908},{
    -739,-1208,-1138,-1208,-1358},{ -379, -848, -778, -848, -998}},
1312 /* CG.G..GU */
1313 {{ DEF, -939, -939, -939, -939},{ -649,-1538,-1538,-1538,-1538},{ -289,-1178,-1178,-1178,-1178},{
    -739,-1628,-1628,-1628,-1628},{ -379,-1268,-1268,-1268,-1268}},
1314 /* CG.U..UG */
1315 {{ DEF, -809, -739, -809, -859},{ -649,-1408,-1338,-1408,-1458},{ -289,-1048, -978,-1048,-1098},{
    -739,-1498,-1428,-1498,-1548},{ -379,-1138,-1068,-1138,-1188}}
1316 },
1317 {
1318 /* CG.@..UG */
1319 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
    DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1320 /* CG.A..UG */
1321 {{ DEF,-1029, -949,-1029,-1029},{ -769,-1748,-1668,-1748,-1748},{ -529,-1508,-1428,-1508,-1508},{
    -709,-1688,-1608,-1688,-1688},{ -599,-1578,-1498,-1578,-1578}},
1322 /* CG.C..UG */
1323 {{ DEF, -519, -449, -519, -669},{ -839,-1308,-1238,-1308,-1458},{ -529, -998, -928, -998,-1148},{
    -859,-1328,-1258,-1328,-1478},{ -489, -958, -888, -958,-1108}},
1324 /* CG.G..UG */
1325 {{ DEF, -939, -939, -939, -939},{-1009,-1898,-1898,-1898,-1898},{ -409,-1298,-1298,-1298,-1298},{
    -969,-1858,-1858,-1858,-1858},{ -599,-1488,-1488,-1488,-1488}},
1326 /* CG.U..UG */
1327 {{ DEF, -809, -739, -809, -859},{ -859,-1618,-1548,-1618,-1668},{ -529,-1288,-1218,-1288,-1338},{
    -859,-1618,-1548,-1618,-1668},{ -409,-1168,-1098,-1168,-1218}}
1328 },
1329 {
1330 /* CG.@..AU */
1331 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
    DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1332 /* CG.A..AU */
1333 {{ DEF,-1029, -949,-1029,-1029},{ -479,-1458,-1378,-1458,-1458},{ -309,-1288,-1208,-1288,-1288},{
    -389,-1368,-1288,-1368,-1368},{ -379,-1358,-1278,-1358,-1358}},
1334 /* CG.C..AU */
1335 {{ DEF, -519, -449, -519, -669},{ -649,-1118,-1048,-1118,-1268},{ -289, -758, -688, -758, -908},{
    -739,-1208,-1138,-1208,-1358},{ -379, -848, -778, -848, -998}},
1336 /* CG.G..AU */
1337 {{ DEF, -939, -939, -939, -939},{ -649,-1538,-1538,-1538,-1538},{ -289,-1178,-1178,-1178,-1178},{
    -739,-1628,-1628,-1628,-1628},{ -379,-1268,-1268,-1268,-1268}},
1338 /* CG.U..AU */
1339 {{ DEF, -809, -739, -809, -859},{ -649,-1408,-1338,-1408,-1458},{ -289,-1048, -978,-1048,-1098},{
    -739,-1498,-1428,-1498,-1548},{ -379,-1138,-1068,-1138,-1188}}
1340 },
1341 {
1342 /* CG.@..UA */
1343 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
    DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1344 /* CG.A..UA */
1345 {{ DEF,-1029, -949,-1029,-1029},{ -449,-1428,-1348,-1428,-1428},{ -479,-1458,-1378,-1458,-1458},{
    -429,-1408,-1328,-1408,-1408},{ -329,-1308,-1228,-1308,-1308}},
1346 /* CG.C..UA */
1347 {{ DEF, -519, -449, -519, -669},{ -679,-1148,-1078,-1148,-1298},{ -559,-1028, -958,-1028,-1178},{
    -729,-1198,-1128,-1198,-1348},{ -189, -658, -588, -658, -808}},
1348 /* CG.G..UA */
1349 {{ DEF, -939, -939, -939, -939},{ -939,-1828,-1828,-1828,-1828},{ -249,-1138,-1138,-1138,-1138},{
    -939,-1828,-1828,-1828,-1828},{ -329,-1218,-1218,-1218,-1218}},
1350 /* CG.U..UA */
1351 {{ DEF, -809, -739, -809, -859},{ -639,-1398,-1328,-1398,-1448},{ -229, -988, -918, -988,-1038},{
    -729,-1488,-1418,-1488,-1538},{ -190, -949, -879, -949, -999}}
1352 },
1353 {
1354 /* CG.@..@ */
1355 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
    DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1356 /* CG.A..@ */
1357 {{ -100,-1079, -999,-1079,-1079},{ -100,-1079, -999,-1079,-1079},{ -100,-1079, -999,-1079,-1079},{
    -100,-1079, -999,-1079,-1079},{ -100,-1079, -999,-1079,-1079}},
1358 /* CG.C..@ */
1359 {{ -100,-569, -499, -569, -719},{ -100, -569, -499, -569, -719},{ -100, -569, -499, -569, -719},{
    -100, -569, -499, -569, -719},{ -100, -569, -499, -569, -719}},
1360 /* CG.G..@ */
1361 {{ -100,-989, -989, -989, -989},{ -100, -989, -989, -989, -989},{ -100, -989, -989, -989, -989},{
    -100, -989, -989, -989, -989},{ -100, -989, -989, -989, -989}},
1362 /* CG.U..@ */
1363 {{ -100,-859, -789, -859, -909},{ -100, -859, -789, -859, -909},{ -100, -859, -789, -859, -909},{
    -100, -859, -789, -859, -909},{ -100, -859, -789, -859, -909}}
1364 },
1365 },
1366 { /* noPair */ {{0}}},
1367 {
1368 /* GC.@..CG */
1369 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
    DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1370 /* GC.A..CG */
1371 {{ DEF, -519, -879, -559, -879},{-1079,-1548,-1908,-1588,-1908},{ -569,-1038,-1398,-1078,-1398},{
    -989,-1458,-1818,-1498,-1818},{ -859,-1328,-1688,-1368,-1688}},
1372 /* GC.C..CG */

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1373 {{ DEF, -719, -309, -309, -389},{ -999,-1668,-1258,-1258,-1338},{ -499,-1168, -758, -758, -838},{
-989,-1658,-1248,-1248,-1328},{ -789,-1458,-1048,-1048,-1128}},
1374 /* GC.G..CG */
1375 {{ DEF, -709, -739, -619, -739},{-1079,-1738,-1768,-1648,-1768},{ -569,-1228,-1258,-1138,-1258},{
-989,-1648,-1678,-1558,-1678},{ -859,-1518,-1548,-1428,-1548}},
1376 /* GC.U..CG */
1377 {{ DEF, -499, -499, -499, -569},{-1079,-1528,-1528,-1528,-1598},{ -719,-1168,-1168,-1168,-1238},{
-989,-1438,-1438,-1438,-1508},{ -909,-1358,-1358,-1358,-1428}}
1378 },
1379 {
1380 /* GC.@..GC */
1381 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1382 /* GC.A..GC */
1383 {{ DEF, -519, -879, -559, -879},{ -569,-1038,-1398,-1078,-1398},{ -769,-1238,-1598,-1278,-1598},{
-759,-1228,-1588,-1268,-1588},{ -549,-1018,-1378,-1058,-1378}},
1384 /* GC.C..GC */
1385 {{ DEF, -719, -309, -309, -389},{ -929,-1598,-1188,-1188,-1268},{ -359,-1028, -618, -618, -698},{
-789,-1458,-1048,-1048,-1128},{ -549,-1218, -808, -808, -888}},
1386 /* GC.G..GC */
1387 {{ DEF, -709, -739, -619, -739},{ -609,-1268,-1298,-1178,-1298},{ -359,-1018,-1048, -928,-1048},{
-669,-1328,-1358,-1238,-1358},{ -549,-1208,-1238,-1118,-1238}},
1388 /* GC.U..GC */
1389 {{ DEF, -499, -499, -499, -569},{ -929,-1378,-1378,-1378,-1448},{ -439, -888, -888, -888, -958},{
-789,-1238,-1238,-1238,-1308},{ -619,-1068,-1068,-1068,-1138}}
1390 },
1391 {
1392 /* GC.@..GU */
1393 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1394 /* GC.A..GU */
1395 {{ DEF, -519, -879, -559, -879},{ -479, -948,-1308, -988,-1308},{ -309, -778,-1138, -818,-1138},{
-389, -858,-1218, -898,-1218},{ -379, -848,-1208, -888,-1208}},
1396 /* GC.C..GU */
1397 {{ DEF, -719, -309, -309, -389},{ -649,-1318, -908, -908, -988},{ -289, -958, -548, -548, -628},{
-739,-1408, -998, -998,-1078},{ -379,-1048, -638, -638, -718}},
1398 /* GC.G..GU */
1399 {{ DEF, -709, -739, -619, -739},{ -649,-1308,-1338,-1218,-1338},{ -289, -948, -978, -858, -978},{
-739,-1398,-1428,-1308,-1428},{ -379,-1038,-1068, -948,-1068}},
1400 /* GC.U..GU */
1401 {{ DEF, -499, -499, -499, -569},{ -649,-1098,-1098,-1098,-1168},{ -289, -738, -738, -738, -808},{
-739,-1188,-1188,-1188,-1258},{ -379, -828, -828, -828, -898}}
1402 },
1403 {
1404 /* GC.@..UG */
1405 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1406 /* GC.A..UG */
1407 {{ DEF, -519, -879, -559, -879},{ -769,-1238,-1598,-1278,-1598},{ -529, -998,-1358,-1038,-1358},{
-709,-1178,-1538,-1218,-1538},{ -599,-1068,-1428,-1108,-1428}},
1408 /* GC.C..UG */
1409 {{ DEF, -719, -309, -309, -389},{ -839,-1508,-1098,-1098,-1178},{ -529,-1198, -788, -788, -868},{
-859,-1528,-1118,-1118,-1198},{ -489,-1158, -748, -748, -828}},
1410 /* GC.G..UG */
1411 {{ DEF, -709, -739, -619, -739},{-1009,-1668,-1698,-1578,-1698},{ -409,-1068,-1098, -978,-1098},{
-969,-1628,-1658,-1538,-1658},{ -599,-1258,-1288,-1168,-1288}},
1412 /* GC.U..UG */
1413 {{ DEF, -499, -499, -499, -569},{ -859,-1308,-1308,-1308,-1378},{ -529, -978, -978, -978,-1048},{
-859,-1308,-1308,-1308,-1378},{ -409, -858, -858, -858, -928}}
1414 },
1415 {
1416 /* GC.@..AU */
1417 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1418 /* GC.A..AU */
1419 {{ DEF, -519, -879, -559, -879},{ -479, -948,-1308, -988,-1308},{ -309, -778,-1138, -818,-1138},{
-389, -858,-1218, -898,-1218},{ -379, -848,-1208, -888,-1208}},
1420 /* GC.C..AU */
1421 {{ DEF, -719, -309, -309, -389},{ -649,-1318, -908, -908, -988},{ -289, -958, -548, -548, -628},{
-739,-1408, -998, -998,-1078},{ -379,-1048, -638, -638, -718}},
1422 /* GC.G..AU */
1423 {{ DEF, -709, -739, -619, -739},{ -649,-1308,-1338,-1218,-1338},{ -289, -948, -978, -858, -978},{
-739,-1398,-1428,-1308,-1428},{ -379,-1038,-1068, -948,-1068}},
1424 /* GC.U..AU */
1425 {{ DEF, -499, -499, -499, -569},{ -649,-1098,-1098,-1098,-1168},{ -289, -738, -738, -738, -808},{
-739,-1188,-1188,-1188,-1258},{ -379, -828, -828, -828, -898}}
1426 },
1427 {
1428 /* GC.@..UA */
1429 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1430 /* GC.A..UA */
1431 {{ DEF, -519, -879, -559, -879},{ -449, -918,-1278, -958,-1278},{ -479, -948,-1308, -988,-1308},{
-429, -898,-1258, -938,-1258},{ -329, -798,-1158, -838,-1158}},
1432 /* GC.C..UA */
1433 {{ DEF, -719, -309, -309, -389},{ -679,-1348, -938, -938,-1018},{ -559,-1228, -818, -818, -898},{
-729,-1398, -988, -988,-1068},{ -189, -858, -448, -448, -528}},
```

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1434 /* GC.G..UA */
1435 {{ DEF, -709, -739, -619, -739},{ -939,-1598,-1628,-1508,-1628},{ -249, -908, -938, -818, -938},{
-939,-1598,-1628,-1508,-1628},{ -329, -988,-1018, -898,-1018}},
1436 /* GC.U..UA */
1437 {{ DEF, -499, -499, -499, -569},{ -639,-1088,-1088,-1088,-1158},{ -229, -678, -678, -678, -748},{
-729,-1178,-1178,-1178,-1248},{ -190, -639, -639, -639, -709}}
1438 },
1439 {
1440 /* GC.@.. @ */
1441 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1442 /* GC.A.. @ */
1443 {{ -100, -569, -929, -609, -929},{ -100, -569, -929, -609, -929},{ -100, -569, -929, -609, -929},{
-100, -569, -929, -609, -929},{ -100, -569, -929, -609, -929}},
1444 /* GC.C.. @ */
1445 {{ -100, -769, -359, -359, -439},{ -100, -769, -359, -359, -439},{ -100, -769, -359, -359, -439},{
-100, -769, -359, -359, -439},{ -100, -769, -359, -359, -439}},
1446 /* GC.G.. @ */
1447 {{ -100, -759, -789, -669, -789},{ -100, -759, -789, -669, -789},{ -100, -759, -789, -669, -789},{
-100, -759, -789, -669, -789},{ -100, -759, -789, -669, -789}},
1448 /* GC.U.. @ */
1449 {{ -100, -549, -549, -549, -619},{ -100, -549, -549, -549, -619},{ -100, -549, -549, -549, -619},{
-100, -549, -549, -549, -619},{ -100, -549, -549, -549, -619}}
1450 },
1451 },
1452 { /* noPair */ {{0}}},
1453 {
1454 /* GU.@..CG */
1455 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1456 /* GU.A..CG */
1457 {{ DEF, -429, -599, -599, -599},{ -1079,-1458,-1628,-1628,-1628},{ -569, -948,-1118,-1118,-1118},{
-989,-1368,-1538,-1538,-1538},{ -859,-1238,-1408,-1408,-1408}},
1458 /* GU.C..CG */
1459 {{ DEF, -259, -239, -239, -239},{ -999,-1208,-1188,-1188,-1188},{ -499, -708, -688, -688, -688},{
-989,-1198,-1178,-1178,-1178},{ -789, -998, -978, -978, -978}},
1460 /* GU.G..CG */
1461 {{ DEF, -339, -689, -689, -689},{ -1079,-1368,-1718,-1718,-1718},{ -569, -858,-1208,-1208,-1208},{
-989,-1278,-1628,-1628,-1628},{ -859,-1148,-1498,-1498,-1498}},
1462 /* GU.U..CG */
1463 {{ DEF, -329, -329, -329, -329},{ -1079,-1358,-1358,-1358,-1358},{ -719, -998, -998, -998, -998},{
-989,-1268,-1268,-1268,-1268},{ -909,-1188,-1188,-1188,-1188}}
1464 },
1465 {
1466 /* GU.@..GC */
1467 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1468 /* GU.A..GC */
1469 {{ DEF, -429, -599, -599, -599},{ -569, -948,-1118,-1118,-1118},{ -769,-1148,-1318,-1318,-1318},{
-759,-1138,-1308,-1308,-1308},{ -549, -928,-1098,-1098,-1098}},
1470 /* GU.C..GC */
1471 {{ DEF, -259, -239, -239, -239},{ -929,-1138,-1118,-1118,-1118},{ -359, -568, -548, -548, -548},{
-789, -998, -978, -978, -978},{ -549, -758, -738, -738, -738}},
1472 /* GU.G..GC */
1473 {{ DEF, -339, -689, -689, -689},{ -609, -898,-1248,-1248,-1248},{ -359, -648, -998, -998, -998},{
-669, -958,-1308,-1308,-1308},{ -549, -838,-1188,-1188,-1188}},
1474 /* GU.U..GC */
1475 {{ DEF, -329, -329, -329, -329},{ -929,-1208,-1208,-1208,-1208},{ -439, -718, -718, -718, -718},{
-789,-1068,-1068,-1068,-1068},{ -619, -898, -898, -898, -898}}
1476 },
1477 {
1478 /* GU.@..GU */
1479 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1480 /* GU.A..GU */
1481 {{ DEF, -429, -599, -599, -599},{ -479, -858,-1028,-1028,-1028},{ -309, -688, -858, -858, -858},{
-389, -768, -938, -938, -938},{ -379, -758, -928, -928, -928}},
1482 /* GU.C..GU */
1483 {{ DEF, -259, -239, -239, -239},{ -649, -858, -838, -838, -838},{ -289, -498, -478, -478, -478},{
-739, -948, -928, -928, -928},{ -379, -588, -568, -568, -568}},
1484 /* GU.G..GU */
1485 {{ DEF, -339, -689, -689, -689},{ -649, -938,-1288,-1288,-1288},{ -289, -578, -928, -928, -928},{
-739,-1028,-1378,-1378,-1378},{ -379, -668,-1018,-1018,-1018}},
1486 /* GU.U..GU */
1487 {{ DEF, -329, -329, -329, -329},{ -649, -928, -928, -928, -928},{ -289, -568, -568, -568, -568},{
-739,-1018,-1018,-1018,-1018},{ -379, -658, -658, -658, -658}}
1488 },
1489 {
1490 /* GU.@..UG */
1491 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1492 /* GU.A..UG */
1493 {{ DEF, -429, -599, -599, -599},{ -769,-1148,-1318,-1318,-1318},{ -529, -908,-1078,-1078,-1078},{
-709,-1088,-1258,-1258,-1258},{ -599, -978,-1148,-1148,-1148}},
1494 /* GU.C..UG */
1495 {{ DEF, -259, -239, -239, -239},{ -839,-1048,-1028,-1028,-1028},{ -529, -738, -718, -718, -718},{
-859,-1068,-1048,-1048,-1048},{ -489, -698, -678, -678, -678}},

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1496 /* GU.G..UG */
1497 {{ DEF, -339, -689, -689, -689},{-1009,-1298,-1648,-1648,-1648},{ -409, -698,-1048,-1048,-1048},{
-969,-1258,-1608,-1608,-1608},{ -599, -888,-1238,-1238,-1238}},
1498 /* GU.U..UG */
1499 {{ DEF, -329, -329, -329, -329},{ -859,-1138,-1138,-1138,-1138},{ -529, -808, -808, -808, -808},{
-859,-1138,-1138,-1138,-1138},{ -409, -688, -688, -688, -688}}
1500 },
1501 {
1502 /* GU.@..AU */
1503 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1504 /* GU.A..AU */
1505 {{ DEF, -429, -599, -599, -599},{ -479, -858,-1028,-1028,-1028},{ -309, -688, -858, -858, -858},{
-389, -768, -938, -938, -938},{ -379, -758, -928, -928, -928}},
1506 /* GU.C..AU */
1507 {{ DEF, -259, -239, -239, -239},{ -649, -858, -838, -838, -838},{ -289, -498, -478, -478, -478},{
-739, -948, -928, -928, -928},{ -379, -588, -568, -568, -568}},
1508 /* GU.G..AU */
1509 {{ DEF, -339, -689, -689, -689},{ -649, -938,-1288,-1288,-1288},{ -289, -578, -928, -928, -928},{
-739,-1028,-1378,-1378,-1378},{ -379, -668,-1018,-1018,-1018}},
1510 /* GU.U..AU */
1511 {{ DEF, -329, -329, -329, -329},{ -649, -928, -928, -928, -928},{ -289, -568, -568, -568, -568},{
-739,-1018,-1018,-1018,-1018},{ -379, -658, -658, -658, -658}}
1512 },
1513 {
1514 /* GU.@..UA */
1515 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1516 /* GU.A..UA */
1517 {{ DEF, -429, -599, -599, -599},{ -449, -828, -998, -998, -998},{ -479, -858,-1028,-1028,-1028},{
-429, -808, -978, -978, -978},{ -329, -708, -878, -878, -878}},
1518 /* GU.C..UA */
1519 {{ DEF, -259, -239, -239, -239},{ -679, -888, -868, -868, -868},{ -559, -768, -748, -748, -748},{
-729, -938, -918, -918, -918},{ -189, -398, -378, -378, -378}},
1520 /* GU.G..UA */
1521 {{ DEF, -339, -689, -689, -689},{ -939,-1228,-1578,-1578,-1578},{ -249, -538, -888, -888, -888},{
-939,-1228,-1578,-1578,-1578},{ -329, -618, -968, -968, -968}},
1522 /* GU.U..UA */
1523 {{ DEF, -329, -329, -329, -329},{ -639, -918, -918, -918, -918},{ -229, -508, -508, -508, -508},{
-729,-1008,-1008,-1008,-1008},{ -190, -469, -469, -469, -469}}
1524 },
1525 {
1526 /* GU.@.. @ */
1527 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1528 /* GU.A.. @ */
1529 {{ -100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649},{
-100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649}},
1530 /* GU.C.. @ */
1531 {{ -100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289},{
-100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289}},
1532 /* GU.G.. @ */
1533 {{ -100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739},{
-100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739}},
1534 /* GU.U.. @ */
1535 {{ -100, -379, -379, -379, -379},{ -100, -379, -379, -379, -379},{ -100, -379, -379, -379, -379},{
-100, -379, -379, -379, -379},{ -100, -379, -379, -379, -379}}
1536 },
1537 },
1538 { /* noPair */ {{0}}},
1539 {
1540 /* UG.@..CG */
1541 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1542 /* UG.A..CG */
1543 {{ DEF, -719, -789, -959, -809},{-1079,-1748,-1818,-1988,-1838},{ -569,-1238,-1308,-1478,-1328},{
-989,-1658,-1728,-1898,-1748},{ -859,-1528,-1598,-1768,-1618}},
1544 /* UG.C..CG */
1545 {{ DEF, -479, -479, -359, -479},{ -999,-1428,-1428,-1308,-1428},{ -499, -928, -928, -808, -928},{
-989,-1418,-1418,-1298,-1418},{ -789,-1218,-1218,-1098,-1218}},
1546 /* UG.G..CG */
1547 {{ DEF, -659, -809, -919, -809},{-1079,-1688,-1838,-1948,-1838},{ -569,-1178,-1328,-1438,-1328},{
-989,-1598,-1748,-1858,-1748},{ -859,-1468,-1618,-1728,-1618}},
1548 /* UG.U..CG */
1549 {{ DEF, -549, -439, -549, -359},{-1079,-1578,-1468,-1578,-1388},{ -719,-1218,-1108,-1218,-1028},{
-989,-1488,-1378,-1488,-1298},{ -909,-1408,-1298,-1408,-1218}}
1550 },
1551 {
1552 /* UG.@..GC */
1553 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1554 /* UG.A..GC */
1555 {{ DEF, -719, -789, -959, -809},{ -569,-1238,-1308,-1478,-1328},{ -769,-1438,-1508,-1678,-1528},{
-759,-1428,-1498,-1668,-1518},{ -549,-1218,-1288,-1458,-1308}},
1556 /* UG.C..GC */
1557 {{ DEF, -479, -479, -359, -479},{ -929,-1358,-1358,-1238,-1358},{ -359, -788, -788, -668, -788},{
-789,-1218,-1218,-1098,-1218},{ -549, -978, -978, -858, -978}},

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1558 /* UG.G..GC */
1559 {{ DEF, -659, -809, -919, -809},{ -609,-1218,-1368,-1478,-1368},{ -359, -968,-1118,-1228,-1118},{
-669,-1278,-1428,-1538,-1428},{ -549,-1158,-1308,-1418,-1308}},
1560 /* UG.U..GC */
1561 {{ DEF, -549, -439, -549, -359},{ -929,-1428,-1318,-1428,-1238},{ -439, -938, -828, -938, -748},{
-789,-1288,-1178,-1288,-1098},{ -619,-1118,-1008,-1118, -928}}
1562 },
1563 {
1564 /* UG.@..GU */
1565 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1566 /* UG.A..GU */
1567 {{ DEF, -719, -789, -959, -809},{ -479,-1148,-1218,-1388,-1238},{ -309, -978,-1048,-1218,-1068},{
-389,-1058,-1128,-1298,-1148},{ -379,-1048,-1118,-1288,-1138}},
1568 /* UG.C..GU */
1569 {{ DEF, -479, -479, -359, -479},{ -649,-1078,-1078, -958,-1078},{ -289, -718, -718, -598, -718},{
-739,-1168,-1168,-1048,-1168},{ -379, -808, -808, -688, -808}},
1570 /* UG.G..GU */
1571 {{ DEF, -659, -809, -919, -809},{ -649,-1258,-1408,-1518,-1408},{ -289, -898,-1048,-1158,-1048},{
-739,-1348,-1498,-1608,-1498},{ -379, -988,-1138,-1248,-1138}},
1572 /* UG.U..GU */
1573 {{ DEF, -549, -439, -549, -359},{ -649,-1148,-1038,-1148, -958},{ -289, -788, -678, -788, -598},{
-739,-1238,-1128,-1238,-1048},{ -379, -878, -768, -878, -688}}
1574 },
1575 {
1576 /* UG.@..UG */
1577 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1578 /* UG.A..UG */
1579 {{ DEF, -719, -789, -959, -809},{ -769,-1438,-1508,-1678,-1528},{ -529,-1198,-1268,-1438,-1288},{
-709,-1378,-1448,-1618,-1468},{ -599,-1268,-1338,-1508,-1358}},
1580 /* UG.C..UG */
1581 {{ DEF, -479, -479, -359, -479},{ -839,-1268,-1268,-1148,-1268},{ -529, -958, -958, -838, -958},{
-859,-1288,-1288,-1168,-1288},{ -489, -918, -918, -798, -918}},
1582 /* UG.G..UG */
1583 {{ DEF, -659, -809, -919, -809},{-1009,-1618,-1768,-1878,-1768},{ -409,-1018,-1168,-1278,-1168},{
-969,-1578,-1728,-1838,-1728},{ -599,-1208,-1358,-1468,-1358}},
1584 /* UG.U..UG */
1585 {{ DEF, -549, -439, -549, -359},{ -859,-1358,-1248,-1358,-1168},{ -529,-1028, -918,-1028, -838},{
-859,-1358,-1248,-1358,-1168},{ -409, -908, -798, -908, -718}}
1586 },
1587 {
1588 /* UG.@..AU */
1589 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1590 /* UG.A..AU */
1591 {{ DEF, -719, -789, -959, -809},{ -479,-1148,-1218,-1388,-1238},{ -309, -978,-1048,-1218,-1068},{
-389,-1058,-1128,-1298,-1148},{ -379,-1048,-1118,-1288,-1138}},
1592 /* UG.C..AU */
1593 {{ DEF, -479, -479, -359, -479},{ -649,-1078,-1078, -958,-1078},{ -289, -718, -718, -598, -718},{
-739,-1168,-1168,-1048,-1168},{ -379, -808, -808, -688, -808}},
1594 /* UG.G..AU */
1595 {{ DEF, -659, -809, -919, -809},{ -649,-1258,-1408,-1518,-1408},{ -289, -898,-1048,-1158,-1048},{
-739,-1348,-1498,-1608,-1498},{ -379, -988,-1138,-1248,-1138}},
1596 /* UG.U..AU */
1597 {{ DEF, -549, -439, -549, -359},{ -649,-1148,-1038,-1148, -958},{ -289, -788, -678, -788, -598},{
-739,-1238,-1128,-1238,-1048},{ -379, -878, -768, -878, -688}}
1598 },
1599 {
1600 /* UG.@..UA */
1601 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1602 /* UG.A..UA */
1603 {{ DEF, -719, -789, -959, -809},{ -449,-1118,-1188,-1358,-1208},{ -479,-1148,-1218,-1388,-1238},{
-429,-1098,-1168,-1338,-1188},{ -329, -998,-1068,-1238,-1088}},
1604 /* UG.C..UA */
1605 {{ DEF, -479, -479, -359, -479},{ -679,-1108,-1108, -988,-1108},{ -559, -988, -988, -868, -988},{
-729,-1158,-1158,-1038,-1158},{ -189, -618, -618, -498, -618}},
1606 /* UG.G..UA */
1607 {{ DEF, -659, -809, -919, -809},{ -939,-1548,-1698,-1808,-1698},{ -249, -858,-1008,-1118,-1008},{
-939,-1548,-1698,-1808,-1698},{ -329, -938,-1088,-1198,-1088}},
1608 /* UG.U..UA */
1609 {{ DEF, -549, -439, -549, -359},{ -639,-1138,-1028,-1138, -948},{ -229, -728, -618, -728, -538},{
-729,-1228,-1118,-1228,-1038},{ -190, -689, -579, -689, -499}}
1610 },
1611 {
1612 /* UG.@..@ */
1613 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1614 /* UG.A..@ */
1615 {{ -100, -769, -839,-1009, -859},{ -100, -769, -839,-1009, -859},{ -100, -769, -839,-1009, -859},{
-100, -769, -839,-1009, -859},{ -100, -769, -839,-1009, -859}},
1616 /* UG.C..@ */
1617 {{ -100, -529, -529, -409, -529},{ -100, -529, -529, -409, -529},{ -100, -529, -529, -409, -529},{
-100, -529, -529, -409, -529},{ -100, -529, -529, -409, -529}},
1618 /* UG.G..@ */
1619 {{ -100, -709, -859, -969, -859},{ -100, -709, -859, -969, -859},{ -100, -709, -859, -969, -859},{

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-100, -709, -859, -969, -859},{ -100, -709, -859, -969, -859}},
1620 /* UG.U.. @ */
1621 {{ -100, -599, -489, -599, -409},{ -100, -599, -489, -599, -409},{ -100, -599, -489, -599, -409},{
-100, -599, -489, -599, -409},{ -100, -599, -489, -599, -409}}
1622 }
1623 },
1624 { /* noPair */ {{0}},
1625 {
1626 /* AU.@..CG */
1627 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1628 /* AU.A..CG */
1629 {{ DEF, -429, -599, -599, -599},{-1079,-1458,-1628,-1628,-1628},{ -569, -948,-1118,-1118,-1118},{
-989,-1368,-1538,-1538,-1538},{ -859,-1238,-1408,-1408,-1408}},
1630 /* AU.C..CG */
1631 {{ DEF, -259, -239, -239, -239},{ -999,-1208,-1188,-1188,-1188},{ -499, -708, -688, -688, -688},{
-989,-1198,-1178,-1178,-1178},{ -789, -998, -978, -978, -978}},
1632 /* AU.G..CG */
1633 {{ DEF, -339, -689, -689, -689},{-1079,-1368,-1718,-1718,-1718},{ -569, -858,-1208,-1208,-1208},{
-989,-1278,-1628,-1628,-1628},{ -859,-1148,-1498,-1498,-1498}},
1634 /* AU.U..CG */
1635 {{ DEF, -329, -329, -329, -329},{-1079,-1358,-1358,-1358,-1358},{ -719, -998, -998, -998, -998},{
-989,-1268,-1268,-1268,-1268},{ -909,-1188,-1188,-1188,-1188}}
1636 },
1637 {
1638 /* AU.@..GC */
1639 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1640 /* AU.A..GC */
1641 {{ DEF, -429, -599, -599, -599},{ -569, -948,-1118,-1118,-1118},{ -769,-1148,-1318,-1318,-1318},{
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1642 /* AU.C..GC */
1643 {{ DEF, -259, -239, -239, -239},{ -929,-1138,-1118,-1118,-1118},{ -359, -568, -548, -548, -548},{
-789, -998, -978, -978, -978},{ -549, -758, -738, -738, -738}},
1644 /* AU.G..GC */
1645 {{ DEF, -339, -689, -689, -689},{ -609, -898,-1248,-1248,-1248},{ -359, -648, -998, -998, -998},{
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1646 /* AU.U..GC */
1647 {{ DEF, -329, -329, -329, -329},{ -929,-1208,-1208,-1208,-1208},{ -439, -718, -718, -718, -718},{
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1648 },
1649 {
1650 /* AU.@..GU */
1651 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1652 /* AU.A..GU */
1653 {{ DEF, -429, -599, -599, -599},{ -479, -858,-1028,-1028,-1028},{ -309, -688, -858, -858, -858},{
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1654 /* AU.C..GU */
1655 {{ DEF, -259, -239, -239, -239},{ -649, -858, -838, -838, -838},{ -289, -498, -478, -478, -478},{
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1656 /* AU.G..GU */
1657 {{ DEF, -339, -689, -689, -689},{ -649, -938,-1288,-1288,-1288},{ -289, -578, -928, -928, -928},{
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1658 /* AU.U..GU */
1659 {{ DEF, -329, -329, -329, -329},{ -649, -928, -928, -928, -928},{ -289, -568, -568, -568, -568},{
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1660 },
1661 {
1662 /* AU.@..UG */
1663 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1664 /* AU.A..UG */
1665 {{ DEF, -429, -599, -599, -599},{ -769,-1148,-1318,-1318,-1318},{ -529, -908,-1078,-1078,-1078},{
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1666 /* AU.C..UG */
1667 {{ DEF, -259, -239, -239, -239},{ -839,-1048,-1028,-1028,-1028},{ -529, -738, -718, -718, -718},{
-859,-1068,-1048,-1048,-1048},{ -489, -698, -678, -678, -678}},
1668 /* AU.G..UG */
1669 {{ DEF, -339, -689, -689, -689},{-1009,-1298,-1648,-1648,-1648},{ -409, -698,-1048,-1048,-1048},{
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1670 /* AU.U..UG */
1671 {{ DEF, -329, -329, -329, -329},{ -859,-1138,-1138,-1138,-1138},{ -529, -808, -808, -808, -808},{
-859,-1138,-1138,-1138,-1138},{ -409, -688, -688, -688, -688}}
1672 },
1673 {
1674 /* AU.@..AU */
1675 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1676 /* AU.A..AU */
1677 {{ DEF, -429, -599, -599, -599},{ -479, -858,-1028,-1028,-1028},{ -309, -688, -858, -858, -858},{
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1678 /* AU.C..AU */
1679 {{ DEF, -259, -239, -239, -239},{ -649, -858, -838, -838, -838},{ -289, -498, -478, -478, -478},{
-739, -948, -928, -928, -928},{ -379, -588, -568, -568, -568}},
1680 /* AU.G..AU */
1681 {{ DEF, -339, -689, -689, -689},{ -649, -938,-1288,-1288,-1288},{ -289, -578, -928, -928, -928},{

```

```

-739,-1028,-1378,-1378,-1378},{ -379, -668,-1018,-1018,-1018}},
1682 /* AU.U..AU */
1683 {{ DEF, -329, -329, -329, -329},{ -649, -928, -928, -928, -928},{ -289, -568, -568, -568, -568},{
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1684 },
1685 {
1686 /* AU.@..UA */
1687 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1688 /* AU.A..UA */
1689 {{ DEF, -429, -599, -599, -599},{ -449, -828, -998, -998, -998},{ -479, -858,-1028,-1028,-1028},{
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1690 /* AU.C..UA */
1691 {{ DEF, -259, -239, -239, -239},{ -679, -888, -868, -868, -868},{ -559, -768, -748, -748, -748},{
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1692 /* AU.G..UA */
1693 {{ DEF, -339, -689, -689, -689},{ -939,-1228,-1578,-1578,-1578},{ -249, -538, -888, -888, -888},{
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1694 /* AU.U..UA */
1695 {{ DEF, -329, -329, -329, -329},{ -639, -918, -918, -918, -918},{ -229, -508, -508, -508, -508},{
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1696 },
1697 {
1698 /* AU.@..@ */
1699 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1700 /* AU.A..@ */
1701 {{ -100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649},{
-100, -479, -649, -649, -649},{ -100, -479, -649, -649, -649}},
1702 /* AU.C..@ */
1703 {{ -100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289},{
-100, -309, -289, -289, -289},{ -100, -309, -289, -289, -289}},
1704 /* AU.G..@ */
1705 {{ -100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739},{
-100, -389, -739, -739, -739},{ -100, -389, -739, -739, -739}},
1706 /* AU.U..@ */
1707 {{ -100, -379, -379, -379, -379},{ -100, -379, -379, -379, -379},{ -100, -379, -379, -379, -379},{
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1708 }
1709 },
1710 { /* noPair */ {{0}}},
1711 {
1712 /* UA.@..CG */
1713 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1714 /* UA.A..CG */
1715 {{ DEF, -399, -629, -889, -589},{ -1079,-1428,-1658,-1918,-1618},{ -569, -918,-1148,-1408,-1108},{
-989,-1338,-1568,-1828,-1528},{ -859,-1208,-1438,-1698,-1398}},
1716 /* UA.C..CG */
1717 {{ DEF, -429, -509, -199, -179},{ -999,-1378,-1458,-1148,-1128},{ -499, -878, -958, -648, -628},{
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1718 /* UA.G..CG */
1719 {{ DEF, -379, -679, -889, -679},{ -1079,-1408,-1708,-1918,-1708},{ -569, -898,-1198,-1408,-1198},{
-989,-1318,-1618,-1828,-1618},{ -859,-1188,-1488,-1698,-1488}},
1720 /* UA.U..CG */
1721 {{ DEF, -279, -139, -279, -140},{ -1079,-1308,-1168,-1308,-1169},{ -719, -948, -808, -948, -809},{
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1722 },
1723 {
1724 /* UA.@..GC */
1725 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1726 /* UA.A..GC */
1727 {{ DEF, -399, -629, -889, -589},{ -569, -918,-1148,-1408,-1108},{ -769,-1118,-1348,-1608,-1308},{
-759,-1108,-1338,-1598,-1298},{ -549, -898,-1128,-1388,-1088}},
1728 /* UA.C..GC */
1729 {{ DEF, -429, -509, -199, -179},{ -929,-1308,-1388,-1078,-1058},{ -359, -738, -818, -508, -488},{
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1730 /* UA.G..GC */
1731 {{ DEF, -379, -679, -889, -679},{ -609, -938,-1238,-1448,-1238},{ -359, -688, -988,-1198, -988},{
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1732 /* UA.U..GC */
1733 {{ DEF, -279, -139, -279, -140},{ -929,-1158,-1018,-1158,-1019},{ -439, -668, -528, -668, -529},{
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1734 },
1735 {
1736 /* UA.@..GU */
1737 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1738 /* UA.A..GU */
1739 {{ DEF, -399, -629, -889, -589},{ -479, -828,-1058,-1318,-1018},{ -309, -658, -888,-1148, -848},{
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1740 /* UA.C..GU */
1741 {{ DEF, -429, -509, -199, -179},{ -649,-1028,-1108, -798, -778},{ -289, -668, -748, -438, -418},{
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1742 /* UA.G..GU */
1743 {{ DEF, -379, -679, -889, -679},{ -649, -978,-1278,-1488,-1278},{ -289, -618, -918,-1128, -918},{

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-739,-1068,-1368,-1578,-1368},{ -379, -708,-1008,-1218,-1008}},
1744 /* UA.U..GU */
1745 {{ DEF, -279, -139, -279, -140},{ -649, -878, -738, -878, -739},{ -289, -518, -378, -518, -379},{
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1746 },
1747 {
1748 /* UA.@..UG */
1749 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1750 /* UA.A..UG */
1751 {{ DEF, -399, -629, -889, -589},{ -769,-1118,-1348,-1608,-1308},{ -529, -878,-1108,-1368,-1068},{
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1752 /* UA.C..UG */
1753 {{ DEF, -429, -509, -199, -179},{ -839,-1218,-1298, -988, -968},{ -529, -908, -988, -678, -658},{
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1754 /* UA.G..UG */
1755 {{ DEF, -379, -679, -889, -679},{ -1009,-1338,-1638,-1848,-1638},{ -409, -738,-1038,-1248,-1038},{
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1756 /* UA.U..UG */
1757 {{ DEF, -279, -139, -279, -140},{ -859,-1088, -948,-1088, -949},{ -529, -758, -618, -758, -619},{
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1758 },
1759 {
1760 /* UA.@..AU */
1761 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1762 /* UA.A..AU */
1763 {{ DEF, -399, -629, -889, -589},{ -479, -828,-1058,-1318,-1018},{ -309, -658, -888,-1148, -848},{
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1764 /* UA.C..AU */
1765 {{ DEF, -429, -509, -199, -179},{ -649,-1028,-1108, -798, -778},{ -289, -668, -748, -438, -418},{
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1766 /* UA.G..AU */
1767 {{ DEF, -379, -679, -889, -679},{ -649, -978,-1278,-1488,-1278},{ -289, -618, -918,-1128, -918},{
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1768 /* UA.U..AU */
1769 {{ DEF, -279, -139, -279, -140},{ -649, -878, -738, -878, -739},{ -289, -518, -378, -518, -379},{
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1770 },
1771 {
1772 /* UA.@..UA */
1773 {{ 0, 0, 0, 0, 0},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1774 /* UA.A..UA */
1775 {{ DEF, -399, -629, -889, -589},{ -449, -798,-1028,-1288, -988},{ -479, -828,-1058,-1318,-1018},{
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1776 /* UA.C..UA */
1777 {{ DEF, -429, -509, -199, -179},{ -679,-1058,-1138, -828, -808},{ -559, -938,-1018, -708, -688},{
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1778 /* UA.G..UA */
1779 {{ DEF, -379, -679, -889, -679},{ -939,-1268,-1568,-1778,-1568},{ -249, -578, -878,-1088, -878},{
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1780 /* UA.U..UA */
1781 {{ DEF, -279, -139, -279, -140},{ -639, -868, -728, -868, -729},{ -229, -458, -318, -458, -319},{
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1782 },
1783 {
1784 /* UA.@.. @ */
1785 {{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF},{
DEF, DEF, DEF, DEF, DEF},{ DEF, DEF, DEF, DEF, DEF}},
1786 /* UA.A.. @ */
1787 {{ -100, -449, -679, -939, -639},{ -100, -449, -679, -939, -639},{ -100, -449, -679, -939, -639},{
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1788 /* UA.C.. @ */
1789 {{ -100, -479, -559, -249, -229},{ -100, -479, -559, -249, -229},{ -100, -479, -559, -249, -229},{
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1790 /* UA.G.. @ */
1791 {{ -100, -429, -729, -939, -729},{ -100, -429, -729, -939, -729},{ -100, -429, -729, -939, -729},{
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1792 /* UA.U.. @ */
1793 {{ -100, -329, -189, -329, -190},{ -100, -329, -189, -329, -190},{ -100, -329, -189, -329, -190},{
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1794 },
1795 {
1796 /* noPair */ {{{} }},
1797 {
1798 /* @.@..CG */
1799 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
-100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1800 /* @.A..CG */
1801 {{ DEF, DEF, DEF, DEF, DEF},{ -1079,-1079,-1079,-1079,-1079},{ -569, -569, -569, -569, -569},{
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1802 /* @.C..CG */
1803 {{ DEF, DEF, DEF, DEF, DEF},{ -999, -999, -999, -999, -999},{ -499, -499, -499, -499, -499},{
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1804 /* @.G..CG */
1805 {{ DEF, DEF, DEF, DEF, DEF},{ -1079,-1079,-1079,-1079,-1079},{ -569, -569, -569, -569, -569},{

```



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-989, -989, -989, -989, -989},{ -859, -859, -859, -859, -859}},
1806 /* @.U..CG */
1807 {{ DEF, DEF, DEF, DEF, DEF},{ -1079,-1079,-1079,-1079,-1079},{ -719, -719, -719, -719, -719},{
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1808 },
1809 {
1810 /* @.@..GC */
1811 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
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1812 /* @.A..GC */
1813 {{ DEF, DEF, DEF, DEF, DEF},{ -569, -569, -569, -569, -569},{ -769, -769, -769, -769, -769},{
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1814 /* @.C..GC */
1815 {{ DEF, DEF, DEF, DEF, DEF},{ -929, -929, -929, -929, -929},{ -359, -359, -359, -359, -359},{
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1816 /* @.G..GC */
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1818 /* @.U..GC */
1819 {{ DEF, DEF, DEF, DEF, DEF},{ -929, -929, -929, -929, -929},{ -439, -439, -439, -439, -439},{
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1820 },
1821 {
1822 /* @.@..GU */
1823 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
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1824 /* @.A..GU */
1825 {{ DEF, DEF, DEF, DEF, DEF},{ -479, -479, -479, -479, -479},{ -309, -309, -309, -309, -309},{
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1826 /* @.C..GU */
1827 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
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1828 /* @.G..GU */
1829 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
-739, -739, -739, -739, -739},{ -379, -379, -379, -379, -379}},
1830 /* @.U..GU */
1831 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
-739, -739, -739, -739, -739},{ -379, -379, -379, -379, -379}}
1832 },
1833 {
1834 /* @.@..UG */
1835 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
-100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1836 /* @.A..UG */
1837 {{ DEF, DEF, DEF, DEF, DEF},{ -769, -769, -769, -769, -769},{ -529, -529, -529, -529, -529},{
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1838 /* @.C..UG */
1839 {{ DEF, DEF, DEF, DEF, DEF},{ -839, -839, -839, -839, -839},{ -529, -529, -529, -529, -529},{
-859, -859, -859, -859, -859},{ -489, -489, -489, -489, -489}},
1840 /* @.G..UG */
1841 {{ DEF, DEF, DEF, DEF, DEF},{ -1009,-1009,-1009,-1009,-1009},{ -409, -409, -409, -409, -409},{
-969, -969, -969, -969, -969},{ -599, -599, -599, -599, -599}},
1842 /* @.U..UG */
1843 {{ DEF, DEF, DEF, DEF, DEF},{ -859, -859, -859, -859, -859},{ -529, -529, -529, -529, -529},{
-859, -859, -859, -859, -859},{ -409, -409, -409, -409, -409}}
1844 },
1845 {
1846 /* @.@..AU */
1847 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
-100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1848 /* @.A..AU */
1849 {{ DEF, DEF, DEF, DEF, DEF},{ -479, -479, -479, -479, -479},{ -309, -309, -309, -309, -309},{
-389, -389, -389, -389, -389},{ -379, -379, -379, -379, -379}},
1850 /* @.C..AU */
1851 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
-739, -739, -739, -739, -739},{ -379, -379, -379, -379, -379}},
1852 /* @.G..AU */
1853 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
-739, -739, -739, -739, -739},{ -379, -379, -379, -379, -379}},
1854 /* @.U..AU */
1855 {{ DEF, DEF, DEF, DEF, DEF},{ -649, -649, -649, -649, -649},{ -289, -289, -289, -289, -289},{
-739, -739, -739, -739, -739},{ -379, -379, -379, -379, -379}}
1856 },
1857 {
1858 /* @.@..UA */
1859 {{ DEF, DEF, DEF, DEF, DEF},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
-100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1860 /* @.A..UA */
1861 {{ DEF, DEF, DEF, DEF, DEF},{ -449, -449, -449, -449, -449},{ -479, -479, -479, -479, -479},{
-429, -429, -429, -429, -429},{ -329, -329, -329, -329, -329}},
1862 /* @.C..UA */
1863 {{ DEF, DEF, DEF, DEF, DEF},{ -679, -679, -679, -679, -679},{ -559, -559, -559, -559, -559},{
-729, -729, -729, -729, -729},{ -189, -189, -189, -189, -189}},
1864 /* @.G..UA */
1865 {{ DEF, DEF, DEF, DEF, DEF},{ -939, -939, -939, -939, -939},{ -249, -249, -249, -249, -249},{
-939, -939, -939, -939, -939},{ -329, -329, -329, -329, -329}},
1866 /* @.U..UA */

```

```
1867 {{ DEF, DEF, DEF, DEF, DEF},{ -639, -639, -639, -639, -639},{ -229, -229, -229, -229, -229},{
      -729, -729, -729, -729, -729},{ -190, -190, -190, -190, -190}}
1868 },
1869 {
1870 /* @.@.. @ */
1871 {{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
      -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1872 /* @.A.. @ */
1873 {{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
      -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1874 /* @.C.. @ */
1875 {{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
      -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1876 /* @.G.. @ */
1877 {{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
      -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}},
1878 /* @.U.. @ */
1879 {{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100},{
      -100, -100, -100, -100, -100},{ -100, -100, -100, -100, -100}}
1880 }
1881 }
1882 };
1883
1884 PRIVATE int int22_37_184[NBPAIRS+1][NBPAIRS+1][5][5][5][5] = {
1885 /* noPair */ {{{{0}}}},
1886 { /* noPair */ {{{{0}}}},
1887 /* CG....CG */
1888 {{
1889 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1890 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1891 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1892 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1893 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}}
1894 },
1895 {
1896 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1897 {{ 340, 340, 340, 340, 340},{ 340, 130, 160, 30, 200},{ 340, 120, 150, 20, 200},{ 340, 30, 60, -70,
      200},{ 340, 200, 200, 200, 200}},
1898 {{ 340, 340, 340, 340, 340},{ 340, 160, 200, 60, 200},{ 340, 210, 180, 150, 200},{ 340, 200, 200, 200,
      200},{ 340, 190, 170, 130, 200}},
1899 {{ 340, 340, 340, 340, 340},{ 340, 30, 60, -70, 200},{ 340, 200, 200, 200, 200},{ 340, 100, 140, 0,
      200},{ 340, -40, -110, -60, 200}},
1900 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 190, 170, 130, 200},{ 340, 110, 40, 90,
      200},{ 340, 140, 80, 130, 200}}
1901 },
1902 {
1903 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1904 {{ 340, 340, 340, 340, 340},{ 340, 120, 210, 200, 190},{ 340, 110, 140, 200, 120},{ 340, 20, 150, 200,
      130},{ 340, 200, 200, 200, 200}},
1905 {{ 340, 340, 340, 340, 340},{ 340, 150, 180, 200, 170},{ 340, 140, 170, 200, 150},{ 340, 200, 200, 200,
      200},{ 340, 120, 150, 200, 140}},
1906 {{ 340, 340, 340, 340, 340},{ 340, 20, 150, 200, 130},{ 340, 200, 200, 200, 200},{ 340, 90, 180, 200,
      170},{ 340, -150, -20, 200, -40}},
1907 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 120, 150, 200, 140},{ 340, 0, 130, 200,
      110},{ 340, 30, 60, 200, 50}}
1908 },
1909 {
1910 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1911 {{ 340, 340, 340, 340, 340},{ 340, 30, 200, 100, 110},{ 340, 20, 200, 90, 0},{ 340, -70, 200, 0,
      90},{ 340, 200, 200, 200, 200}},
1912 {{ 340, 340, 340, 340, 340},{ 340, 60, 200, 140, 40},{ 340, 150, 200, 180, 130},{ 340, 200, 200, 200,
      200},{ 340, 130, 200, 170, 110}},
1913 {{ 340, 340, 340, 340, 340},{ 340, -70, 200, 0, 90},{ 340, 200, 200, 200, 200},{ 340, 0, 200, 80,
      90},{ 340, -60, 200, -70, -260}},
1914 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 130, 200, 170, 110},{ 340, 90, 200, 90,
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1915 },
1916 {
1917 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
      340},{ 340, 340, 340, 340, 340}},
1918 {{ 340, 340, 340, 340, 340},{ 340, 200, 190, -40, 140},{ 340, 200, 120, -150, 30},{ 340, 200, 130,
      -60, 130},{ 340, 200, 200, 200, 200}},
1919 {{ 340, 340, 340, 340, 340},{ 340, 200, 170, -110, 80},{ 340, 200, 150, -20, 60},{ 340, 200, 200,
      200, 200},{ 340, 200, 140, -40, 50}},
1920 {{ 340, 340, 340, 340, 340},{ 340, 200, 130, -60, 130},{ 340, 200, 200, 200, 200},{ 340, 200, 170, -70,
      120},{ 340, 200, -40, -420, -50}},
1921 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 200, 140, -40, 50},{ 340, 200, 110,
      -260, 110},{ 340, 200, 50, -50, -40}}
1922 }
```

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1923 },
1924 /* CG...GC */
1925 {{
1926 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1927 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1928 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1929 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1930 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1931 },
1932 {
1933 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1934 {{ 340, 340, 340, 340, 340, 340},{ 340, 50, 60, 0, 200},{ 340, 110, 150, -70, 200},{ 340, -30, 10,
    -160, 200},{ 340, 200, 200, 200, 200}},
1935 {{ 340, 340, 340, 340, 340},{ 340, 110, 110, -100, 200},{ 340, 170, 150, -60, 200},{ 340, 200, 200,
    200, 200},{ 340, 70, 50, 20, 200}},
1936 {{ 340, 340, 340, 340, 340},{ 340, 40, 50, -70, 200},{ 340, 200, 200, 200, 200},{ 340, 100, 140, 0,
    200},{ 340, 10, -70, -80, 200}},
1937 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 180, 150, 120, 200},{ 340, -50, -60, -60,
    200},{ 340, 150, 0, 90, 200}},
1938 },
1939 {
1940 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1941 {{ 340, 340, 340, 340, 340, 340},{ 340, 130, 220, 200, 200},{ 340, 100, 130, 200, 120},{ 340, -70, 70, 200,
    40},{ 340, 200, 200, 200, 200}},
1942 {{ 340, 340, 340, 340, 340},{ 340, 100, 190, 200, 110},{ 340, 100, 130, 200, 120},{ 340, 200, 200, 200,
    200},{ 340, 0, 30, 200, 170}},
1943 {{ 340, 340, 340, 340, 340},{ 340, 70, 70, 200, 100},{ 340, 200, 200, 200, 200},{ 340, 90, 180, 200,
    170},{ 340, -190, -30, 200, -70}},
1944 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 110, 140, 200, 120},{ 340, -150, -20,
    200, -30},{ 340, -20, -10, 200, 20}},
1945 },
1946 {
1947 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1948 {{ 340, 340, 340, 340, 340, 340},{ 340, -20, 200, 110, 90},{ 340, -40, 200, 90, 0},{ 340, -170, 200,
    -90, 30},{ 340, 200, 200, 200, 200}},
1949 {{ 340, 340, 340, 340, 340},{ 340, 70, 200, 80, -10},{ 340, 110, 200, 150, 100},{ 340, 200, 200, 200,
    200},{ 340, 20, 200, 50, 0}},
1950 {{ 340, 340, 340, 340, 340},{ 340, -50, 200, -20, 60},{ 340, 200, 200, 200, 200},{ 340, 0, 200, 80,
    90},{ 340, -90, 200, -100, -300}},
1951 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 120, 200, 150, 100},{ 340, -130, 200,
    -60, -240},{ 340, 90, 200, 110, 60}},
1952 },
1953 {
1954 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1955 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, -10, 140},{ 340, 200, 120, -160, 30},{ 340, 200, 40,
    -160, 50},{ 340, 200, 200, 200, 200}},
1956 {{ 340, 340, 340, 340, 340},{ 340, 200, 110, -160, 30},{ 340, 200, 120, -60, 30},{ 340, 200, 200,
    200, 200},{ 340, 200, 20, -160, 10}},
1957 {{ 340, 340, 340, 340, 340},{ 340, 200, 50, -60, 140},{ 340, 200, 200, 200, 200},{ 340, 200, 170, -70,
    120},{ 340, 200, -70, -440, -100}},
1958 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 200, 120, -50, 30},{ 340, 200, -10,
    -410, 10},{ 340, 200, 40, -100, 60}},
1959 },
1960 },
1961 /* CG...GU */
1962 {{
1963 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1964 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340}},
1965 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1966 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1967 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1968 },
1969 {
1970 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1971 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 240, 100, 200},{ 340, 180, 210, 80, 200},{ 340, 80, 110, -20,
    200},{ 340, 200, 200, 200, 200}},
1972 {{ 340, 340, 340, 340, 340},{ 340, 190, 220, 90, 200},{ 340, 230, 210, 170, 200},{ 340, 200, 200, 200,
    200},{ 340, 230, 210, 170, 200}},
1973 {{ 340, 340, 340, 340, 340},{ 340, 80, 110, -20, 200},{ 340, 200, 200, 200, 200},{ 340, 130, 170, 30,
    200},{ 340, 60, 0, 40, 200}},
1974 {{ 340, 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 230, 210, 170, 200},{ 340, 160, 90, 140,
    200},{ 340, 190, 130, 180, 200}}
```

```
1975 },
1976 {
1977 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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1978 {{ 340, 340, 340, 340, 340},{ 340, 190, 280, 200, 270},{ 340, 170, 200, 200, 180},{ 340, 70, 200, 200,
180},{ 340, 200, 200, 200, 200}},
1979 {{ 340, 340, 340, 340, 340},{ 340, 180, 210, 200, 190},{ 340, 160, 190, 200, 180},{ 340, 200, 200, 200,
200},{ 340, 160, 190, 200, 180}},
1980 {{ 340, 340, 340, 340, 340},{ 340, 70, 200, 200, 180},{ 340, 200, 200, 200, 200},{ 340, 120, 210, 200,
200},{ 340, -50, 80, 200, 70}},
1981 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 160, 190, 200, 180},{ 340, 50, 180, 200,
160},{ 340, 80, 110, 200, 100}}
1982 },
1983 {
1984 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
1985 {{ 340, 340, 340, 340, 340},{ 340, 100, 200, 180, 180},{ 340, 80, 200, 150, 60},{ 340, -20, 200, 50,
140},{ 340, 200, 200, 200, 200}},
1986 {{ 340, 340, 340, 340, 340},{ 340, 90, 200, 160, 70},{ 340, 170, 200, 210, 150},{ 340, 200, 200, 200,
200},{ 340, 170, 200, 210, 150}},
1987 {{ 340, 340, 340, 340, 340},{ 340, -20, 200, 50, 140},{ 340, 200, 200, 200, 200},{ 340, 30, 200, 110,
110},{ 340, 40, 200, 40, -160}},
1988 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 170, 200, 210, 150},{ 340, 140, 200, 130,
-60},{ 340, 180, 200, 170, 160}}
1989 },
1990 {
1991 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
1992 {{ 340, 340, 340, 340, 340},{ 340, 200, 270, 30, 220},{ 340, 200, 180, -90, 90},{ 340, 200, 180, -10,
180},{ 340, 200, 200, 200, 200}},
1993 {{ 340, 340, 340, 340, 340},{ 340, 200, 190, -80, 100},{ 340, 200, 180, 0, 90},{ 340, 200, 200, 200,
200},{ 340, 200, 180, 0, 90}},
1994 {{ 340, 340, 340, 340, 340},{ 340, 200, 180, -10, 180},{ 340, 200, 200, 200, 200},{ 340, 200, 200, -40,
150},{ 340, 200, 70, -310, 60}},
1995 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 200, 180, 0, 90},{ 340, 200, 160,
-210, 160},{ 340, 200, 100, 0, 10}}
1996 },
1997 },
1998 /* CG....UG */
1999 {{
2000 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2001 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2002 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2003 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2004 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2005 },
2006 {
2007 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2008 {{ 340, 340, 340, 340, 340},{ 340, 200, 240, 100, 200},{ 340, 160, 190, 60, 200},{ 340, 100, 130, 0,
200},{ 340, 200, 200, 200, 200}},
2009 {{ 340, 340, 340, 340, 340},{ 340, 200, 240, 100, 200},{ 340, 260, 240, 200, 200},{ 340, 200, 200, 200,
200},{ 340, 260, 240, 200, 200}},
2010 {{ 340, 340, 340, 340, 340},{ 340, 100, 130, 0, 200},{ 340, 200, 200, 200, 200},{ 340, 140, 170, 40,
200},{ 340, 20, -40, 0, 200}},
2011 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 230, 210, 170, 200},{ 340, 150, 80, 130,
200},{ 340, 220, 150, 200, 200}}
2012 },
2013 {
2014 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2015 {{ 340, 340, 340, 340, 340},{ 340, 190, 280, 200, 270},{ 340, 150, 180, 200, 160},{ 340, 90, 220, 200,
200},{ 340, 200, 200, 200, 200}},
2016 {{ 340, 340, 340, 340, 340},{ 340, 190, 220, 200, 210},{ 340, 190, 220, 200, 210},{ 340, 200, 200, 200,
200},{ 340, 190, 220, 200, 210}},
2017 {{ 340, 340, 340, 340, 340},{ 340, 90, 220, 200, 200},{ 340, 200, 200, 200, 200},{ 340, 130, 220, 200,
200},{ 340, -90, 40, 200, 30}},
2018 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 160, 190, 200, 180},{ 340, 40, 170, 200,
150},{ 340, 110, 140, 200, 120}}
2019 },
2020 {
2021 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2022 {{ 340, 340, 340, 340, 340},{ 340, 100, 200, 180, 180},{ 340, 60, 200, 130, 40},{ 340, 0, 200, 70,
160},{ 340, 200, 200, 200, 200}},
2023 {{ 340, 340, 340, 340, 340},{ 340, 100, 200, 180, 80},{ 340, 200, 200, 240, 180},{ 340, 200, 200, 200,
200},{ 340, 200, 200, 240, 180}},
2024 {{ 340, 340, 340, 340, 340},{ 340, 0, 200, 70, 160},{ 340, 200, 200, 200, 200},{ 340, 40, 200, 110,
120},{ 340, 0, 200, 0, -200}},
2025 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 170, 200, 210, 150},{ 340, 130, 200, 120,
-70},{ 340, 200, 200, 190, 180}}
2026 },
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2027 {
2028 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2029 {{ 340, 340, 340, 340, 340},{ 340, 200, 270, 30, 220},{ 340, 200, 160, -110, 70},{ 340, 200, 200,
10, 190},{ 340, 200, 200, 200, 200}},
2030 {{ 340, 340, 340, 340, 340},{ 340, 200, 210, -70, 120},{ 340, 200, 210, 30, 120},{ 340, 200, 200, 200,
200},{ 340, 200, 210, 30, 120}},
2031 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 10, 190},{ 340, 200, 200, 200, 200},{ 340, 200, 200, -30,
150},{ 340, 200, 30, -350, 20}},
2032 {{ 340, 340, 340, 340, 340},{ 340, 200, 200, 200, 200},{ 340, 200, 180, 0, 90},{ 340, 200, 150,
-220, 150},{ 340, 200, 120, 30, 30}}
2033 }
2034 },
2035 /* CG...AU */
2036 {{
2037 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2038 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2039 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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2040 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}},
2041 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
340},{ 340, 340, 340, 340, 340}}
2042 },
2043 {
2044 {{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
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3705 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340, 340}},
3706 {{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340},{ 340, 340, 340, 340, 340, 340}},
3707 {{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340, 340, 340, 340}},
3708 {{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340, 340, 340, 340}},
3709 {{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340, 340, 340, 340},{ 340, 340, 340, 340,
    340, 340, 340, 340}},
3710 }
3711 }
3712 }
3713 };
3714
3715 PRIVATE int int22_H184[NBPAIRS+1][NBPAIRS+1][5][5][5][5] =
3716 { /* noPair */ {{{{0}}}},
3717 { /* noPair */ {{{{0}}}},
3718 /* CG.@..CG */
3719 { { { 0, 0, 0, 0, 0},
3720 { DEF, DEF, DEF, DEF, DEF},
3721 { DEF, DEF, DEF, DEF, DEF},
3722 { DEF, DEF, DEF, DEF, DEF},
3723 { DEF, DEF, DEF, DEF, DEF}},
3724 /* CG.@A..CG */
3725 { { 0, 0, 0, 0, 0},
3726 {-1029,-1029,-1029,-1029,-1029},
3727 {-519, -519, -519, -519, -519},
3728 {-939, -939, -939, -939, -939},
3729 {-809, -809, -809, -809, -809}},
3730 /* CG.@C..CG */
3731 { { 0, 0, 0, 0, 0},
3732 {-949, -949, -949, -949, -949},
3733 {-449, -449, -449, -449, -449},
3734 {-939, -939, -939, -939, -939},
3735 {-739, -739, -739, -739, -739}},
3736 /* CG.@G..CG */
3737 { { 0, 0, 0, 0, 0},
3738 {-1029,-1029,-1029,-1029,-1029},
3739 {-519, -519, -519, -519, -519},
3740 {-939, -939, -939, -939, -939},
3741 {-809, -809, -809, -809, -809}},
3742 /* CG.@U..CG */
3743 { { 0, 0, 0, 0, 0},
3744 {-1029,-1029,-1029,-1029,-1029},
3745 {-669, -669, -669, -669, -669},
3746 {-939, -939, -939, -939, -939},
3747 {-859, -859, -859, -859, -859}},
3748 /* CG.A@..CG */
3749 {{{ DEF,-1029, -949,-1029,-1029},
3750 {-100,-1079, -999,-1079,-1079},
3751 {-100,-1079, -999,-1079,-1079},
3752 {-100,-1079, -999,-1079,-1079},
3753 {-100,-1079, -999,-1079,-1079}},
3754 /* CG.AA..CG */
3755 {{{ DEF,-1029, -949,-1029,-1029},
3756 {-1079,-2058,-1978,-2058,-2058},
3757 {-569,-1548,-1468,-1548,-1548},
3758 {-989,-1968,-1888,-1968,-1968},
3759 {-859,-1838,-1758,-1838,-1838}},
3760 /* CG.AC..CG */
3761 {{{ DEF,-1029, -949,-1029,-1029},
3762 {-999,-1978,-1898,-1978,-1978},
3763 {-499,-1478,-1398,-1478,-1478},
3764 {-989,-1968,-1888,-1968,-1968},
3765 {-789,-1768,-1688,-1768,-1768}},
3766 /* CG.AG..CG */
3767 {{{ DEF,-1029, -949,-1029,-1029},

```

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3768 {-1079,-2058,-1978,-2058,-2058},
3769 {-569,-1548,-1468,-1548,-1548},
3770 {-989,-1968,-1888,-1968,-1968},
3771 {-859,-1838,-1758,-1838,-1838}},
3772 /* CG.AU..CG */
3773 {{ DEF, -1029, -949, -1029, -1029},
3774 {-1079,-2058,-1978,-2058,-2058},
3775 {-719,-1698,-1618,-1698,-1698},
3776 {-989,-1968,-1888,-1968,-1968},
3777 {-909,-1888,-1808,-1888,-1888}}},
3778 /* CG.C@..CG */
3779 {{{ DEF, -519, -449, -519, -669},
3780 {-100, -569, -499, -569, -719},
3781 {-100, -569, -499, -569, -719},
3782 {-100, -569, -499, -569, -719},
3783 {-100, -569, -499, -569, -719}},
3784 /* CG.CA..CG */
3785 {{ DEF, -519, -449, -519, -669},
3786 {-1079,-1548,-1478,-1548,-1698},
3787 {-569,-1038, -968,-1038,-1188},
3788 {-989,-1458,-1388,-1458,-1608},
3789 {-859,-1328,-1258,-1328,-1478}},
3790 /* CG.CC..CG */
3791 {{ DEF, -519, -449, -519, -669},
3792 {-999,-1468,-1398,-1468,-1618},
3793 {-499, -968, -898, -968,-1118},
3794 {-989,-1458,-1388,-1458,-1608},
3795 {-789,-1258,-1188,-1258,-1408}},
3796 /* CG.CG..CG */
3797 {{ DEF, -519, -449, -519, -669},
3798 {-1079,-1548,-1478,-1548,-1698},
3799 {-569,-1038, -968,-1038,-1188},
3800 {-989,-1458,-1388,-1458,-1608},
3801 {-859,-1328,-1258,-1328,-1478}},
3802 /* CG.CU..CG */
3803 {{ DEF, -519, -449, -519, -669},
3804 {-1079,-1548,-1478,-1548,-1698},
3805 {-719,-1188,-1118,-1188,-1338},
3806 {-989,-1458,-1388,-1458,-1608},
3807 {-909,-1378,-1308,-1378,-1528}}},
3808 /* CG.G@..CG */
3809 {{{ DEF, -939, -939, -939, -939},
3810 {-100, -989, -989, -989, -989},
3811 {-100, -989, -989, -989, -989},
3812 {-100, -989, -989, -989, -989},
3813 {-100, -989, -989, -989, -989}},
3814 /* CG.GA..CG */
3815 {{ DEF, -939, -939, -939, -939},
3816 {-1079,-1968,-1968,-1968,-1968},
3817 {-569,-1458,-1458,-1458,-1458},
3818 {-989,-1878,-1878,-1878,-1878},
3819 {-859,-1748,-1748,-1748,-1748}},
3820 /* CG.GC..CG */
3821 {{ DEF, -939, -939, -939, -939},
3822 {-999,-1888,-1888,-1888,-1888},
3823 {-499,-1388,-1388,-1388,-1388},
3824 {-989,-1878,-1878,-1878,-1878},
3825 {-789,-1678,-1678,-1678,-1678}},
3826 /* CG.GG..CG */
3827 {{ DEF, -939, -939, -939, -939},
3828 {-1079,-1968,-1968,-1968,-1968},
3829 {-569,-1458,-1458,-1458,-1458},
3830 {-989,-1878,-1878,-1878,-1878},
3831 {-859,-1748,-1748,-1748,-1748}},
3832 /* CG.GU..CG */
3833 {{ DEF, -939, -939, -939, -939},
3834 {-1079,-1968,-1968,-1968,-1968},
3835 {-719,-1608,-1608,-1608,-1608},
3836 {-989,-1878,-1878,-1878,-1878},
3837 {-909,-1798,-1798,-1798,-1798}}},
3838 /* CG.U@..CG */
3839 {{{ DEF, -809, -739, -809, -859},
3840 {-100, -859, -789, -859, -909},
3841 {-100, -859, -789, -859, -909},
3842 {-100, -859, -789, -859, -909},
3843 {-100, -859, -789, -859, -909}},
3844 /* CG.UA..CG */
3845 {{ DEF, -809, -739, -809, -859},
3846 {-1079,-1838,-1768,-1838,-1888},
3847 {-569,-1328,-1258,-1328,-1378},
3848 {-989,-1748,-1678,-1748,-1798},
3849 {-859,-1618,-1548,-1618,-1668}},
3850 /* CG.UC..CG */
3851 {{ DEF, -809, -739, -809, -859},
3852 {-999,-1758,-1688,-1758,-1808},
3853 {-499,-1258,-1188,-1258,-1308},
3854 {-989,-1748,-1678,-1748,-1798},
```

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3855 { -789,-1548,-1478,-1548,-1598}},
3856 /* CG.UG..CG */
3857 {{ DEF, -809, -739, -809, -859},
3858 {-1079,-1838,-1768,-1838,-1888},
3859 { -569,-1328,-1258,-1328,-1378},
3860 { -989,-1748,-1678,-1748,-1798},
3861 { -859,-1618,-1548,-1618,-1668}},
3862 /* CG.UU..CG */
3863 {{ DEF, -809, -739, -809, -859},
3864 {-1079,-1838,-1768,-1838,-1888},
3865 { -719,-1478,-1408,-1478,-1528},
3866 { -989,-1748,-1678,-1748,-1798},
3867 { -909,-1668,-1598,-1668,-1718}}}},
3868 /* CG.@..GC */
3869 {{{ 0, 0, 0, 0, 0},
3870 { DEF, DEF, DEF, DEF, DEF},
3871 { DEF, DEF, DEF, DEF, DEF},
3872 { DEF, DEF, DEF, DEF, DEF},
3873 { DEF, DEF, DEF, DEF, DEF}},
3874 /* CG.@A..GC */
3875 {{ 0, 0, 0, 0, 0},
3876 { -519, -519, -519, -519, -519},
3877 { -719, -719, -719, -719, -719},
3878 { -709, -709, -709, -709, -709},
3879 { -499, -499, -499, -499, -499}},
3880 /* CG.@C..GC */
3881 {{ 0, 0, 0, 0, 0},
3882 { -879, -879, -879, -879, -879},
3883 { -309, -309, -309, -309, -309},
3884 { -739, -739, -739, -739, -739},
3885 { -499, -499, -499, -499, -499}},
3886 /* CG.@G..GC */
3887 {{ 0, 0, 0, 0, 0},
3888 { -559, -559, -559, -559, -559},
3889 { -309, -309, -309, -309, -309},
3890 { -619, -619, -619, -619, -619},
3891 { -499, -499, -499, -499, -499}},
3892 /* CG.@U..GC */
3893 {{ 0, 0, 0, 0, 0},
3894 { -879, -879, -879, -879, -879},
3895 { -389, -389, -389, -389, -389},
3896 { -739, -739, -739, -739, -739},
3897 { -569, -569, -569, -569, -569}}}},
3898 /* CG.A@..GC */
3899 {{{ DEF,-1029, -949,-1029,-1029},
3900 { -100,-1079, -999,-1079,-1079},
3901 { -100,-1079, -999,-1079,-1079},
3902 { -100,-1079, -999,-1079,-1079},
3903 { -100,-1079, -999,-1079,-1079}},
3904 /* CG.AA..GC */
3905 {{ DEF,-1029, -949,-1029,-1029},
3906 { -569,-1548,-1468,-1548,-1548},
3907 { -769,-1748,-1668,-1748,-1748},
3908 { -759,-1738,-1658,-1738,-1738},
3909 { -549,-1528,-1448,-1528,-1528}},
3910 /* CG.AC..GC */
3911 {{ DEF,-1029, -949,-1029,-1029},
3912 { -929,-1908,-1828,-1908,-1908},
3913 { -359,-1338,-1258,-1338,-1338},
3914 { -789,-1768,-1688,-1768,-1768},
3915 { -549,-1528,-1448,-1528,-1528}},
3916 /* CG.AG..GC */
3917 {{ DEF,-1029, -949,-1029,-1029},
3918 { -609,-1588,-1508,-1588,-1588},
3919 { -359,-1338,-1258,-1338,-1338},
3920 { -669,-1648,-1568,-1648,-1648},
3921 { -549,-1528,-1448,-1528,-1528}},
3922 /* CG.AU..GC */
3923 {{ DEF,-1029, -949,-1029,-1029},
3924 { -929,-1908,-1828,-1908,-1908},
3925 { -439,-1418,-1338,-1418,-1418},
3926 { -789,-1768,-1688,-1768,-1768},
3927 { -619,-1598,-1518,-1598,-1598}}}},
3928 /* CG.C@..GC */
3929 {{{ DEF, -519, -449, -519, -669},
3930 { -100, -569, -499, -569, -719},
3931 { -100, -569, -499, -569, -719},
3932 { -100, -569, -499, -569, -719},
3933 { -100, -569, -499, -569, -719}},
3934 /* CG.CA..GC */
3935 {{ DEF, -519, -449, -519, -669},
3936 { -569,-1038, -968,-1038,-1188},
3937 { -769,-1238,-1168,-1238,-1388},
3938 { -759,-1228,-1158,-1228,-1378},
3939 { -549,-1018, -948,-1018,-1168}},
3940 /* CG.CC..GC */
3941 {{ DEF, -519, -449, -519, -669},

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3942 { -929,-1398,-1328,-1398,-1548},
3943 { -359, -828, -758, -828, -978},
3944 { -789,-1258,-1188,-1258,-1408},
3945 { -549,-1018, -948,-1018,-1168}},
3946 /* CG.CG..GC */
3947 {{ DEF, -519, -449, -519, -669},
3948 { -609,-1078,-1008,-1078,-1228},
3949 { -359, -828, -758, -828, -978},
3950 { -669,-1138,-1068,-1138,-1288},
3951 { -549,-1018, -948,-1018,-1168}},
3952 /* CG.CU..GC */
3953 {{ DEF, -519, -449, -519, -669},
3954 { -929,-1398,-1328,-1398,-1548},
3955 { -439, -908, -838, -908,-1058},
3956 { -789,-1258,-1188,-1258,-1408},
3957 { -619,-1088,-1018,-1088,-1238}}},
3958 /* CG.G@..GC */
3959 {{{ DEF, -939, -939, -939, -939},
3960 { -100, -989, -989, -989, -989},
3961 { -100, -989, -989, -989, -989},
3962 { -100, -989, -989, -989, -989},
3963 { -100, -989, -989, -989, -989}}},
3964 /* CG.GA..GC */
3965 {{ DEF, -939, -939, -939, -939},
3966 { -569,-1458,-1458,-1458,-1458},
3967 { -769,-1658,-1658,-1658,-1658},
3968 { -759,-1648,-1648,-1648,-1648},
3969 { -549,-1438,-1438,-1438,-1438}},
3970 /* CG.GC..GC */
3971 {{ DEF, -939, -939, -939, -939},
3972 { -929,-1818,-1818,-1818,-1818},
3973 { -359,-1248,-1248,-1248,-1248},
3974 { -789,-1678,-1678,-1678,-1678},
3975 { -549,-1438,-1438,-1438,-1438}},
3976 /* CG.GG..GC */
3977 {{ DEF, -939, -939, -939, -939},
3978 { -609,-1498,-1498,-1498,-1498},
3979 { -359,-1248,-1248,-1248,-1248},
3980 { -669,-1558,-1558,-1558,-1558},
3981 { -549,-1438,-1438,-1438,-1438}},
3982 /* CG.GU..GC */
3983 {{ DEF, -939, -939, -939, -939},
3984 { -929,-1818,-1818,-1818,-1818},
3985 { -439,-1328,-1328,-1328,-1328},
3986 { -789,-1678,-1678,-1678,-3080},
3987 { -619,-1508,-1508,-1508,-1508}}},
3988 /* CG.U@..GC */
3989 {{{ DEF, -809, -739, -809, -859},
3990 { -100, -859, -789, -859, -909},
3991 { -100, -859, -789, -859, -909},
3992 { -100, -859, -789, -859, -909},
3993 { -100, -859, -789, -859, -909}}},
3994 /* CG.UA..GC */
3995 {{ DEF, -809, -739, -809, -859},
3996 { -569,-1328,-1258,-1328,-1378},
3997 { -769,-1528,-1458,-1528,-1578},
3998 { -759,-1518,-1448,-1518,-1568},
3999 { -549,-1308,-1238,-1308,-1358}},
4000 /* CG.UC..GC */
4001 {{ DEF, -809, -739, -809, -859},
4002 { -929,-1688,-1618,-1688,-1738},
4003 { -359,-1118,-1048,-1118,-1168},
4004 { -789,-1548,-1478,-1548,-1598},
4005 { -549,-1308,-1238,-1308,-1358}},
4006 /* CG.UG..GC */
4007 {{ DEF, -809, -739, -809, -859},
4008 { -609,-1368,-1298,-1368,-1418},
4009 { -359,-1118,-1048,-1118,-1168},
4010 { -669,-1428,-1358,-1428,-1478},
4011 { -549,-1308,-1238,-1308,-1358}},
4012 /* CG.UU..GC */
4013 {{ DEF, -809, -739, -809, -859},
4014 { -929,-1688,-1618,-1688,-1738},
4015 { -439,-1198,-1128,-1198,-1248},
4016 { -789,-1548,-1478,-1548,-1598},
4017 { -619,-1378,-1308,-1378,-1428}}},
4018 /* CG.@@..GU */
4019 {{{{ 0, 0, 0, 0, 0},
4020 { DEF, DEF, DEF, DEF, DEF},
4021 { DEF, DEF, DEF, DEF, DEF},
4022 { DEF, DEF, DEF, DEF, DEF},
4023 { DEF, DEF, DEF, DEF, DEF}}},
4024 /* CG.@A..GU */
4025 {{ 0, 0, 0, 0, 0},
4026 { -429, -429, -429, -429, -429},
4027 { -259, -259, -259, -259, -259},
4028 { -339, -339, -339, -339, -339},

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4029 { -329, -329, -329, -329, -329}},
4030 /* CG.@C..GU */
4031 {{ 0, 0, 0, 0, 0}},
4032 { -599, -599, -599, -599, -599}},
4033 { -239, -239, -239, -239, -239}},
4034 { -689, -689, -689, -689, -689}},
4035 { -329, -329, -329, -329, -329}},
4036 /* CG.@G..GU */
4037 {{ 0, 0, 0, 0, 0}},
4038 { -599, -599, -599, -599, -599}},
4039 { -239, -239, -239, -239, -239}},
4040 { -689, -689, -689, -689, -689}},
4041 { -329, -329, -329, -329, -329}},
4042 /* CG.@U..GU */
4043 {{ 0, 0, 0, 0, 0}},
4044 { -599, -599, -599, -599, -599}},
4045 { -239, -239, -239, -239, -239}},
4046 { -689, -689, -689, -689, -689}},
4047 { -329, -329, -329, -329, -329}}}},
4048 /* CG.A@..GU */
4049 {{{ DEF, -1029, -949, -1029, -1029}},
4050 { -100, -1079, -999, -1079, -1079}},
4051 { -100, -1079, -999, -1079, -1079}},
4052 { -100, -1079, -999, -1079, -1079}},
4053 { -100, -1079, -999, -1079, -1079}}}},
4054 /* CG.AA..GU */
4055 {{{ DEF, -1029, -949, -1029, -1029}},
4056 { -479, -1458, -1378, -1458, -1458}},
4057 { -309, -1288, -1208, -1288, -1288}},
4058 { -389, -1368, -1288, -1368, -1368}},
4059 { -379, -1358, -1278, -1358, -1358}}}},
4060 /* CG.AC..GU */
4061 {{{ DEF, -1029, -949, -1029, -1029}},
4062 { -649, -1628, -1548, -1628, -1628}},
4063 { -289, -1268, -1188, -1268, -1268}},
4064 { -739, -1718, -1638, -1718, -1718}},
4065 { -379, -1358, -1278, -1358, -1358}}}},
4066 /* CG.AG..GU */
4067 {{{ DEF, -1029, -949, -1029, -1029}},
4068 { -649, -1628, -1548, -1628, -1628}},
4069 { -289, -1268, -1188, -1268, -1268}},
4070 { -739, -1718, -1638, -1718, -1718}},
4071 { -379, -1358, -1278, -1358, -1358}}}},
4072 /* CG.AU..GU */
4073 {{{ DEF, -1029, -949, -1029, -1029}},
4074 { -649, -1628, -1548, -1628, -1628}},
4075 { -289, -1268, -1188, -1268, -1268}},
4076 { -739, -1718, -1638, -1718, -1718}},
4077 { -379, -1358, -1278, -1358, -1358}}}},
4078 /* CG.C@..GU */
4079 {{{ DEF, -519, -449, -519, -669}},
4080 { -100, -569, -499, -569, -719}},
4081 { -100, -569, -499, -569, -719}},
4082 { -100, -569, -499, -569, -719}},
4083 { -100, -569, -499, -569, -719}}}},
4084 /* CG.CA..GU */
4085 {{{ DEF, -519, -449, -519, -669}},
4086 { -479, -948, -878, -948, -1098}},
4087 { -309, -778, -708, -778, -928}},
4088 { -389, -858, -788, -858, -1008}},
4089 { -379, -848, -778, -848, -998}}}},
4090 /* CG.CC..GU */
4091 {{{ DEF, -519, -449, -519, -669}},
4092 { -649, -1118, -1048, -1118, -1268}},
4093 { -289, -758, -688, -758, -908}},
4094 { -739, -1208, -1138, -1208, -1358}},
4095 { -379, -848, -778, -848, -998}}}},
4096 /* CG.CG..GU */
4097 {{{ DEF, -519, -449, -519, -669}},
4098 { -649, -1118, -1048, -1118, -1268}},
4099 { -289, -758, -688, -758, -908}},
4100 { -739, -1208, -1138, -1208, -1358}},
4101 { -379, -848, -778, -848, -998}}}},
4102 /* CG.CU..GU */
4103 {{{ DEF, -519, -449, -519, -669}},
4104 { -649, -1118, -1048, -1118, -1268}},
4105 { -289, -758, -688, -758, -908}},
4106 { -739, -1208, -1138, -1208, -1358}},
4107 { -379, -848, -778, -848, -998}}}},
4108 /* CG.G@..GU */
4109 {{{ DEF, -939, -939, -939, -939}},
4110 { -100, -989, -989, -989, -989}},
4111 { -100, -989, -989, -989, -989}},
4112 { -100, -989, -989, -989, -989}},
4113 { -100, -989, -989, -989, -989}}}},
4114 /* CG.GA..GU */
4115 {{{ DEF, -939, -939, -939, -939}},

```

```

4116 { -479,-1368,-1368,-1368,-1368},
4117 { -309,-1198,-1198,-1198,-1198},
4118 { -389,-1278,-1278,-1278,-1278},
4119 { -379,-1268,-1268,-1268,-1268}},
4120 /* CG.GC..GU */
4121 {{ DEF, -939, -939, -939, -939},
4122 { -649,-1538,-1538,-1538,-1538},
4123 { -289,-1178,-1178,-1178,-1178},
4124 { -739,-1628,-1628,-1628,-1628},
4125 { -379,-1268,-1268,-1268,-1268}},
4126 /* CG.GG..GU */
4127 {{ DEF, -939, -939, -939, -939},
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4129 { -289,-1178,-1178,-1178,-1178},
4130 { -739,-1628,-1628,-1628,-1628},
4131 { -379,-1268,-1268,-1268,-1268}},
4132 /* CG.GU..GU */
4133 {{ DEF, -939, -939, -939, -939},
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4135 { -289,-1178,-1178,-1178,-1178},
4136 { -739,-1628,-1628,-1628,-1628},
4137 { -379,-1268,-1268,-1268,-1268}}},
4138 /* CG.U@..GU */
4139 {{{ DEF, -809, -739, -809, -859},
4140 { -100, -859, -789, -859, -909},
4141 { -100, -859, -789, -859, -909},
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4143 { -100, -859, -789, -859, -909}}},
4144 /* CG.UA..GU */
4145 {{ DEF, -809, -739, -809, -859},
4146 { -479,-1238,-1168,-1238,-1288},
4147 { -309,-1068, -998,-1068,-1118},
4148 { -389,-1148,-1078,-1148,-1198},
4149 { -379,-1138,-1068,-1138,-1188}},
4150 /* CG.UC..GU */
4151 {{ DEF, -809, -739, -809, -859},
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4153 { -289,-1048, -978,-1048,-1098},
4154 { -739,-1498,-1428,-1498,-1548},
4155 { -379,-1138,-1068,-1138,-1188}},
4156 /* CG.UG..GU */
4157 {{ DEF, -809, -739, -809, -859},
4158 { -649,-1408,-1338,-1408,-1458},
4159 { -289,-1048, -978,-1048,-1098},
4160 { -739,-1498,-1428,-1498,-1548},
4161 { -379,-1138,-1068,-1138,-1188}},
4162 /* CG.UU..GU */
4163 {{ DEF, -809, -739, -809, -859},
4164 { -649,-1408,-1338,-1408,-1458},
4165 { -289,-1048, -978,-1048,-1098},
4166 { -739,-1498,-1428,-1498,-1548},
4167 { -379,-1138,-1068,-1138,-1188}}}},
4168 /* CG.@@..UG */
4169 {{{ 0, 0, 0, 0, 0},
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4174 /* CG.@A..UG */
4175 {{ 0, 0, 0, 0, 0},
4176 { -719, -719, -719, -719, -719},
4177 { -479, -479, -479, -479, -479},
4178 { -659, -659, -659, -659, -659},
4179 { -549, -549, -549, -549, -549}}},
4180 /* CG.@C..UG */
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4183 { -479, -479, -479, -479, -479},
4184 { -809, -809, -809, -809, -809},
4185 { -439, -439, -439, -439, -439}},
4186 /* CG.@G..UG */
4187 {{ 0, 0, 0, 0, 0},
4188 { -959, -959, -959, -959, -959},
4189 { -359, -359, -359, -359, -359},
4190 { -919, -919, -919, -919, -919},
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4192 /* CG.@U..UG */
4193 {{ 0, 0, 0, 0, 0},
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4197 { -359, -359, -359, -359, -359}}}},
4198 /* CG.A@..UG */
4199 {{{ DEF,-1029, -949,-1029,-1029},
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4202 { -100,-1079, -999,-1079,-1079},

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4203 { -100,-1079, -999,-1079,-1079}},
4204 /* CG.AA..UG */
4205 {{ DEF,-1029, -949,-1029,-1029},
4206 { -769,-1748,-1668,-1748,-1748},
4207 { -529,-1508,-1428,-1508,-1508},
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4209 { -599,-1578,-1498,-1578,-1578}},
4210 /* CG.AC..UG */
4211 {{ DEF,-1029, -949,-1029,-1029},
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4215 { -489,-1468,-1388,-1468,-1468}},
4216 /* CG.AG..UG */
4217 {{ DEF,-1029, -949,-1029,-1029},
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4219 { -409,-1388,-1308,-1388,-1388},
4220 { -969,-1948,-1868,-1948,-1948},
4221 { -599,-1578,-1498,-1578,-1578}},
4222 /* CG.AU..UG */
4223 {{ DEF,-1029, -949,-1029,-1029},
4224 { -859,-1838,-1758,-1838,-1838},
4225 { -529,-1508,-1428,-1508,-1508},
4226 { -859,-1838,-1758,-1838,-1838},
4227 { -409,-1388,-1308,-1388,-1388}}},
4228 /* CG.C@..UG */
4229 {{{ DEF, -519, -449, -519, -669},
4230 { -100, -569, -499, -569, -719},
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4234 /* CG.CA..UG */
4235 {{ DEF, -519, -449, -519, -669},
4236 { -769,-1238,-1168,-1238,-1388},
4237 { -529, -998, -928, -998,-1148},
4238 { -709,-1178,-1108,-1178,-1328},
4239 { -599,-1068, -998,-1068,-1218}},
4240 /* CG.CC..UG */
4241 {{ DEF, -519, -449, -519, -669},
4242 { -839,-1308,-1238,-1308,-1458},
4243 { -529, -998, -928, -998,-1148},
4244 { -859,-1328,-1258,-1328,-1478},
4245 { -489, -958, -888, -958,-1108}},
4246 /* CG.CG..UG */
4247 {{ DEF, -519, -449, -519, -669},
4248 {-1009,-1478,-1408,-1478,-1628},
4249 { -409, -878, -808, -878,-1028},
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4251 { -599,-1068, -998,-1068,-1218}},
4252 /* CG.CU..UG */
4253 {{ DEF, -519, -449, -519, -669},
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4258 /* CG.G@..UG */
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4264 /* CG.GA..UG */
4265 {{ DEF, -939, -939, -939, -939},
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4269 { -599,-1488,-1488,-1488,-1488}},
4270 /* CG.GC..UG */
4271 {{ DEF, -939, -939, -939, -939},
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4275 { -489,-1378,-1378,-1378,-1378}},
4276 /* CG.GG..UG */
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4281 { -599,-1488,-1488,-1488,-1488}},
4282 /* CG.GU..UG */
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4285 { -529,-1418,-1418,-1418,-1418},
4286 { -859,-1748,-1748,-1748,-1748},
4287 { -409,-1298,-1298,-1298,-1298}}},
4288 /* CG.U@..UG */
4289 {{{ DEF, -809, -739, -809, -859},

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4290 { -100, -859, -789, -859, -909},
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4292 { -100, -859, -789, -859, -909},
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4295 {{ DEF, -809, -739, -809, -859},
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4301 {{ DEF, -809, -739, -809, -859},
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4305 { -489,-1248,-1178,-1248,-1298}},
4306 /* CG.UG..UG */
4307 {{ DEF, -809, -739, -809, -859},
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4312 /* CG.UU..UG */
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4315 { -529,-1288,-1218,-1288,-1338},
4316 { -859,-1618,-1548,-1618,-1668},
4317 { -409,-1168,-1098,-1168,-1218}}}},
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4336 /* CG.@G..AU */
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4348 /* CG.A@..AU */
4349 {{{ DEF,-1029, -949,-1029,-1029},
4350 { -100,-1079, -999,-1079,-1079},
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4354 /* CG.AA..AU */
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4377 { -379,-1358,-1278,-1358,-1358}}},
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4438 /* CG.U@..AU */
4439 {{{ DEF, -809, -739, -809, -859},
4440 { -100, -859, -789, -859, -909},
4441 { -100, -859, -789, -859, -909},
4442 { -100, -859, -789, -859, -909},
4443 { -100, -859, -789, -859, -909}},
4444 /* CG.UA..AU */
4445 {{{ DEF, -809, -739, -809, -859},
4446 { -479,-1238,-1168,-1238,-1288},
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4449 { -379,-1138,-1068,-1138,-1188}},
4450 /* CG.UC..AU */
4451 {{{ DEF, -809, -739, -809, -859},
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4453 { -289,-1048, -978,-1048,-1098},
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4455 { -379,-1138,-1068,-1138,-1188}},
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4462 /* CG.UU..AU */
4463 {{{ DEF, -809, -739, -809, -859},
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4464 { -649,-1408,-1338,-1408,-1458},
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4466 { -739,-1498,-1428,-1498,-1548},
4467 { -379,-1138,-1068,-1138,-1188}}},
4468 /* CG.@@..UA */
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4472 { DEF, DEF, DEF, DEF, DEF},
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4478 { -379,-379,-379,-379,-379},
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4510 /* CG.AC..UA */
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4515 { -189,-1168,-1088,-1168,-1168}},
4516 /* CG.AG..UA */
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4528 /* CG.C@..UA */
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4533 { -100, -569, -499, -569, -719}},
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4535 {{{ DEF, -519, -449, -519, -669},
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4540 /* CG.CC..UA */
4541 {{{ DEF, -519, -449, -519, -669},
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4545 { -189,-658, -588, -658, -808}},
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4551 { -329, -798, -728, -798, -948}},
4552 /* CG.CU..UA */
4553 {{ DEF, -519, -449, -519, -669},
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4563 { -100, -989, -989, -989, -989}},
4564 /* CG.GA..UA */
4565 {{ DEF, -939, -939, -939, -939},
4566 { -449,-1338,-1338,-1338,-1338},
4567 { -479,-1368,-1368,-1368,-1368},
4568 { -429,-1318,-1318,-1318,-1318},
4569 { -329,-1218,-1218,-1218,-1218}},
4570 /* CG.GC..UA */
4571 {{ DEF, -939, -939, -939, -939},
4572 { -679,-1568,-1568,-1568,-1568},
4573 { -559,-1448,-1448,-1448,-1448},
4574 { -729,-1618,-1618,-1618,-1618},
4575 { -189,-1078,-1078,-1078,-1078}},
4576 /* CG.GG..UA */
4577 {{ DEF, -939, -939, -939, -939},
4578 { -939,-1828,-1828,-1828,-1828},
4579 { -249,-1138,-1138,-1138,-1138},
4580 { -939,-1828,-1828,-1828,-1828},
4581 { -329,-1218,-1218,-1218,-1218}},
4582 /* CG.GU..UA */
4583 {{ DEF, -939, -939, -939, -939},
4584 { -639,-1528,-1528,-1528,-1528},
4585 { -229,-1118,-1118,-1118,-1118},
4586 { -729,-1618,-1618,-1618,-1618},
4587 { -190,-1079,-1079,-1079,-1079}}},
4588 /* CG.U@..UA */
4589 {{{ DEF, -809, -739, -809, -859},
4590 { -100, -859, -789, -859, -909},
4591 { -100, -859, -789, -859, -909},
4592 { -100, -859, -789, -859, -909},
4593 { -100, -859, -789, -859, -909}},
4594 /* CG.UA..UA */
4595 {{ DEF, -809, -739, -809, -859},
4596 { -449,-1208,-1138,-1208,-1258},
4597 { -479,-1238,-1168,-1238,-1288},
4598 { -429,-1188,-1118,-1188,-1238},
4599 { -329,-1088,-1018,-1088,-1138}},
4600 /* CG.UC..UA */
4601 {{ DEF, -809, -739, -809, -859},
4602 { -679,-1438,-1368,-1438,-1488},
4603 { -559,-1318,-1248,-1318,-1368},
4604 { -729,-1488,-1418,-1488,-1538},
4605 { -189, -948, -878, -948, -998}},
4606 /* CG.UG..UA */
4607 {{ DEF, -809, -739, -809, -859},
4608 { -939,-1698,-1628,-1698,-1748},
4609 { -249,-1008, -938,-1008,-1058},
4610 { -939,-1698,-1628,-1698,-1748},
4611 { -329,-1088,-1018,-1088,-1138}},
4612 /* CG.UU..UA */
4613 {{ DEF, -809, -739, -809, -859},
4614 { -639,-1398,-1328,-1398,-1448},
4615 { -229, -988, -918, -988,-1038},
4616 { -729,-1488,-1418,-1488,-1538},
4617 { -190, -949, -879, -949, -999}}},
4618 /* CG.@@.. @ */
4619 {{{{ DEF, DEF, DEF, DEF, DEF},
4620 { DEF, DEF, DEF, DEF, DEF},
4621 { DEF, DEF, DEF, DEF, DEF},
4622 { DEF, DEF, DEF, DEF, DEF},
4623 { DEF, DEF, DEF, DEF, DEF}}},
4624 /* CG.@A.. @ */
4625 {{ DEF, DEF, DEF, DEF, DEF},
4626 { DEF, DEF, DEF, DEF, DEF},
4627 { DEF, DEF, DEF, DEF, DEF},
4628 { DEF, DEF, DEF, DEF, DEF},
4629 { DEF, DEF, DEF, DEF, DEF}},
4630 /* CG.@C.. @ */
4631 {{{ DEF, DEF, DEF, DEF, DEF},
4632 { DEF, DEF, DEF, DEF, DEF},
4633 { DEF, DEF, DEF, DEF, DEF},
4634 { DEF, DEF, DEF, DEF, DEF},
4635 { DEF, DEF, DEF, DEF, DEF}},
4636 /* CG.@G.. @ */
4637 {{ DEF, DEF, DEF, DEF, DEF},

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4638 { DEF, DEF, DEF, DEF, DEF},
4639 { DEF, DEF, DEF, DEF, DEF},
4640 { DEF, DEF, DEF, DEF, DEF},
4641 { DEF, DEF, DEF, DEF, DEF}},
4642 /* CG.UU.. @ */
4643 {{ DEF, DEF, DEF, DEF, DEF},
4644 { DEF, DEF, DEF, DEF, DEF},
4645 { DEF, DEF, DEF, DEF, DEF},
4646 { DEF, DEF, DEF, DEF, DEF},
4647 { DEF, DEF, DEF, DEF, DEF}}},
4648 /* CG.A@.. @ */
4649 {{{ -100,-1079, -999,-1079,-1079},
4650 { -100,-1079, -999,-1079,-1079},
4651 { -100,-1079, -999,-1079,-1079},
4652 { -100,-1079, -999,-1079,-1079},
4653 { -100,-1079, -999,-1079,-1079}},
4654 /* CG.AA.. @ */
4655 {{{ -100,-1079, -999,-1079,-1079},
4656 { -100,-1079, -999,-1079,-1079},
4657 { -100,-1079, -999,-1079,-1079},
4658 { -100,-1079, -999,-1079,-1079},
4659 { -100,-1079, -999,-1079,-1079}},
4660 /* CG.AC.. @ */
4661 {{{ -100,-1079, -999,-1079,-1079},
4662 { -100,-1079, -999,-1079,-1079},
4663 { -100,-1079, -999,-1079,-1079},
4664 { -100,-1079, -999,-1079,-1079},
4665 { -100,-1079, -999,-1079,-1079}},
4666 /* CG.AG.. @ */
4667 {{{ -100,-1079, -999,-1079,-1079},
4668 { -100,-1079, -999,-1079,-1079},
4669 { -100,-1079, -999,-1079,-1079},
4670 { -100,-1079, -999,-1079,-1079},
4671 { -100,-1079, -999,-1079,-1079}},
4672 /* CG.AU.. @ */
4673 {{{ -100,-1079, -999,-1079,-1079},
4674 { -100,-1079, -999,-1079,-1079},
4675 { -100,-1079, -999,-1079,-1079},
4676 { -100,-1079, -999,-1079,-1079},
4677 { -100,-1079, -999,-1079,-1079}}},
4678 /* CG.C@.. @ */
4679 {{{ -100, -569, -499, -569, -719},
4680 { -100, -569, -499, -569, -719},
4681 { -100, -569, -499, -569, -719},
4682 { -100, -569, -499, -569, -719},
4683 { -100, -569, -499, -569, -719}},
4684 /* CG.CA.. @ */
4685 {{{ -100, -569, -499, -569, -719},
4686 { -100, -569, -499, -569, -719},
4687 { -100, -569, -499, -569, -719},
4688 { -100, -569, -499, -569, -719},
4689 { -100, -569, -499, -569, -719}},
4690 /* CG.CC.. @ */
4691 {{{ -100, -569, -499, -569, -719},
4692 { -100, -569, -499, -569, -719},
4693 { -100, -569, -499, -569, -719},
4694 { -100, -569, -499, -569, -719},
4695 { -100, -569, -499, -569, -719}},
4696 /* CG.CG.. @ */
4697 {{{ -100, -569, -499, -569, -719},
4698 { -100, -569, -499, -569, -719},
4699 { -100, -569, -499, -569, -719},
4700 { -100, -569, -499, -569, -719},
4701 { -100, -569, -499, -569, -719}},
4702 /* CG.CU.. @ */
4703 {{{ -100, -569, -499, -569, -719},
4704 { -100, -569, -499, -569, -719},
4705 { -100, -569, -499, -569, -719},
4706 { -100, -569, -499, -569, -719},
4707 { -100, -569, -499, -569, -719}}},
4708 /* CG.G@.. @ */
4709 {{{ -100, -989, -989, -989, -989},
4710 { -100, -989, -989, -989, -989},
4711 { -100, -989, -989, -989, -989},
4712 { -100, -989, -989, -989, -989},
4713 { -100, -989, -989, -989, -989}},
4714 /* CG.GA.. @ */
4715 {{{ -100, -989, -989, -989, -989},
4716 { -100, -989, -989, -989, -989},
4717 { -100, -989, -989, -989, -989},
4718 { -100, -989, -989, -989, -989},
4719 { -100, -989, -989, -989, -989}},
4720 /* CG.GC.. @ */
4721 {{{ -100, -989, -989, -989, -989},
4722 { -100, -989, -989, -989, -989},
4723 { -100, -989, -989, -989, -989},
4724 { -100, -989, -989, -989, -989},

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4725 { -100, -989, -989, -989, -989}},
4726 /* CG.GG.. @ */
4727 {{ -100, -989, -989, -989, -989}},
4728 { -100, -989, -989, -989, -989}},
4729 { -100, -989, -989, -989, -989}},
4730 { -100, -989, -989, -989, -989}},
4731 { -100, -989, -989, -989, -989}},
4732 /* CG.GU.. @ */
4733 {{ -100, -989, -989, -989, -989}},
4734 { -100, -989, -989, -989, -989}},
4735 { -100, -989, -989, -989, -989}},
4736 { -100, -989, -989, -989, -989}},
4737 { -100, -989, -989, -989, -989}}},
4738 /* CG.U@.. @ */
4739 {{{ -100, -859, -789, -859, -909}},
4740 { -100, -859, -789, -859, -909}},
4741 { -100, -859, -789, -859, -909}},
4742 { -100, -859, -789, -859, -909}},
4743 { -100, -859, -789, -859, -909}},
4744 /* CG.UA.. @ */
4745 {{{ -100, -859, -789, -859, -909}},
4746 { -100, -859, -789, -859, -909}},
4747 { -100, -859, -789, -859, -909}},
4748 { -100, -859, -789, -859, -909}},
4749 { -100, -859, -789, -859, -909}}},
4750 /* CG.UC.. @ */
4751 {{{ -100, -859, -789, -859, -909}},
4752 { -100, -859, -789, -859, -909}},
4753 { -100, -859, -789, -859, -909}},
4754 { -100, -859, -789, -859, -909}},
4755 { -100, -859, -789, -859, -909}}},
4756 /* CG.UG.. @ */
4757 {{{ -100, -859, -789, -859, -909}},
4758 { -100, -859, -789, -859, -909}},
4759 { -100, -859, -789, -859, -909}},
4760 { -100, -859, -789, -859, -909}},
4761 { -100, -859, -789, -859, -909}}},
4762 /* CG.UU.. @ */
4763 {{{ -100, -859, -789, -859, -909}},
4764 { -100, -859, -789, -859, -909}},
4765 { -100, -859, -789, -859, -909}},
4766 { -100, -859, -789, -859, -909}},
4767 { -100, -859, -789, -859, -909}}}}},
4768 { /* noPair */ {{{0}}}},
4769 /* GC.@@..CG */
4770 {{{ 0, 0, 0, 0, 0}},
4771 { DEF, DEF, DEF, DEF, DEF}},
4772 { DEF, DEF, DEF, DEF, DEF}},
4773 { DEF, DEF, DEF, DEF, DEF}},
4774 { DEF, DEF, DEF, DEF, DEF}},
4775 /* GC.@A..CG */
4776 {{ 0, 0, 0, 0, 0}},
4777 {-1029,-1029,-1029,-1029,-1029}},
4778 { -519, -519, -519, -519, -519}},
4779 { -939, -939, -939, -939, -939}},
4780 { -809, -809, -809, -809, -809}},
4781 /* GC.@C..CG */
4782 {{ 0, 0, 0, 0, 0}},
4783 { -949, -949, -949, -949, -949}},
4784 { -449, -449, -449, -449, -449}},
4785 { -939, -939, -939, -939, -939}},
4786 { -739, -739, -739, -739, -739}},
4787 /* GC.@G..CG */
4788 {{ 0, 0, 0, 0, 0}},
4789 {-1029,-1029,-1029,-1029,-1029}},
4790 { -519, -519, -519, -519, -519}},
4791 { -939, -939, -939, -939, -939}},
4792 { -809, -809, -809, -809, -809}},
4793 /* GC.@U..CG */
4794 {{ 0, 0, 0, 0, 0}},
4795 {-1029,-1029,-1029,-1029,-1029}},
4796 { -669, -669, -669, -669, -669}},
4797 { -939, -939, -939, -939, -939}},
4798 { -859, -859, -859, -859, -859}}},
4799 /* GC.A@..CG */
4800 {{{ DEF, -519, -879, -559, -879}},
4801 { -100, -569, -929, -609, -929}},
4802 { -100, -569, -929, -609, -929}},
4803 { -100, -569, -929, -609, -929}},
4804 { -100, -569, -929, -609, -929}},
4805 /* GC.AA..CG */
4806 {{ DEF, -519, -879, -559, -879}},
4807 {-1079,-1548,-1908,-1588,-1908}},
4808 { -569,-1038,-1398,-1078,-1398}},
4809 { -989,-1458,-1818,-1498,-1818}},
4810 { -859,-1328,-1688,-1368,-1688}},
4811 /* GC.AC..CG */

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4812 {{ DEF, -519, -879, -559, -879}},
4813 { -999,-1468,-1828,-1508,-1828}},
4814 { -499, -968,-1328,-1008,-1328}},
4815 { -989,-1458,-1818,-1498,-1818}},
4816 { -789,-1258,-1618,-1298,-1618}},
4817 /* GC.AG..CG */
4818 {{ DEF, -519, -879, -559, -879}},
4819 {-1079,-1548,-1908,-1588,-1908}},
4820 { -569,-1038,-1398,-1078,-1398}},
4821 { -989,-1458,-1818,-1498,-1818}},
4822 { -859,-1328,-1688,-1368,-1688}},
4823 /* GC.AU..CG */
4824 {{ DEF, -519, -879, -559, -879}},
4825 {-1079,-1548,-1908,-1588,-1908}},
4826 { -719,-1188,-1548,-1228,-1548}},
4827 { -989,-1458,-1818,-1498,-1818}},
4828 { -909,-1378,-1738,-1418,-1738}}},
4829 /* GC.C@..CG */
4830 {{{ DEF, -719, -309, -309, -389}},
4831 { -100, -769, -359, -359, -439}},
4832 { -100, -769, -359, -359, -439}},
4833 { -100, -769, -359, -359, -439}},
4834 { -100, -769, -359, -359, -439}}},
4835 /* GC.CA..CG */
4836 {{ DEF, -719, -309, -309, -389}},
4837 {-1079,-1748,-1338,-1338,-1418}},
4838 { -569,-1238, -828, -828, -908}},
4839 { -989,-1658,-1248,-1248,-1328}},
4840 { -859,-1528,-1118,-1118,-1198}},
4841 /* GC.CC..CG */
4842 {{ DEF, -719, -309, -309, -389}},
4843 { -999,-1668,-1258,-1258,-1338}},
4844 { -499,-1168, -758, -758, -838}},
4845 { -989,-1658,-1248,-1248,-1328}},
4846 { -789,-1458,-1048,-1048,-1128}},
4847 /* GC.CG..CG */
4848 {{ DEF, -719, -309, -309, -389}},
4849 {-1079,-1748,-1338,-1338,-1418}},
4850 { -569,-1238, -828, -828, -908}},
4851 { -989,-1658,-1248,-1248,-1328}},
4852 { -859,-1528,-1118,-1118,-1198}},
4853 /* GC.CU..CG */
4854 {{ DEF, -719, -309, -309, -389}},
4855 {-1079,-1748,-1338,-1338,-1418}},
4856 { -719,-1388, -978, -978,-1058}},
4857 { -989,-1658,-1248,-1248,-1328}},
4858 { -909,-1578,-1168,-1168,-1248}}},
4859 /* GC.G@..CG */
4860 {{{ DEF, -709, -739, -619, -739}},
4861 { -100, -759, -789, -669, -789}},
4862 { -100, -759, -789, -669, -789}},
4863 { -100, -759, -789, -669, -789}},
4864 { -100, -759, -789, -669, -789}}},
4865 /* GC.GA..CG */
4866 {{ DEF, -709, -739, -619, -739}},
4867 {-1079,-1738,-1768,-1648,-1768}},
4868 { -569,-1228,-1258,-1138,-1258}},
4869 { -989,-1648,-1678,-1558,-1678}},
4870 { -859,-1518,-1548,-1428,-1548}},
4871 /* GC.GC..CG */
4872 {{ DEF, -709, -739, -619, -739}},
4873 { -999,-1658,-1688,-1568,-1688}},
4874 { -499,-1158,-1188,-1068,-1188}},
4875 { -989,-1648,-1678,-1558,-1678}},
4876 { -789,-1448,-1478,-1358,-1478}},
4877 /* GC.GG..CG */
4878 {{ DEF, -709, -739, -619, -739}},
4879 {-1079,-1738,-1768,-1648,-1768}},
4880 { -569,-1228,-1258,-1138,-1258}},
4881 { -989,-1648,-1678,-1558,-1678}},
4882 { -859,-1518,-1548,-1428,-1548}},
4883 /* GC.GU..CG */
4884 {{ DEF, -709, -739, -619, -739}},
4885 {-1079,-1738,-1768,-1648,-1768}},
4886 { -719,-1378,-1408,-1288,-1408}},
4887 { -989,-1648,-1678,-1558,-3080}},
4888 { -909,-1568,-1598,-1478,-1598}}},
4889 /* GC.U@..CG */
4890 {{{ DEF, -499, -499, -499, -569}},
4891 { -100, -549, -549, -549, -619}},
4892 { -100, -549, -549, -549, -619}},
4893 { -100, -549, -549, -549, -619}},
4894 { -100, -549, -549, -549, -619}}},
4895 /* GC.UA..CG */
4896 {{ DEF, -499, -499, -499, -569}},
4897 {-1079,-1528,-1528,-1528,-1598}},
4898 { -569,-1018,-1018,-1018,-1088}},
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4899 { -989,-1438,-1438,-1438,-1508},
4900 { -859,-1308,-1308,-1308,-1378}},
4901 /* GC.UC..CG */
4902 {{ DEF, -499, -499, -499, -569},
4903 { -999,-1448,-1448,-1448,-1518},
4904 { -499, -948, -948, -948,-1018},
4905 { -989,-1438,-1438,-1438,-1508},
4906 { -789,-1238,-1238,-1238,-1308}},
4907 /* GC.UG..CG */
4908 {{ DEF, -499, -499, -499, -569},
4909 {-1079,-1528,-1528,-1528,-1598},
4910 { -569,-1018,-1018,-1018,-1088},
4911 { -989,-1438,-1438,-1438,-1508},
4912 { -859,-1308,-1308,-1308,-1378}},
4913 /* GC.UU..CG */
4914 {{ DEF, -499, -499, -499, -569},
4915 {-1079,-1528,-1528,-1528,-1598},
4916 { -719,-1168,-1168,-1168,-1238},
4917 { -989,-1438,-1438,-1438,-1508},
4918 { -909,-1358,-1358,-1358,-1428}}},
4919 /* GC.@@..GC */
4920 {{{ 0, 0, 0, 0, 0},
4921 { DEF, DEF, DEF, DEF, DEF},
4922 { DEF, DEF, DEF, DEF, DEF},
4923 { DEF, DEF, DEF, DEF, DEF},
4924 { DEF, DEF, DEF, DEF, DEF}}},
4925 /* GC.@A..GC */
4926 {{ 0, 0, 0, 0, 0},
4927 { -519, -519, -519, -519, -519},
4928 { -719, -719, -719, -719, -719},
4929 { -709, -709, -709, -709, -709},
4930 { -499, -499, -499, -499, -499}},
4931 /* GC.@C..GC */
4932 {{ 0, 0, 0, 0, 0},
4933 { -879, -879, -879, -879, -879},
4934 { -309, -309, -309, -309, -309},
4935 { -739, -739, -739, -739, -739},
4936 { -499, -499, -499, -499, -499}},
4937 /* GC.@G..GC */
4938 {{ 0, 0, 0, 0, 0},
4939 { -559, -559, -559, -559, -559},
4940 { -309, -309, -309, -309, -309},
4941 { -619, -619, -619, -619, -619},
4942 { -499, -499, -499, -499, -499}},
4943 /* GC.@U..GC */
4944 {{ 0, 0, 0, 0, 0},
4945 { -879, -879, -879, -879, -879},
4946 { -389, -389, -389, -389, -389},
4947 { -739, -739, -739, -739, -739},
4948 { -569, -569, -569, -569, -569}}},
4949 /* GC.A@..GC */
4950 {{{ DEF, -519, -879, -559, -879},
4951 { -100, -569, -929, -609, -929},
4952 { -100, -569, -929, -609, -929},
4953 { -100, -569, -929, -609, -929},
4954 { -100, -569, -929, -609, -929}}},
4955 /* GC.AA..GC */
4956 {{ DEF, -519, -879, -559, -879},
4957 { -569,-1038,-1398,-1078,-1398},
4958 { -769,-1238,-1598,-1278,-1598},
4959 { -759,-1228,-1588,-1268,-1588},
4960 { -549,-1018,-1378,-1058,-1378}},
4961 /* GC.AC..GC */
4962 {{ DEF, -519, -879, -559, -879},
4963 { -929,-1398,-1758,-1438,-1758},
4964 { -359, -828,-1188, -868,-1188},
4965 { -789,-1258,-1618,-1298,-1618},
4966 { -549,-1018,-1378,-1058,-1378}},
4967 /* GC.AG..GC */
4968 {{ DEF, -519, -879, -559, -879},
4969 { -609,-1078,-1438,-1118,-1438},
4970 { -359, -828,-1188, -868,-1188},
4971 { -669,-1138,-1498,-1178,-1498},
4972 { -549,-1018,-1378,-1058,-1378}},
4973 /* GC.AU..GC */
4974 {{ DEF, -519, -879, -559, -879},
4975 { -929,-1398,-1758,-1438,-1758},
4976 { -439, -908,-1268, -948,-1268},
4977 { -789,-1258,-1618,-1298,-1618},
4978 { -619,-1088,-1448,-1128,-1448}}},
4979 /* GC.C@..GC */
4980 {{{ DEF, -719, -309, -309, -389},
4981 { -100, -769, -359, -359, -439},
4982 { -100, -769, -359, -359, -439},
4983 { -100, -769, -359, -359, -439},
4984 { -100, -769, -359, -359, -439}},
4985 /* GC.CA..GC */

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4986 {{ DEF, -719, -309, -309, -389},
4987 { -569,-1238, -828, -828, -908},
4988 { -769,-1438,-1028,-1028,-1108},
4989 { -759,-1428,-1018,-1018,-1098},
4990 { -549,-1218, -808, -808, -888}},
4991 /* GC.CC..GC */
4992 {{ DEF, -719, -309, -309, -389},
4993 { -929,-1598,-1188,-1188,-1268},
4994 { -359,-1028, -618, -618, -698},
4995 { -789,-1458,-1048,-1048,-1128},
4996 { -549,-1218, -808, -808, -888}},
4997 /* GC.CG..GC */
4998 {{ DEF, -719, -309, -309, -389},
4999 { -609,-1278, -868, -868, -948},
5000 { -359,-1028, -618, -618, -698},
5001 { -669,-1338, -928, -928,-1008},
5002 { -549,-1218, -808, -808, -888}},
5003 /* GC.CU..GC */
5004 {{ DEF, -719, -309, -309, -389},
5005 { -929,-1598,-1188,-1188,-1268},
5006 { -439,-1108, -698, -698, -778},
5007 { -789,-1458,-1048,-1048,-1128},
5008 { -619,-1288, -878, -878, -958}}},
5009 /* GC.G@..GC */
5010 {{{ DEF, -709, -739, -619, -739},
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5012 { -100, -759, -789, -669, -789},
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5016 {{ DEF, -709, -739, -619, -739},
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5020 { -549,-1208,-1238,-1118,-1238}},
5021 /* GC.GC..GC */
5022 {{ DEF, -709, -739, -619, -739},
5023 { -929,-1588,-1618,-1498,-1618},
5024 { -359,-1018,-1048, -928,-1048},
5025 { -789,-1448,-1478,-1358,-1478},
5026 { -549,-1208,-1238,-1118,-1238}},
5027 /* GC.GG..GC */
5028 {{ DEF, -709, -739, -619, -739},
5029 { -609,-1268,-1298,-1178,-1298},
5030 { -359,-1018,-1048, -928,-1048},
5031 { -669,-1328,-1358,-1238,-1358},
5032 { -549,-1208,-1238,-1118,-1238}},
5033 /* GC.GU..GC */
5034 {{ DEF, -709, -739, -619, -739},
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5036 { -439,-1098,-1128,-1008,-1128},
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5038 { -619,-1278,-1308,-1188,-1308}}},
5039 /* GC.U@..GC */
5040 {{{ DEF, -499, -499, -499, -569},
5041 { -100, -549, -549, -549, -619},
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5049 { -759,-1208,-1208,-1208,-1278},
5050 { -549, -998, -998, -998,-1068}},
5051 /* GC.UC..GC */
5052 {{ DEF, -499, -499, -499, -569},
5053 { -929,-1378,-1378,-1378,-1448},
5054 { -359, -808, -808, -808, -878},
5055 { -789,-1238,-1238,-1238,-1308},
5056 { -549, -998, -998, -998,-1068}},
5057 /* GC.UG..GC */
5058 {{ DEF, -499, -499, -499, -569},
5059 { -609,-1058,-1058,-1058,-1128},
5060 { -359, -808, -808, -808, -878},
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5062 { -549, -998, -998, -998,-1068}},
5063 /* GC.UU..GC */
5064 {{ DEF, -499, -499, -499, -569},
5065 { -929,-1378,-1378,-1378,-1448},
5066 { -439, -888, -888, -888, -958},
5067 { -789,-1238,-1238,-1238,-1308},
5068 { -619,-1068,-1068,-1068,-1138}}}},
5069 /* GC.@@..GU */
5070 {{{ 0, 0, 0, 0, 0},
5071 { DEF, DEF, DEF, DEF, DEF},
5072 { DEF, DEF, DEF, DEF, DEF},

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5073 { DEF, DEF, DEF, DEF, DEF},
5074 { DEF, DEF, DEF, DEF, DEF}},
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5076 {{ 0, 0, 0, 0, 0},
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5078 {-259, -259, -259, -259, -259},
5079 {-339, -339, -339, -339, -339},
5080 {-329, -329, -329, -329, -329}},
5081 /* GC.@C..GU */
5082 {{ 0, 0, 0, 0, 0},
5083 {-599, -599, -599, -599, -599},
5084 {-239, -239, -239, -239, -239},
5085 {-689, -689, -689, -689, -689},
5086 {-329, -329, -329, -329, -329}},
5087 /* GC.@G..GU */
5088 {{ 0, 0, 0, 0, 0},
5089 {-599, -599, -599, -599, -599},
5090 {-239, -239, -239, -239, -239},
5091 {-689, -689, -689, -689, -689},
5092 {-329, -329, -329, -329, -329}},
5093 /* GC.@U..GU */
5094 {{ 0, 0, 0, 0, 0},
5095 {-599, -599, -599, -599, -599},
5096 {-239, -239, -239, -239, -239},
5097 {-689, -689, -689, -689, -689},
5098 {-329, -329, -329, -329, -329}}},
5099 /* GC.A@..GU */
5100 {{{ DEF, -519, -879, -559, -879},
5101 {-100, -569, -929, -609, -929},
5102 {-100, -569, -929, -609, -929},
5103 {-100, -569, -929, -609, -929},
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5105 /* GC.AA..GU */
5106 {{ DEF, -519, -879, -559, -879},
5107 {-479, -948, -1308, -988, -1308},
5108 {-309, -778, -1138, -818, -1138},
5109 {-389, -858, -1218, -898, -1218},
5110 {-379, -848, -1208, -888, -1208}},
5111 /* GC.AC..GU */
5112 {{ DEF, -519, -879, -559, -879},
5113 {-649, -1118, -1478, -1158, -1478},
5114 {-289, -758, -1118, -798, -1118},
5115 {-739, -1208, -1568, -1248, -1568},
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5117 /* GC.AG..GU */
5118 {{ DEF, -519, -879, -559, -879},
5119 {-649, -1118, -1478, -1158, -1478},
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5121 {-739, -1208, -1568, -1248, -1568},
5122 {-379, -848, -1208, -888, -1208}},
5123 /* GC.AU..GU */
5124 {{ DEF, -519, -879, -559, -879},
5125 {-649, -1118, -1478, -1158, -1478},
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5127 {-739, -1208, -1568, -1248, -1568},
5128 {-379, -848, -1208, -888, -1208}}},
5129 /* GC.C@..GU */
5130 {{{ DEF, -719, -309, -309, -389},
5131 {-100, -769, -359, -359, -439},
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5135 /* GC.CA..GU */
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5137 {-479, -1148, -738, -738, -818},
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5140 {-379, -1048, -638, -638, -718}},
5141 /* GC.CC..GU */
5142 {{ DEF, -719, -309, -309, -389},
5143 {-649, -1318, -908, -908, -988},
5144 {-289, -958, -548, -548, -628},
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5146 {-379, -1048, -638, -638, -718}},
5147 /* GC.CG..GU */
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5149 {-649, -1318, -908, -908, -988},
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5151 {-739, -1408, -998, -998, -1078},
5152 {-379, -1048, -638, -638, -718}},
5153 /* GC.CU..GU */
5154 {{ DEF, -719, -309, -309, -389},
5155 {-649, -1318, -908, -908, -988},
5156 {-289, -958, -548, -548, -628},
5157 {-739, -1408, -998, -998, -1078},
5158 {-379, -1048, -638, -638, -718}}},
5159 /* GC.G@..GU */

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5160 {{{ DEF, -709, -739, -619, -739}},
5161 { -100, -759, -789, -669, -789}},
5162 { -100, -759, -789, -669, -789}},
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5165 /* GC.GA..GU */
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5171 /* GC.GC..GU */
5172 {{{ DEF, -709, -739, -619, -739}},
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5177 /* GC.GG..GU */
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5189 /* GC.U@..GU */
5190 {{{ DEF, -499, -499, -499, -569}},
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5207 /* GC.UG..GU */
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5209 { -649, -1098, -1098, -1098, -1168}},
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5213 /* GC.UU..GU */
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5217 { -739, -1188, -1188, -1188, -1258}},
5218 { -379, -828, -828, -828, -898}}}},
5219 /* GC.@@..UG */
5220 {{{ 0, 0, 0, 0, 0}},
5221 { DEF, DEF, DEF, DEF, DEF}},
5222 { DEF, DEF, DEF, DEF, DEF}},
5223 { DEF, DEF, DEF, DEF, DEF}},
5224 { DEF, DEF, DEF, DEF, DEF}},
5225 /* GC.@A..UG */
5226 {{{ 0, 0, 0, 0, 0}},
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5230 { -549, -549, -549, -549, -549}},
5231 /* GC.@C..UG */
5232 {{{ 0, 0, 0, 0, 0}},
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5246 { -479, -479, -479, -479, -479}},

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```

5247 { -809, -809, -809, -809, -809},
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5250 {{{ DEF, -519, -879, -559, -879},
5251 { -100, -569, -929, -609, -929},
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5278 { -409, -878, -1238, -918, -1238}}},
5279 /* GC.C@..UG */
5280 {{{ DEF, -719, -309, -309, -389},
5281 { -100, -769, -359, -359, -439},
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5297 /* GC.CG..UG */
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5309 /* GC.G@..UG */
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5315 /* GC.GA..UG */
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5325 { -859, -1518, -1548, -1428, -1548},
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5327 /* GC.GG..UG */
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5330 { -409, -1068, -1098, -978, -1098},
5331 { -969, -1628, -1658, -1538, -1658},
5332 { -599, -1258, -1288, -1168, -1288}}},
5333 /* GC.GU..UG */

```

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5334 {{ DEF, -709, -739, -619, -739},
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5336 { -529,-1188,-1218,-1098,-1218},
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5338 { -409,-1068,-1098, -978,-1098}}},
5339 /* GC.U@..UG */
5340 {{{ DEF, -499, -499, -499, -569},
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5357 /* GC.UG..UG */
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5375 /* GC.@A..AU */
5376 {{ 0, 0, 0, 0, 0},
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5378 { -259, -259, -259, -259, -259},
5379 { -339, -339, -339, -339, -339},
5380 { -329, -329, -329, -329, -329}}},
5381 /* GC.@C..AU */
5382 {{ 0, 0, 0, 0, 0},
5383 { -599, -599, -599, -599, -599},
5384 { -239, -239, -239, -239, -239},
5385 { -689, -689, -689, -689, -689},
5386 { -329, -329, -329, -329, -329}}},
5387 /* GC.@G..AU */
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5391 { -689, -689, -689, -689, -689},
5392 { -329, -329, -329, -329, -329}}},
5393 /* GC.@U..AU */
5394 {{ 0, 0, 0, 0, 0},
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5396 { -239, -239, -239, -239, -239},
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5401 { -100, -569, -929, -609, -929},
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5405 /* GC.AA..AU */
5406 {{ DEF, -519, -879, -559, -879},
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5408 { -309, -778,-1138, -818,-1138},
5409 { -389, -858,-1218, -898,-1218},
5410 { -379, -848,-1208, -888,-1208}}},
5411 /* GC.AC..AU */
5412 {{ DEF, -519, -879, -559, -879},
5413 { -649,-1118,-1478,-1158,-1478},
5414 { -289, -758,-1118, -798,-1118},
5415 { -739,-1208,-1568,-1248,-1568},
5416 { -379, -848,-1208, -888,-1208}}},
5417 /* GC.AG..AU */
5418 {{ DEF, -519, -879, -559, -879},
5419 { -649,-1118,-1478,-1158,-1478},
5420 { -289, -758,-1118, -798,-1118},

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5421 { -739,-1208,-1568,-1248,-1568},
5422 { -379, -848,-1208, -888,-1208}},
5423 /* GC.AU..AU */
5424 {{ DEF, -519, -879, -559, -879},
5425 { -649,-1118,-1478,-1158,-1478},
5426 { -289, -758,-1118, -798,-1118},
5427 { -739,-1208,-1568,-1248,-1568},
5428 { -379, -848,-1208, -888,-1208}}},
5429 /* GC.C@..AU */
5430 {{{ DEF, -719, -309, -309, -389},
5431 { -100, -769, -359, -359, -439},
5432 { -100, -769, -359, -359, -439},
5433 { -100, -769, -359, -359, -439},
5434 { -100, -769, -359, -359, -439}}},
5435 /* GC.CA..AU */
5436 {{ DEF, -719, -309, -309, -389},
5437 { -479,-1148, -738, -738, -818},
5438 { -309, -978, -568, -568, -648},
5439 { -389,-1058, -648, -648, -728},
5440 { -379,-1048, -638, -638, -718}}},
5441 /* GC.CC..AU */
5442 {{ DEF, -719, -309, -309, -389},
5443 { -649,-1318, -908, -908, -988},
5444 { -289, -958, -548, -548, -628},
5445 { -739,-1408, -998, -998,-1078},
5446 { -379,-1048, -638, -638, -718}}},
5447 /* GC.CG..AU */
5448 {{ DEF, -719, -309, -309, -389},
5449 { -649,-1318, -908, -908, -988},
5450 { -289, -958, -548, -548, -628},
5451 { -739,-1408, -998, -998,-1078},
5452 { -379,-1048, -638, -638, -718}}},
5453 /* GC.CU..AU */
5454 {{ DEF, -719, -309, -309, -389},
5455 { -649,-1318, -908, -908, -988},
5456 { -289, -958, -548, -548, -628},
5457 { -739,-1408, -998, -998,-1078},
5458 { -379,-1048, -638, -638, -718}}},
5459 /* GC.G@..AU */
5460 {{{ DEF, -709, -739, -619, -739},
5461 { -100, -759, -789, -669, -789},
5462 { -100, -759, -789, -669, -789},
5463 { -100, -759, -789, -669, -789},
5464 { -100, -759, -789, -669, -789}}},
5465 /* GC.GA..AU */
5466 {{ DEF, -709, -739, -619, -739},
5467 { -479,-1138,-1168,-1048,-1168},
5468 { -309, -968, -998, -878, -998},
5469 { -389,-1048,-1078, -958,-1078},
5470 { -379,-1038,-1068, -948,-1068}}},
5471 /* GC.GC..AU */
5472 {{ DEF, -709, -739, -619, -739},
5473 { -649,-1308,-1338,-1218,-1338},
5474 { -289, -948, -978, -858, -978},
5475 { -739,-1398,-1428,-1308,-1428},
5476 { -379,-1038,-1068, -948,-1068}}},
5477 /* GC.GG..AU */
5478 {{ DEF, -709, -739, -619, -739},
5479 { -649,-1308,-1338,-1218,-1338},
5480 { -289, -948, -978, -858, -978},
5481 { -739,-1398,-1428,-1308,-1428},
5482 { -379,-1038,-1068, -948,-1068}}},
5483 /* GC.GU..AU */
5484 {{ DEF, -709, -739, -619, -739},
5485 { -649,-1308,-1338,-1218,-1338},
5486 { -289, -948, -978, -858, -978},
5487 { -739,-1398,-1428,-1308,-1428},
5488 { -379,-1038,-1068, -948,-1068}}},
5489 /* GC.U@..AU */
5490 {{{ DEF, -499, -499, -499, -569},
5491 { -100, -549, -549, -549, -619},
5492 { -100, -549, -549, -549, -619},
5493 { -100, -549, -549, -549, -619},
5494 { -100, -549, -549, -549, -619}}},
5495 /* GC.UA..AU */
5496 {{ DEF, -499, -499, -499, -569},
5497 { -479, -928, -928, -928, -998},
5498 { -309, -758, -758, -758, -828},
5499 { -389, -838, -838, -838, -908},
5500 { -379, -828, -828, -828, -898}}},
5501 /* GC.UC..AU */
5502 {{ DEF, -499, -499, -499, -569},
5503 { -649,-1098,-1098,-1098,-1168},
5504 { -289, -738, -738, -738, -808},
5505 { -739,-1188,-1188,-1188,-1258},
5506 { -379, -828, -828, -828, -898}}},
5507 /* GC.UG..AU */
```

```
5508 {{ DEF, -499, -499, -499, -569},
5509 { -649,-1098,-1098,-1098,-1168},
5510 { -289, -738, -738, -738, -808},
5511 { -739,-1188,-1188,-1188,-1258},
5512 { -379, -828, -828, -828, -898}},
5513 /* GC.UU..AU */
5514 {{ DEF, -499, -499, -499, -569},
5515 { -649,-1098,-1098,-1098,-1168},
5516 { -289, -738, -738, -738, -808},
5517 { -739,-1188,-1188,-1188,-1258},
5518 { -379, -828, -828, -828, -898}}}},
5519 /* GC.@@..UA */
5520 {{{{ 0, 0, 0, 0, 0},
5521 { DEF, DEF, DEF, DEF, DEF},
5522 { DEF, DEF, DEF, DEF, DEF},
5523 { DEF, DEF, DEF, DEF, DEF},
5524 { DEF, DEF, DEF, DEF, DEF}}}},
5525 /* GC.@A..UA */
5526 {{ 0, 0, 0, 0, 0},
5527 { -399, -399, -399, -399, -399},
5528 { -429, -429, -429, -429, -429},
5529 { -379, -379, -379, -379, -379},
5530 { -279, -279, -279, -279, -279}},
5531 /* GC.@C..UA */
5532 {{ 0, 0, 0, 0, 0},
5533 { -629, -629, -629, -629, -629},
5534 { -509, -509, -509, -509, -509},
5535 { -679, -679, -679, -679, -679},
5536 { -139, -139, -139, -139, -139}},
5537 /* GC.@G..UA */
5538 {{ 0, 0, 0, 0, 0},
5539 { -889, -889, -889, -889, -889},
5540 { -199, -199, -199, -199, -199},
5541 { -889, -889, -889, -889, -889},
5542 { -279, -279, -279, -279, -279}},
5543 /* GC.@U..UA */
5544 {{{ 0, 0, 0, 0, 0},
5545 { -589, -589, -589, -589, -589},
5546 { -179, -179, -179, -179, -179},
5547 { -679, -679, -679, -679, -679},
5548 { -140, -140, -140, -140, -140}}}},
5549 /* GC.A@..UA */
5550 {{{ DEF, -519, -879, -559, -879},
5551 { -100, -569, -929, -609, -929},
5552 { -100, -569, -929, -609, -929},
5553 { -100, -569, -929, -609, -929},
5554 { -100, -569, -929, -609, -929}},
5555 /* GC.AA..UA */
5556 {{ DEF, -519, -879, -559, -879},
5557 { -449, -918,-1278, -958,-1278},
5558 { -479, -948,-1308, -988,-1308},
5559 { -429, -898,-1258, -938,-1258},
5560 { -329, -798,-1158, -838,-1158}},
5561 /* GC.AC..UA */
5562 {{ DEF, -519, -879, -559, -879},
5563 { -679,-1148,-1508,-1188,-1508},
5564 { -559,-1028,-1388,-1068,-1388},
5565 { -729,-1198,-1558,-1238,-1558},
5566 { -189,-658,-1018, -698,-1018}},
5567 /* GC.AG..UA */
5568 {{ DEF, -519, -879, -559, -879},
5569 { -939,-1408,-1768,-1448,-1768},
5570 { -249, -718,-1078, -758,-1078},
5571 { -939,-1408,-1768,-1448,-1768},
5572 { -329, -798,-1158, -838,-1158}},
5573 /* GC.AU..UA */
5574 {{ DEF, -519, -879, -559, -879},
5575 { -639,-1108,-1468,-1148,-1468},
5576 { -229, -698,-1058, -738,-1058},
5577 { -729,-1198,-1558,-1238,-1558},
5578 { -190, -659,-1019, -699,-1019}}}},
5579 /* GC.C@..UA */
5580 {{{ DEF, -719, -309, -309, -389},
5581 { -100, -769, -359, -359, -439},
5582 { -100, -769, -359, -359, -439},
5583 { -100, -769, -359, -359, -439},
5584 { -100, -769, -359, -359, -439}},
5585 /* GC.CA..UA */
5586 {{ DEF, -719, -309, -309, -389},
5587 { -449,-1118, -708, -708, -788},
5588 { -479,-1148, -738, -738, -818},
5589 { -429,-1098, -688, -688, -768},
5590 { -329, -998, -588, -588, -668}},
5591 /* GC.CC..UA */
5592 {{ DEF, -719, -309, -309, -389},
5593 { -679,-1348, -938, -938,-1018},
5594 { -559,-1228, -818, -818, -898},
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5595 { -729,-1398, -988, -988,-1068},
5596 { -189, -858, -448, -448, -528}},
5597 /* GC.CG..UA */
5598 {{ DEF, -719, -309, -309, -389},
5599 { -939,-1608,-1198,-1198,-1278},
5600 { -249, -918, -508, -508, -588},
5601 { -939,-1608,-1198,-1198,-1278},
5602 { -329, -998, -588, -588, -668}},
5603 /* GC.CU..UA */
5604 {{ DEF, -719, -309, -309, -389},
5605 { -639,-1308, -898, -898, -978},
5606 { -229, -898, -488, -488, -568},
5607 { -729,-1398, -988, -988,-1068},
5608 { -190, -859, -449, -449, -529}}},
5609 /* GC.G@..UA */
5610 {{{ DEF, -709, -739, -619, -739},
5611 { -100, -759, -789, -669, -789},
5612 { -100, -759, -789, -669, -789},
5613 { -100, -759, -789, -669, -789},
5614 { -100, -759, -789, -669, -789}}},
5615 /* GC.GA..UA */
5616 {{ DEF, -709, -739, -619, -739},
5617 { -449,-1108,-1138,-1018,-1138},
5618 { -479,-1138,-1168,-1048,-1168},
5619 { -429,-1088,-1118, -998,-1118},
5620 { -329, -988, -1018, -898,-1018}},
5621 /* GC.GC..UA */
5622 {{ DEF, -709, -739, -619, -739},
5623 { -679,-1338,-1368,-1248,-1368},
5624 { -559,-1218,-1248,-1128,-1248},
5625 { -729,-1388,-1418,-1298,-1418},
5626 { -189, -848, -878, -758, -878}},
5627 /* GC.GG..UA */
5628 {{ DEF, -709, -739, -619, -739},
5629 { -939,-1598,-1628,-1508,-1628},
5630 { -249, -908, -938, -818, -938},
5631 { -939,-1598,-1628,-1508,-1628},
5632 { -329, -988,-1018, -898,-1018}},
5633 /* GC.GU..UA */
5634 {{ DEF, -709, -739, -619, -739},
5635 { -639,-1298,-1328,-1208,-1328},
5636 { -229, -888, -918, -798, -918},
5637 { -729,-1388,-1418,-1298,-1418},
5638 { -190, -849, -879, -759, -879}}},
5639 /* GC.U@..UA */
5640 {{{ DEF, -499, -499, -499, -569},
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5642 { -100, -549, -549, -549, -619},
5643 { -100, -549, -549, -549, -619},
5644 { -100, -549, -549, -549, -619}},
5645 /* GC.UA..UA */
5646 {{ DEF, -499, -499, -499, -569},
5647 { -449, -898, -898, -898, -968},
5648 { -479, -928, -928, -928, -998},
5649 { -429, -878, -878, -878, -948},
5650 { -329, -778, -778, -778, -848}},
5651 /* GC.UC..UA */
5652 {{ DEF, -499, -499, -499, -569},
5653 { -679,-1128,-1128,-1128,-1198},
5654 { -559,-1008,-1008,-1008,-1078},
5655 { -729,-1178,-1178,-1178,-1248},
5656 { -189, -638, -638, -638, -708}},
5657 /* GC.UG..UA */
5658 {{ DEF, -499, -499, -499, -569},
5659 { -939,-1388,-1388,-1388,-1458},
5660 { -249, -698, -698, -698, -768},
5661 { -939,-1388,-1388,-1388,-1458},
5662 { -329, -778, -778, -778, -848}},
5663 /* GC.UU..UA */
5664 {{ DEF, -499, -499, -499, -569},
5665 { -639,-1088,-1088,-1088,-1158},
5666 { -229, -678, -678, -678, -748},
5667 { -729,-1178,-1178,-1178,-1248},
5668 { -190, -639, -639, -639, -709}}},
5669 /* GC.@@.. @ */
5670 {{{{ DEF, DEF, DEF, DEF, DEF},
5671 { DEF, DEF, DEF, DEF, DEF},
5672 { DEF, DEF, DEF, DEF, DEF},
5673 { DEF, DEF, DEF, DEF, DEF},
5674 { DEF, DEF, DEF, DEF, DEF}},
5675 /* GC.@A.. @ */
5676 {{ DEF, DEF, DEF, DEF, DEF},
5677 { DEF, DEF, DEF, DEF, DEF},
5678 { DEF, DEF, DEF, DEF, DEF},
5679 { DEF, DEF, DEF, DEF, DEF},
5680 { DEF, DEF, DEF, DEF, DEF}},
5681 /* GC.@C.. @ */

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5682 {{ DEF, DEF, DEF, DEF, DEF}},
5683 { DEF, DEF, DEF, DEF, DEF}},
5684 { DEF, DEF, DEF, DEF, DEF}},
5685 { DEF, DEF, DEF, DEF, DEF}},
5686 { DEF, DEF, DEF, DEF, DEF}},
5687 /* GC.@G.. @ */
5688 {{ DEF, DEF, DEF, DEF, DEF}},
5689 { DEF, DEF, DEF, DEF, DEF}},
5690 { DEF, DEF, DEF, DEF, DEF}},
5691 { DEF, DEF, DEF, DEF, DEF}},
5692 { DEF, DEF, DEF, DEF, DEF}},
5693 /* GC.@U.. @ */
5694 {{ DEF, DEF, DEF, DEF, DEF}},
5695 { DEF, DEF, DEF, DEF, DEF}},
5696 { DEF, DEF, DEF, DEF, DEF}},
5697 { DEF, DEF, DEF, DEF, DEF}},
5698 { DEF, DEF, DEF, DEF, DEF}},
5699 /* GC.A@.. @ */
5700 {{{ -100, -569, -929, -609, -929}},
5701 { -100, -569, -929, -609, -929}},
5702 { -100, -569, -929, -609, -929}},
5703 { -100, -569, -929, -609, -929}},
5704 { -100, -569, -929, -609, -929}},
5705 /* GC.AA.. @ */
5706 {{ -100, -569, -929, -609, -929}},
5707 { -100, -569, -929, -609, -929}},
5708 { -100, -569, -929, -609, -929}},
5709 { -100, -569, -929, -609, -929}},
5710 { -100, -569, -929, -609, -929}},
5711 /* GC.AC.. @ */
5712 {{ -100, -569, -929, -609, -929}},
5713 { -100, -569, -929, -609, -929}},
5714 { -100, -569, -929, -609, -929}},
5715 { -100, -569, -929, -609, -929}},
5716 { -100, -569, -929, -609, -929}},
5717 /* GC.AG.. @ */
5718 {{ -100, -569, -929, -609, -929}},
5719 { -100, -569, -929, -609, -929}},
5720 { -100, -569, -929, -609, -929}},
5721 { -100, -569, -929, -609, -929}},
5722 { -100, -569, -929, -609, -929}},
5723 /* GC.AU.. @ */
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5725 { -100, -569, -929, -609, -929}},
5726 { -100, -569, -929, -609, -929}},
5727 { -100, -569, -929, -609, -929}},
5728 { -100, -569, -929, -609, -929}},
5729 /* GC.C@.. @ */
5730 {{{ -100, -769, -359, -359, -439}},
5731 { -100, -769, -359, -359, -439}},
5732 { -100, -769, -359, -359, -439}},
5733 { -100, -769, -359, -359, -439}},
5734 { -100, -769, -359, -359, -439}},
5735 /* GC.CA.. @ */
5736 {{ -100, -769, -359, -359, -439}},
5737 { -100, -769, -359, -359, -439}},
5738 { -100, -769, -359, -359, -439}},
5739 { -100, -769, -359, -359, -439}},
5740 { -100, -769, -359, -359, -439}},
5741 /* GC.CC.. @ */
5742 {{ -100, -769, -359, -359, -439}},
5743 { -100, -769, -359, -359, -439}},
5744 { -100, -769, -359, -359, -439}},
5745 { -100, -769, -359, -359, -439}},
5746 { -100, -769, -359, -359, -439}},
5747 /* GC.CG.. @ */
5748 {{ -100, -769, -359, -359, -439}},
5749 { -100, -769, -359, -359, -439}},
5750 { -100, -769, -359, -359, -439}},
5751 { -100, -769, -359, -359, -439}},
5752 { -100, -769, -359, -359, -439}},
5753 /* GC.CU.. @ */
5754 {{ -100, -769, -359, -359, -439}},
5755 { -100, -769, -359, -359, -439}},
5756 { -100, -769, -359, -359, -439}},
5757 { -100, -769, -359, -359, -439}},
5758 { -100, -769, -359, -359, -439}},
5759 /* GC.G@.. @ */
5760 {{{ -100, -759, -789, -669, -789}},
5761 { -100, -759, -789, -669, -789}},
5762 { -100, -759, -789, -669, -789}},
5763 { -100, -759, -789, -669, -789}},
5764 { -100, -759, -789, -669, -789}},
5765 /* GC.GA.. @ */
5766 {{ -100, -759, -789, -669, -789}},
5767 { -100, -759, -789, -669, -789}},
5768 { -100, -759, -789, -669, -789}},
```

```

5769 { -100, -759, -789, -669, -789},
5770 { -100, -759, -789, -669, -789}},
5771 /* GC.GC.. @ */
5772 {{ -100, -759, -789, -669, -789},
5773 { -100, -759, -789, -669, -789},
5774 { -100, -759, -789, -669, -789},
5775 { -100, -759, -789, -669, -789},
5776 { -100, -759, -789, -669, -789}},
5777 /* GC.GG.. @ */
5778 {{ -100, -759, -789, -669, -789},
5779 { -100, -759, -789, -669, -789},
5780 { -100, -759, -789, -669, -789},
5781 { -100, -759, -789, -669, -789},
5782 { -100, -759, -789, -669, -789}},
5783 /* GC.GU.. @ */
5784 {{ -100, -759, -789, -669, -789},
5785 { -100, -759, -789, -669, -789},
5786 { -100, -759, -789, -669, -789},
5787 { -100, -759, -789, -669, -789},
5788 { -100, -759, -789, -669, -789}},
5789 /* GC.U@.. @ */
5790 {{{ -100, -549, -549, -549, -619},
5791 { -100, -549, -549, -549, -619},
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5793 { -100, -549, -549, -549, -619},
5794 { -100, -549, -549, -549, -619}},
5795 /* GC.UA.. @ */
5796 {{ -100, -549, -549, -549, -619},
5797 { -100, -549, -549, -549, -619},
5798 { -100, -549, -549, -549, -619},
5799 { -100, -549, -549, -549, -619},
5800 { -100, -549, -549, -549, -619}},
5801 /* GC.UC.. @ */
5802 {{ -100, -549, -549, -549, -619},
5803 { -100, -549, -549, -549, -619},
5804 { -100, -549, -549, -549, -619},
5805 { -100, -549, -549, -549, -619},
5806 { -100, -549, -549, -549, -619}},
5807 /* GC.UG.. @ */
5808 {{ -100, -549, -549, -549, -619},
5809 { -100, -549, -549, -549, -619},
5810 { -100, -549, -549, -549, -619},
5811 { -100, -549, -549, -549, -619},
5812 { -100, -549, -549, -549, -619}},
5813 /* GC.UU.. @ */
5814 {{ -100, -549, -549, -549, -619},
5815 { -100, -549, -549, -549, -619},
5816 { -100, -549, -549, -549, -619},
5817 { -100, -549, -549, -549, -619},
5818 { -100, -549, -549, -549, -619}}}},
5819 { /* noPair */ {{{{0}}}},
5820 /* GU.@@..CG */
5821 {{{ 0, 0, 0, 0, 0},
5822 { DEF, DEF, DEF, DEF, DEF},
5823 { DEF, DEF, DEF, DEF, DEF},
5824 { DEF, DEF, DEF, DEF, DEF},
5825 { DEF, DEF, DEF, DEF, DEF}},
5826 /* GU.@A..CG */
5827 {{ 0, 0, 0, 0, 0},
5828 {-1029,-1029,-1029,-1029,-1029},
5829 {-519, -519, -519, -519, -519},
5830 {-939, -939, -939, -939, -939},
5831 {-809, -809, -809, -809, -809}},
5832 /* GU.@C..CG */
5833 {{ 0, 0, 0, 0, 0},
5834 {-949, -949, -949, -949, -949},
5835 {-449, -449, -449, -449, -449},
5836 {-939, -939, -939, -939, -939},
5837 {-739, -739, -739, -739, -739}},
5838 /* GU.@G..CG */
5839 {{ 0, 0, 0, 0, 0},
5840 {-1029,-1029,-1029,-1029,-1029},
5841 {-519, -519, -519, -519, -519},
5842 {-939, -939, -939, -939, -939},
5843 {-809, -809, -809, -809, -809}},
5844 /* GU.@U..CG */
5845 {{ 0, 0, 0, 0, 0},
5846 {-1029,-1029,-1029,-1029,-1029},
5847 {-669, -669, -669, -669, -669},
5848 {-939, -939, -939, -939, -939},
5849 {-859, -859, -859, -859, -859}}}},
5850 /* GU.A@..CG */
5851 {{{ DEF, -429, -599, -599, -599},
5852 {-100, -479, -649, -649, -649},
5853 {-100, -479, -649, -649, -649},
5854 {-100, -479, -649, -649, -649},
5855 {-100, -479, -649, -649, -649}},

```

```

5856 /* GU.AA..CG */
5857 {{ DEF, -429, -599, -599, -599}},
5858 {-1079,-1458,-1628,-1628,-1628},
5859 {-569, -948,-1118,-1118,-1118},
5860 {-989,-1368,-1538,-1538,-1538},
5861 {-859,-1238,-1408,-1408,-1408}},
5862 /* GU.AC..CG */
5863 {{ DEF, -429, -599, -599, -599}},
5864 {-999,-1378,-1548,-1548,-1548},
5865 {-499, -878,-1048,-1048,-1048},
5866 {-989,-1368,-1538,-1538,-1538},
5867 {-789,-1168,-1338,-1338,-1338}},
5868 /* GU.AG..CG */
5869 {{ DEF, -429, -599, -599, -599}},
5870 {-1079,-1458,-1628,-1628,-1628},
5871 {-569, -948,-1118,-1118,-1118},
5872 {-989,-1368,-1538,-1538,-1538},
5873 {-859,-1238,-1408,-1408,-1408}},
5874 /* GU.AU..CG */
5875 {{ DEF, -429, -599, -599, -599}},
5876 {-1079,-1458,-1628,-1628,-1628},
5877 {-719,-1098,-1268,-1268,-1268},
5878 {-989,-1368,-1538,-1538,-1538},
5879 {-909,-1288,-1458,-1458,-1458}},
5880 /* GU.C@..CG */
5881 {{{ DEF, -259, -239, -239, -239}},
5882 {-100, -309, -289, -289, -289}},
5883 {-100, -309, -289, -289, -289}},
5884 {-100, -309, -289, -289, -289}},
5885 {-100, -309, -289, -289, -289}}},
5886 /* GU.CA..CG */
5887 {{ DEF, -259, -239, -239, -239}},
5888 {-1079,-1288,-1268,-1268,-1268},
5889 {-569, -778, -758, -758, -758},
5890 {-989,-1198,-1178,-1178,-1178},
5891 {-859,-1068,-1048,-1048,-1048}},
5892 /* GU.CC..CG */
5893 {{ DEF, -259, -239, -239, -239}},
5894 {-999,-1208,-1188,-1188,-1188},
5895 {-499, -708, -688, -688, -688},
5896 {-989,-1198,-1178,-1178,-1178},
5897 {-789, -998, -978, -978, -978}},
5898 /* GU.CG..CG */
5899 {{ DEF, -259, -239, -239, -239}},
5900 {-1079,-1288,-1268,-1268,-1268},
5901 {-569, -778, -758, -758, -758},
5902 {-989,-1198,-1178,-1178,-1178},
5903 {-859,-1068,-1048,-1048,-1048}},
5904 /* GU.CU..CG */
5905 {{ DEF, -259, -239, -239, -239}},
5906 {-1079,-1288,-1268,-1268,-1268},
5907 {-719, -928, -908, -908, -908},
5908 {-989,-1198,-1178,-1178,-1178},
5909 {-909,-1118,-1098,-1098,-1098}}},
5910 /* GU.G@..CG */
5911 {{{ DEF, -339, -689, -689, -689}},
5912 {-100, -389, -739, -739, -739}},
5913 {-100, -389, -739, -739, -739}},
5914 {-100, -389, -739, -739, -739}},
5915 {-100, -389, -739, -739, -739}}},
5916 /* GU.GA..CG */
5917 {{ DEF, -339, -689, -689, -689}},
5918 {-1079,-1368,-1718,-1718,-1718},
5919 {-569, -858,-1208,-1208,-1208},
5920 {-989,-1278,-1628,-1628,-1628},
5921 {-859,-1148,-1498,-1498,-1498}},
5922 /* GU.GC..CG */
5923 {{ DEF, -339, -689, -689, -689}},
5924 {-999,-1288,-1638,-1638,-1638},
5925 {-499, -788,-1138,-1138,-1138},
5926 {-989,-1278,-1628,-1628,-1628},
5927 {-789,-1078,-1428,-1428,-1428}},
5928 /* GU.GG..CG */
5929 {{ DEF, -339, -689, -689, -689}},
5930 {-1079,-1368,-1718,-1718,-1718},
5931 {-569, -858,-1208,-1208,-1208},
5932 {-989,-1278,-1628,-1628,-1628},
5933 {-859,-1148,-1498,-1498,-1498}},
5934 /* GU.GU..CG */
5935 {{ DEF, -339, -689, -689, -689}},
5936 {-1079,-1368,-1718,-1718,-1718},
5937 {-719,-1008,-1358,-1358,-1358},
5938 {-989,-1278,-1628,-1628,-1628},
5939 {-909,-1198,-1548,-1548,-1548}}},
5940 /* GU.U@..CG */
5941 {{{ DEF, -329, -329, -329, -329}},
5942 {-100, -379, -379, -379, -379}},

```

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5943 { -100, -379, -379, -379, -379},
5944 { -100, -379, -379, -379, -379},
5945 { -100, -379, -379, -379, -379}},
5946 /* GU.UA..CG */
5947 {{ DEF, -329, -329, -329, -329},
5948 {-1079,-1358,-1358,-1358,-1358},
5949 {-569, -848, -848, -848, -848},
5950 {-989,-1268,-1268,-1268,-1268},
5951 {-859,-1138,-1138,-1138,-1138}},
5952 /* GU.UC..CG */
5953 {{ DEF, -329, -329, -329, -329},
5954 {-999,-1278,-1278,-1278,-1278},
5955 {-499, -778, -778, -778, -778},
5956 {-989,-1268,-1268,-1268,-1268},
5957 {-789,-1068,-1068,-1068,-1068}},
5958 /* GU.UG..CG */
5959 {{ DEF, -329, -329, -329, -329},
5960 {-1079,-1358,-1358,-1358,-1358},
5961 {-569, -848, -848, -848, -848},
5962 {-989,-1268,-1268,-1268,-1268},
5963 {-859,-1138,-1138,-1138,-1138}},
5964 /* GU.UU..CG */
5965 {{ DEF, -329, -329, -329, -329},
5966 {-1079,-1358,-1358,-1358,-1358},
5967 {-719, -998, -998, -998, -998},
5968 {-989,-1268,-1268,-1268,-1268},
5969 {-909,-1188,-1188,-1188,-1188}}}},
5970 /* GU.@@..GC */
5971 {{{ 0, 0, 0, 0, 0},
5972 { DEF, DEF, DEF, DEF, DEF},
5973 { DEF, DEF, DEF, DEF, DEF},
5974 { DEF, DEF, DEF, DEF, DEF},
5975 { DEF, DEF, DEF, DEF, DEF}}},
5976 /* GU.@A..GC */
5977 {{ 0, 0, 0, 0, 0},
5978 {-519, -519, -519, -519, -519},
5979 {-719, -719, -719, -719, -719},
5980 {-709, -709, -709, -709, -709},
5981 {-499, -499, -499, -499, -499}},
5982 /* GU.@C..GC */
5983 {{ 0, 0, 0, 0, 0},
5984 {-879, -879, -879, -879, -879},
5985 {-309, -309, -309, -309, -309},
5986 {-739, -739, -739, -739, -739},
5987 {-499, -499, -499, -499, -499}},
5988 /* GU.@G..GC */
5989 {{ 0, 0, 0, 0, 0},
5990 {-559, -559, -559, -559, -559},
5991 {-309, -309, -309, -309, -309},
5992 {-619, -619, -619, -619, -619},
5993 {-499, -499, -499, -499, -499}},
5994 /* GU.@U..GC */
5995 {{ 0, 0, 0, 0, 0},
5996 {-879, -879, -879, -879, -879},
5997 {-389, -389, -389, -389, -389},
5998 {-739, -739, -739, -739, -739},
5999 {-569, -569, -569, -569, -569}}}},
6000 /* GU.A@..GC */
6001 {{{ DEF, -429, -599, -599, -599},
6002 {-100, -479, -649, -649, -649},
6003 {-100, -479, -649, -649, -649},
6004 {-100, -479, -649, -649, -649},
6005 {-100, -479, -649, -649, -649}}},
6006 /* GU.AA..GC */
6007 {{ DEF, -429, -599, -599, -599},
6008 {-569, -948, -1118, -1118, -1118},
6009 {-769, -1148, -1318, -1318, -1318},
6010 {-759, -1138, -1308, -1308, -1308},
6011 {-549, -928, -1098, -1098, -1098}},
6012 /* GU.AC..GC */
6013 {{ DEF, -429, -599, -599, -599},
6014 {-929, -1308, -1478, -1478, -1478},
6015 {-359, -738, -908, -908, -908},
6016 {-789, -1168, -1338, -1338, -1338},
6017 {-549, -928, -1098, -1098, -1098}},
6018 /* GU.AG..GC */
6019 {{ DEF, -429, -599, -599, -599},
6020 {-609, -988, -1158, -1158, -1158},
6021 {-359, -738, -908, -908, -908},
6022 {-669, -1048, -1218, -1218, -1218},
6023 {-549, -928, -1098, -1098, -1098}},
6024 /* GU.AU..GC */
6025 {{ DEF, -429, -599, -599, -599},
6026 {-929, -1308, -1478, -1478, -1478},
6027 {-439, -818, -988, -988, -988},
6028 {-789, -1168, -1338, -1338, -1338},
6029 {-619, -998, -1168, -1168, -1168}}}},

```

```

6030 /* GU.C@..GC */
6031 {{ DEF, -259, -239, -239, -239},
6032 { -100, -309, -289, -289, -289},
6033 { -100, -309, -289, -289, -289},
6034 { -100, -309, -289, -289, -289},
6035 { -100, -309, -289, -289, -289}},
6036 /* GU.CA..GC */
6037 {{ DEF, -259, -239, -239, -239},
6038 { -569, -778, -758, -758, -758},
6039 { -769, -978, -958, -958, -958},
6040 { -759, -968, -948, -948, -948},
6041 { -549, -758, -738, -738, -738}},
6042 /* GU.CC..GC */
6043 {{ DEF, -259, -239, -239, -239},
6044 { -929, -1138, -1118, -1118, -1118},
6045 { -359, -568, -548, -548, -548},
6046 { -789, -998, -978, -978, -978},
6047 { -549, -758, -738, -738, -738}},
6048 /* GU.CG..GC */
6049 {{ DEF, -259, -239, -239, -239},
6050 { -609, -818, -798, -798, -798},
6051 { -359, -568, -548, -548, -548},
6052 { -669, -878, -858, -858, -858},
6053 { -549, -758, -738, -738, -738}},
6054 /* GU.CU..GC */
6055 {{ DEF, -259, -239, -239, -239},
6056 { -929, -1138, -1118, -1118, -1118},
6057 { -439, -648, -628, -628, -628},
6058 { -789, -998, -978, -978, -978},
6059 { -619, -828, -808, -808, -808}},
6060 /* GU.G@..GC */
6061 {{ DEF, -339, -689, -689, -689},
6062 { -100, -389, -739, -739, -739},
6063 { -100, -389, -739, -739, -739},
6064 { -100, -389, -739, -739, -739},
6065 { -100, -389, -739, -739, -739}},
6066 /* GU.GA..GC */
6067 {{ DEF, -339, -689, -689, -689},
6068 { -569, -858, -1208, -1208, -1208},
6069 { -769, -1058, -1408, -1408, -1408},
6070 { -759, -1048, -1398, -1398, -1398},
6071 { -549, -838, -1188, -1188, -1188}},
6072 /* GU.GC..GC */
6073 {{ DEF, -339, -689, -689, -689},
6074 { -929, -1218, -1568, -1568, -1568},
6075 { -359, -648, -998, -998, -998},
6076 { -789, -1078, -1428, -1428, -1428},
6077 { -549, -838, -1188, -1188, -1188}},
6078 /* GU.GG..GC */
6079 {{ DEF, -339, -689, -689, -689},
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6084 /* GU.GU..GC */
6085 {{ DEF, -339, -689, -689, -689},
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6089 { -619, -908, -1258, -1258, -1258}},
6090 /* GU.U@..GC */
6091 {{ DEF, -329, -329, -329, -329},
6092 { -100, -379, -379, -379, -379},
6093 { -100, -379, -379, -379, -379},
6094 { -100, -379, -379, -379, -379},
6095 { -100, -379, -379, -379, -379}},
6096 /* GU.UA..GC */
6097 {{ DEF, -329, -329, -329, -329},
6098 { -569, -848, -848, -848, -848},
6099 { -769, -1048, -1048, -1048, -1048},
6100 { -759, -1038, -1038, -1038, -1038},
6101 { -549, -828, -828, -828, -828}},
6102 /* GU.UC..GC */
6103 {{ DEF, -329, -329, -329, -329},
6104 { -929, -1208, -1208, -1208, -1208},
6105 { -359, -638, -638, -638, -638},
6106 { -789, -1068, -1068, -1068, -1068},
6107 { -549, -828, -828, -828, -828}},
6108 /* GU.UG..GC */
6109 {{ DEF, -329, -329, -329, -329},
6110 { -609, -888, -888, -888, -888},
6111 { -359, -638, -638, -638, -638},
6112 { -669, -948, -948, -948, -948},
6113 { -549, -828, -828, -828, -828}},
6114 /* GU.UU..GC */
6115 {{ DEF, -329, -329, -329, -329},
6116 { -929, -1208, -1208, -1208, -1208},

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6117 { -439, -718, -718, -718, -718},
6118 { -789,-1068,-1068,-1068,-1068},
6119 { -619, -898, -898, -898, -898}}},
6120 /* GU.@@..GU */
6121 {{{ 0, 0, 0, 0, 0},
6122 { DEF, DEF, DEF, DEF, DEF},
6123 { DEF, DEF, DEF, DEF, DEF},
6124 { DEF, DEF, DEF, DEF, DEF},
6125 { DEF, DEF, DEF, DEF, DEF}}},
6126 /* GU.@A..GU */
6127 {{ 0, 0, 0, 0, 0},
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6129 { -259, -259, -259, -259, -259},
6130 { -339, -339, -339, -339, -339},
6131 { -329, -329, -329, -329, -329}}},
6132 /* GU.@C..GU */
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6135 { -239, -239, -239, -239, -239},
6136 { -689, -689, -689, -689, -689},
6137 { -329, -329, -329, -329, -329}}},
6138 /* GU.@G..GU */
6139 {{ 0, 0, 0, 0, 0},
6140 { -599, -599, -599, -599, -599},
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6142 { -689, -689, -689, -689, -689},
6143 { -329, -329, -329, -329, -329}}},
6144 /* GU.@U..GU */
6145 {{ 0, 0, 0, 0, 0},
6146 { -599, -599, -599, -599, -599},
6147 { -239, -239, -239, -239, -239},
6148 { -689, -689, -689, -689, -689},
6149 { -329, -329, -329, -329, -329}}},
6150 /* GU.A@..GU */
6151 {{{ DEF, -429, -599, -599, -599},
6152 { -100, -479, -649, -649, -649},
6153 { -100, -479, -649, -649, -649},
6154 { -100, -479, -649, -649, -649},
6155 { -100, -479, -649, -649, -649}}},
6156 /* GU.AA..GU */
6157 {{ DEF, -429, -599, -599, -599},
6158 { -479, -858, -1028, -1028, -1028},
6159 { -309, -688, -858, -858, -858},
6160 { -389, -768, -938, -938, -938},
6161 { -379, -758, -928, -928, -928}}},
6162 /* GU.AC..GU */
6163 {{ DEF, -429, -599, -599, -599},
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6165 { -289, -668, -838, -838, -838},
6166 { -739, -1118, -1288, -1288, -1288},
6167 { -379, -758, -928, -928, -928}}},
6168 /* GU.AG..GU */
6169 {{ DEF, -429, -599, -599, -599},
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6171 { -289, -668, -838, -838, -838},
6172 { -739, -1118, -1288, -1288, -1288},
6173 { -379, -758, -928, -928, -928}}},
6174 /* GU.AU..GU */
6175 {{ DEF, -429, -599, -599, -599},
6176 { -649, -1028, -1198, -1198, -1198},
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6178 { -739, -1118, -1288, -1288, -1288},
6179 { -379, -758, -928, -928, -928}}},
6180 /* GU.C@..GU */
6181 {{{ DEF, -259, -239, -239, -239},
6182 { -100, -309, -289, -289, -289},
6183 { -100, -309, -289, -289, -289},
6184 { -100, -309, -289, -289, -289},
6185 { -100, -309, -289, -289, -289}}},
6186 /* GU.CA..GU */
6187 {{ DEF, -259, -239, -239, -239},
6188 { -479, -688, -668, -668, -668},
6189 { -309, -518, -498, -498, -498},
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6191 { -379, -588, -568, -568, -568}}},
6192 /* GU.CC..GU */
6193 {{ DEF, -259, -239, -239, -239},
6194 { -649, -858, -838, -838, -838},
6195 { -289, -498, -478, -478, -478},
6196 { -739, -948, -928, -928, -928},
6197 { -379, -588, -568, -568, -568}}},
6198 /* GU.CG..GU */
6199 {{ DEF, -259, -239, -239, -239},
6200 { -649, -858, -838, -838, -838},
6201 { -289, -498, -478, -478, -478},
6202 { -739, -948, -928, -928, -928},
6203 { -379, -588, -568, -568, -568}}},

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6204 /* GU.CU..GU */
6205 {{ DEF, -259, -239, -239, -239},
6206 { -649, -858, -838, -838, -838},
6207 { -289, -498, -478, -478, -478},
6208 { -739, -948, -928, -928, -928},
6209 { -379, -588, -568, -568, -568}}},
6210 /* GU.G@..GU */
6211 {{{ DEF, -339, -689, -689, -689},
6212 { -100, -389, -739, -739, -739},
6213 { -100, -389, -739, -739, -739},
6214 { -100, -389, -739, -739, -739},
6215 { -100, -389, -739, -739, -739}}},
6216 /* GU.GA..GU */
6217 {{ DEF, -339, -689, -689, -689},
6218 { -479, -768, -1118, -1118, -1118},
6219 { -309, -598, -948, -948, -948},
6220 { -389, -678, -1028, -1028, -1028},
6221 { -379, -668, -1018, -1018, -1018}},
6222 /* GU.GC..GU */
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6224 { -649, -938, -1288, -1288, -1288},
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6226 { -739, -1028, -1378, -1378, -1378},
6227 { -379, -668, -1018, -1018, -1018}},
6228 /* GU.GG..GU */
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6231 { -289, -578, -928, -928, -928},
6232 { -739, -1028, -1378, -1378, -1378},
6233 { -379, -668, -1018, -1018, -1018}},
6234 /* GU.GU..GU */
6235 {{ DEF, -339, -689, -689, -689},
6236 { -649, -938, -1288, -1288, -1288},
6237 { -289, -578, -928, -928, -928},
6238 { -739, -1028, -1378, -1378, -1378},
6239 { -379, -668, -1018, -1018, -1018}}},
6240 /* GU.U@..GU */
6241 {{{ DEF, -329, -329, -329, -329},
6242 { -100, -379, -379, -379, -379},
6243 { -100, -379, -379, -379, -379},
6244 { -100, -379, -379, -379, -379},
6245 { -100, -379, -379, -379, -379}}},
6246 /* GU.UA..GU */
6247 {{ DEF, -329, -329, -329, -329},
6248 { -479, -758, -758, -758, -758},
6249 { -309, -588, -588, -588, -588},
6250 { -389, -668, -668, -668, -668},
6251 { -379, -658, -658, -658, -658}},
6252 /* GU.UC..GU */
6253 {{ DEF, -329, -329, -329, -329},
6254 { -649, -928, -928, -928, -928},
6255 { -289, -568, -568, -568, -568},
6256 { -739, -1018, -1018, -1018, -1018},
6257 { -379, -658, -658, -658, -658}},
6258 /* GU.UG..GU */
6259 {{ DEF, -329, -329, -329, -329},
6260 { -649, -928, -928, -928, -928},
6261 { -289, -568, -568, -568, -568},
6262 { -739, -1018, -1018, -1018, -1018},
6263 { -379, -658, -658, -658, -658}},
6264 /* GU.UU..GU */
6265 {{ DEF, -329, -329, -329, -329},
6266 { -649, -928, -928, -928, -928},
6267 { -289, -568, -568, -568, -568},
6268 { -739, -1018, -1018, -1018, -1018},
6269 { -379, -658, -658, -658, -658}}},
6270 /* GU.@@..UG */
6271 {{{ 0, 0, 0, 0, 0},
6272 { DEF, DEF, DEF, DEF, DEF},
6273 { DEF, DEF, DEF, DEF, DEF},
6274 { DEF, DEF, DEF, DEF, DEF},
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6635 { -100, -309, -289, -289, -289}}},
6636 /* GU.CA..UA */
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6698 { -449, -728, -728, -728, -728},
6699 { -479, -758, -758, -758, -758},
6700 { -429, -708, -708, -708, -708},
6701 { -329, -608, -608, -608, -608}},
6702 /* GU.UC..UA */
6703 {{ DEF, -329, -329, -329, -329},
6704 { -679, -958, -958, -958, -958},
6705 { -559, -838, -838, -838, -838},
6706 { -729, -1008, -1008, -1008, -1008},
6707 { -189, -468, -468, -468, -468}},
6708 /* GU.UG..UA */
6709 {{ DEF, -329, -329, -329, -329},
6710 { -939, -1218, -1218, -1218, -1218},
6711 { -249, -528, -528, -528, -528},
6712 { -939, -1218, -1218, -1218, -1218},
6713 { -329, -608, -608, -608, -608}},
6714 /* GU.UU..UA */
6715 {{ DEF, -329, -329, -329, -329},
6716 { -639, -918, -918, -918, -918},
6717 { -229, -508, -508, -508, -508},
6718 { -729, -1008, -1008, -1008, -1008},
6719 { -190, -469, -469, -469, -469}}}},
6720 /* GU.@@..@ */
6721 {{{ DEF, DEF, DEF, DEF, DEF},
6722 { DEF, DEF, DEF, DEF, DEF},
6723 { DEF, DEF, DEF, DEF, DEF},
6724 { DEF, DEF, DEF, DEF, DEF},
6725 { DEF, DEF, DEF, DEF, DEF}}},

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6726 /* GU.@A.. @ */
6727 {{ DEF, DEF, DEF, DEF, DEF},
6728 { DEF, DEF, DEF, DEF, DEF},
6729 { DEF, DEF, DEF, DEF, DEF},
6730 { DEF, DEF, DEF, DEF, DEF},
6731 { DEF, DEF, DEF, DEF, DEF}},
6732 /* GU.@C.. @ */
6733 {{ DEF, DEF, DEF, DEF, DEF},
6734 { DEF, DEF, DEF, DEF, DEF},
6735 { DEF, DEF, DEF, DEF, DEF},
6736 { DEF, DEF, DEF, DEF, DEF},
6737 { DEF, DEF, DEF, DEF, DEF}},
6738 /* GU.@G.. @ */
6739 {{ DEF, DEF, DEF, DEF, DEF},
6740 { DEF, DEF, DEF, DEF, DEF},
6741 { DEF, DEF, DEF, DEF, DEF},
6742 { DEF, DEF, DEF, DEF, DEF},
6743 { DEF, DEF, DEF, DEF, DEF}},
6744 /* GU.@U.. @ */
6745 {{ DEF, DEF, DEF, DEF, DEF},
6746 { DEF, DEF, DEF, DEF, DEF},
6747 { DEF, DEF, DEF, DEF, DEF},
6748 { DEF, DEF, DEF, DEF, DEF},
6749 { DEF, DEF, DEF, DEF, DEF}},
6750 /* GU.@.. @ */
6751 {{{ -100, -479, -649, -649, -649},
6752 { -100, -479, -649, -649, -649},
6753 { -100, -479, -649, -649, -649},
6754 { -100, -479, -649, -649, -649},
6755 { -100, -479, -649, -649, -649}},
6756 /* GU.@A.. @ */
6757 {{ -100, -479, -649, -649, -649},
6758 { -100, -479, -649, -649, -649},
6759 { -100, -479, -649, -649, -649},
6760 { -100, -479, -649, -649, -649},
6761 { -100, -479, -649, -649, -649}},
6762 /* GU.@C.. @ */
6763 {{ -100, -479, -649, -649, -649},
6764 { -100, -479, -649, -649, -649},
6765 { -100, -479, -649, -649, -649},
6766 { -100, -479, -649, -649, -649},
6767 { -100, -479, -649, -649, -649}},
6768 /* GU.@G.. @ */
6769 {{ -100, -479, -649, -649, -649},
6770 { -100, -479, -649, -649, -649},
6771 { -100, -479, -649, -649, -649},
6772 { -100, -479, -649, -649, -649},
6773 { -100, -479, -649, -649, -649}},
6774 /* GU.@U.. @ */
6775 {{ -100, -479, -649, -649, -649},
6776 { -100, -479, -649, -649, -649},
6777 { -100, -479, -649, -649, -649},
6778 { -100, -479, -649, -649, -649},
6779 { -100, -479, -649, -649, -649}},
6780 /* GU.@C.. @ */
6781 {{{ -100, -309, -289, -289, -289},
6782 { -100, -309, -289, -289, -289},
6783 { -100, -309, -289, -289, -289},
6784 { -100, -309, -289, -289, -289},
6785 { -100, -309, -289, -289, -289}},
6786 /* GU.@A.. @ */
6787 {{ -100, -309, -289, -289, -289},
6788 { -100, -309, -289, -289, -289},
6789 { -100, -309, -289, -289, -289},
6790 { -100, -309, -289, -289, -289},
6791 { -100, -309, -289, -289, -289}},
6792 /* GU.@C.. @ */
6793 {{ -100, -309, -289, -289, -289},
6794 { -100, -309, -289, -289, -289},
6795 { -100, -309, -289, -289, -289},
6796 { -100, -309, -289, -289, -289},
6797 { -100, -309, -289, -289, -289}},
6798 /* GU.@G.. @ */
6799 {{ -100, -309, -289, -289, -289},
6800 { -100, -309, -289, -289, -289},
6801 { -100, -309, -289, -289, -289},
6802 { -100, -309, -289, -289, -289},
6803 { -100, -309, -289, -289, -289}},
6804 /* GU.@U.. @ */
6805 {{{ -100, -309, -289, -289, -289},
6806 { -100, -309, -289, -289, -289},
6807 { -100, -309, -289, -289, -289},
6808 { -100, -309, -289, -289, -289},
6809 { -100, -309, -289, -289, -289}},
6810 /* GU.@G.. @ */
6811 {{{ -100, -389, -739, -739, -739},
6812 { -100, -389, -739, -739, -739},

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6813 { -100, -389, -739, -739, -739},
6814 { -100, -389, -739, -739, -739},
6815 { -100, -389, -739, -739, -739}},
6816 /* GU.GA.. @ */
6817 {{ -100, -389, -739, -739, -739},
6818 { -100, -389, -739, -739, -739},
6819 { -100, -389, -739, -739, -739},
6820 { -100, -389, -739, -739, -739},
6821 { -100, -389, -739, -739, -739}},
6822 /* GU.GC.. @ */
6823 {{ -100, -389, -739, -739, -739},
6824 { -100, -389, -739, -739, -739},
6825 { -100, -389, -739, -739, -739},
6826 { -100, -389, -739, -739, -739},
6827 { -100, -389, -739, -739, -739}},
6828 /* GU.GG.. @ */
6829 {{ -100, -389, -739, -739, -739},
6830 { -100, -389, -739, -739, -739},
6831 { -100, -389, -739, -739, -739},
6832 { -100, -389, -739, -739, -739},
6833 { -100, -389, -739, -739, -739}},
6834 /* GU.GU.. @ */
6835 {{ -100, -389, -739, -739, -739},
6836 { -100, -389, -739, -739, -739},
6837 { -100, -389, -739, -739, -739},
6838 { -100, -389, -739, -739, -739},
6839 { -100, -389, -739, -739, -739}},
6840 /* GU.U@.. @ */
6841 {{{ -100, -379, -379, -379, -379},
6842 { -100, -379, -379, -379, -379},
6843 { -100, -379, -379, -379, -379},
6844 { -100, -379, -379, -379, -379},
6845 { -100, -379, -379, -379, -379}},
6846 /* GU.UA.. @ */
6847 {{ -100, -379, -379, -379, -379},
6848 { -100, -379, -379, -379, -379},
6849 { -100, -379, -379, -379, -379},
6850 { -100, -379, -379, -379, -379},
6851 { -100, -379, -379, -379, -379}},
6852 /* GU.UC.. @ */
6853 {{ -100, -379, -379, -379, -379},
6854 { -100, -379, -379, -379, -379},
6855 { -100, -379, -379, -379, -379},
6856 { -100, -379, -379, -379, -379},
6857 { -100, -379, -379, -379, -379}},
6858 /* GU.UG.. @ */
6859 {{ -100, -379, -379, -379, -379},
6860 { -100, -379, -379, -379, -379},
6861 { -100, -379, -379, -379, -379},
6862 { -100, -379, -379, -379, -379},
6863 { -100, -379, -379, -379, -379}},
6864 /* GU.UU.. @ */
6865 {{ -100, -379, -379, -379, -379},
6866 { -100, -379, -379, -379, -379},
6867 { -100, -379, -379, -379, -379},
6868 { -100, -379, -379, -379, -379},
6869 { -100, -379, -379, -379, -379}}}},
6870 { /* noPair */ {{{0}}}},
6871 /* UG.@@..CG */
6872 {{{ 0, 0, 0, 0, 0},
6873 { DEF, DEF, DEF, DEF, DEF},
6874 { DEF, DEF, DEF, DEF, DEF},
6875 { DEF, DEF, DEF, DEF, DEF},
6876 { DEF, DEF, DEF, DEF, DEF}},
6877 /* UG.@A..CG */
6878 {{ 0, 0, 0, 0, 0},
6879 {-1029,-1029,-1029,-1029,-1029},
6880 { -519, -519, -519, -519, -519},
6881 { -939, -939, -939, -939, -939},
6882 { -809, -809, -809, -809, -809}},
6883 /* UG.@C..CG */
6884 {{ 0, 0, 0, 0, 0},
6885 { -949, -949, -949, -949, -949},
6886 { -449, -449, -449, -449, -449},
6887 { -939, -939, -939, -939, -939},
6888 { -739, -739, -739, -739, -739}},
6889 /* UG.@G..CG */
6890 {{ 0, 0, 0, 0, 0},
6891 {-1029,-1029,-1029,-1029,-1029},
6892 { -519, -519, -519, -519, -519},
6893 { -939, -939, -939, -939, -939},
6894 { -809, -809, -809, -809, -809}},
6895 /* UG.@U..CG */
6896 {{ 0, 0, 0, 0, 0},
6897 {-1029,-1029,-1029,-1029,-1029},
6898 { -669, -669, -669, -669, -669},
6899 { -939, -939, -939, -939, -939},

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```

6900 { -859, -859, -859, -859, -859}},
6901 /* UG.A@..CG */
6902 {{{ DEF, -719, -789, -959, -809},
6903 { -100, -769, -839, -1009, -859},
6904 { -100, -769, -839, -1009, -859},
6905 { -100, -769, -839, -1009, -859},
6906 { -100, -769, -839, -1009, -859}},
6907 /* UG.AA..CG */
6908 {{{ DEF, -719, -789, -959, -809},
6909 {-1079, -1748, -1818, -1988, -1838},
6910 { -569, -1238, -1308, -1478, -1328},
6911 { -989, -1658, -1728, -1898, -1748},
6912 { -859, -1528, -1598, -1768, -1618}},
6913 /* UG.AC..CG */
6914 {{{ DEF, -719, -789, -959, -809},
6915 { -999, -1668, -1738, -1908, -1758},
6916 { -499, -1168, -1238, -1408, -1258},
6917 { -989, -1658, -1728, -1898, -1748},
6918 { -789, -1458, -1528, -1698, -1548}},
6919 /* UG.AG..CG */
6920 {{{ DEF, -719, -789, -959, -809},
6921 {-1079, -1748, -1818, -1988, -1838},
6922 { -569, -1238, -1308, -1478, -1328},
6923 { -989, -1658, -1728, -1898, -1748},
6924 { -859, -1528, -1598, -1768, -1618}},
6925 /* UG.AU..CG */
6926 {{{ DEF, -719, -789, -959, -809},
6927 {-1079, -1748, -1818, -1988, -1838},
6928 { -719, -1388, -1458, -1628, -1478},
6929 { -989, -1658, -1728, -1898, -1748},
6930 { -909, -1578, -1648, -1818, -1668}}},
6931 /* UG.C@..CG */
6932 {{{ DEF, -479, -479, -359, -479},
6933 { -100, -529, -529, -409, -529},
6934 { -100, -529, -529, -409, -529},
6935 { -100, -529, -529, -409, -529},
6936 { -100, -529, -529, -409, -529}},
6937 /* UG.CA..CG */
6938 {{{ DEF, -479, -479, -359, -479},
6939 {-1079, -1508, -1508, -1388, -1508},
6940 { -569, -998, -998, -878, -998},
6941 { -989, -1418, -1418, -1298, -1418},
6942 { -859, -1288, -1288, -1168, -1288}},
6943 /* UG.CC..CG */
6944 {{{ DEF, -479, -479, -359, -479},
6945 { -999, -1428, -1428, -1308, -1428},
6946 { -499, -928, -928, -808, -928},
6947 { -989, -1418, -1418, -1298, -1418},
6948 { -789, -1218, -1218, -1098, -1218}},
6949 /* UG.CG..CG */
6950 {{{ DEF, -479, -479, -359, -479},
6951 {-1079, -1508, -1508, -1388, -1508},
6952 { -569, -998, -998, -878, -998},
6953 { -989, -1418, -1418, -1298, -1418},
6954 { -859, -1288, -1288, -1168, -1288}},
6955 /* UG.CU..CG */
6956 {{{ DEF, -479, -479, -359, -479},
6957 {-1079, -1508, -1508, -1388, -1508},
6958 { -719, -1148, -1148, -1028, -1148},
6959 { -989, -1418, -1418, -1298, -1418},
6960 { -909, -1338, -1338, -1218, -1338}}},
6961 /* UG.G@..CG */
6962 {{{ DEF, -659, -809, -919, -809},
6963 { -100, -709, -859, -969, -859},
6964 { -100, -709, -859, -969, -859},
6965 { -100, -709, -859, -969, -859},
6966 { -100, -709, -859, -969, -859}},
6967 /* UG.GA..CG */
6968 {{{ DEF, -659, -809, -919, -809},
6969 {-1079, -1688, -1838, -1948, -1838},
6970 { -569, -1178, -1328, -1438, -1328},
6971 { -989, -1598, -1748, -1858, -1748},
6972 { -859, -1468, -1618, -1728, -1618}},
6973 /* UG.GC..CG */
6974 {{{ DEF, -659, -809, -919, -809},
6975 { -999, -1608, -1758, -1868, -1758},
6976 { -499, -1108, -1258, -1368, -1258},
6977 { -989, -1598, -1748, -1858, -1748},
6978 { -789, -1398, -1548, -1658, -1548}},
6979 /* UG.GG..CG */
6980 {{{ DEF, -659, -809, -919, -809},
6981 {-1079, -1688, -1838, -1948, -1838},
6982 { -569, -1178, -1328, -1438, -1328},
6983 { -989, -1598, -1748, -1858, -1748},
6984 { -859, -1468, -1618, -1728, -1618}},
6985 /* UG.GU..CG */
6986 {{{ DEF, -659, -809, -919, -809},

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6987 {-1079,-1688,-1838,-1948,-1838},
6988 {-719,-1328,-1478,-1588,-1478},
6989 {-989,-1598,-1748,-1858,-1748},
6990 {-909,-1518,-1668,-1778,-1668}}},
6991 /* UG.U@..CG */
6992 {{{ DEF, -549, -439, -549, -359},
6993 {-100, -599, -489, -599, -409},
6994 {-100, -599, -489, -599, -409},
6995 {-100, -599, -489, -599, -409},
6996 {-100, -599, -489, -599, -409}}},
6997 /* UG.UA..CG */
6998 {{ DEF, -549, -439, -549, -359},
6999 {-1079,-1578,-1468,-1578,-1388},
7000 {-569,-1068, -958,-1068, -878},
7001 {-989,-1488,-1378,-1488,-1298},
7002 {-859,-1358,-1248,-1358,-1168}},
7003 /* UG.UC..CG */
7004 {{{ DEF, -549, -439, -549, -359},
7005 {-999,-1498,-1388,-1498,-1308},
7006 {-499, -998, -888, -998, -808},
7007 {-989,-1488,-1378,-1488,-1298},
7008 {-789,-1288,-1178,-1288,-1098}},
7009 /* UG.UG..CG */
7010 {{{ DEF, -549, -439, -549, -359},
7011 {-1079,-1578,-1468,-1578,-1388},
7012 {-569,-1068, -958,-1068, -878},
7013 {-989,-1488,-1378,-1488,-1298},
7014 {-859,-1358,-1248,-1358,-1168}},
7015 /* UG.UU..CG */
7016 {{{ DEF, -549, -439, -549, -359},
7017 {-1079,-1578,-1468,-1578,-1388},
7018 {-719,-1218,-1108,-1218,-1028},
7019 {-989,-1488,-1378,-1488,-1298},
7020 {-909,-1408,-1298,-1408,-1218}}}},
7021 /* UG.@@..GC */
7022 {{{{ 0, 0, 0, 0, 0},
7023 { DEF, DEF, DEF, DEF, DEF},
7024 { DEF, DEF, DEF, DEF, DEF},
7025 { DEF, DEF, DEF, DEF, DEF},
7026 { DEF, DEF, DEF, DEF, DEF}}},
7027 /* UG.@A..GC */
7028 {{{ 0, 0, 0, 0, 0},
7029 {-519, -519, -519, -519, -519},
7030 {-719, -719, -719, -719, -719},
7031 {-709, -709, -709, -709, -709},
7032 {-499, -499, -499, -499, -499}}},
7033 /* UG.@C..GC */
7034 {{{ 0, 0, 0, 0, 0},
7035 {-879, -879, -879, -879, -879},
7036 {-309, -309, -309, -309, -309},
7037 {-739, -739, -739, -739, -739},
7038 {-499, -499, -499, -499, -499}}},
7039 /* UG.@G..GC */
7040 {{{ 0, 0, 0, 0, 0},
7041 {-559, -559, -559, -559, -559},
7042 {-309, -309, -309, -309, -309},
7043 {-619, -619, -619, -619, -619},
7044 {-499, -499, -499, -499, -499}}},
7045 /* UG.@U..GC */
7046 {{{ 0, 0, 0, 0, 0},
7047 {-879, -879, -879, -879, -879},
7048 {-389, -389, -389, -389, -389},
7049 {-739, -739, -739, -739, -739},
7050 {-569, -569, -569, -569, -569}}}},
7051 /* UG.A@..GC */
7052 {{{{ DEF, -719, -789, -959, -809},
7053 {-100, -769, -839, -1009, -859},
7054 {-100, -769, -839, -1009, -859},
7055 {-100, -769, -839, -1009, -859},
7056 {-100, -769, -839, -1009, -859}}},
7057 /* UG.AA..GC */
7058 {{{ DEF, -719, -789, -959, -809},
7059 {-569,-1238,-1308,-1478,-1328},
7060 {-769,-1438,-1508,-1678,-1528},
7061 {-759,-1428,-1498,-1668,-1518},
7062 {-549,-1218,-1288,-1458,-1308}}},
7063 /* UG.AC..GC */
7064 {{{ DEF, -719, -789, -959, -809},
7065 {-929,-1598,-1668,-1838,-1688},
7066 {-359,-1028,-1098,-1268,-1118},
7067 {-789,-1458,-1528,-1698,-1548},
7068 {-549,-1218,-1288,-1458,-1308}}},
7069 /* UG.AG..GC */
7070 {{{ DEF, -719, -789, -959, -809},
7071 {-609,-1278,-1348,-1518,-1368},
7072 {-359,-1028,-1098,-1268,-1118},
7073 {-669,-1338,-1408,-1578,-1428},

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7074 { -549,-1218,-1288,-1458,-1308}},
7075 /* UG.AU..GC */
7076 {{ DEF, -719, -789, -959, -809},
7077 { -929,-1598,-1668,-1838,-1688},
7078 { -439,-1108,-1178,-1348,-1198},
7079 { -789,-1458,-1528,-1698,-1548},
7080 { -619,-1288,-1358,-1528,-1378}}},
7081 /* UG.C@..GC */
7082 {{ DEF, -479, -479, -359, -479},
7083 { -100, -529, -529, -409, -529},
7084 { -100, -529, -529, -409, -529},
7085 { -100, -529, -529, -409, -529},
7086 { -100, -529, -529, -409, -529}}},
7087 /* UG.CA..GC */
7088 {{ DEF, -479, -479, -359, -479},
7089 { -569, -998, -998, -878, -998},
7090 { -769,-1198,-1198,-1078,-1198},
7091 { -759,-1188,-1188,-1068,-1188},
7092 { -549, -978, -978, -858, -978}},
7093 /* UG.CC..GC */
7094 {{ DEF, -479, -479, -359, -479},
7095 { -929,-1358,-1358,-1238,-1358},
7096 { -359, -788, -788, -668, -788},
7097 { -789,-1218,-1218,-1098,-1218},
7098 { -549, -978, -978, -858, -978}},
7099 /* UG.CG..GC */
7100 {{ DEF, -479, -479, -359, -479},
7101 { -609,-1038,-1038, -918,-1038},
7102 { -359, -788, -788, -668, -788},
7103 { -669,-1098,-1098, -978,-1098},
7104 { -549, -978, -978, -858, -978}},
7105 /* UG.CU..GC */
7106 {{ DEF, -479, -479, -359, -479},
7107 { -929,-1358,-1358,-1238,-1358},
7108 { -439, -868, -868, -748, -868},
7109 { -789,-1218,-1218,-1098,-1218},
7110 { -619,-1048,-1048, -928,-1048}}},
7111 /* UG.G@..GC */
7112 {{ DEF, -659, -809, -919, -809},
7113 { -100, -709, -859, -969, -859},
7114 { -100, -709, -859, -969, -859},
7115 { -100, -709, -859, -969, -859},
7116 { -100, -709, -859, -969, -859}}},
7117 /* UG.GA..GC */
7118 {{ DEF, -659, -809, -919, -809},
7119 { -569,-1178,-1328,-1438,-1328},
7120 { -769,-1378,-1528,-1638,-1528},
7121 { -759,-1368,-1518,-1628,-1518},
7122 { -549,-1158,-1308,-1418,-1308}},
7123 /* UG.GC..GC */
7124 {{ DEF, -659, -809, -919, -809},
7125 { -929,-1538,-1688,-1798,-1688},
7126 { -359, -968,-1118,-1228,-1118},
7127 { -789,-1398,-1548,-1658,-1548},
7128 { -549,-1158,-1308,-1418,-1308}},
7129 /* UG.GG..GC */
7130 {{ DEF, -659, -809, -919, -809},
7131 { -609,-1218,-1368,-1478,-1368},
7132 { -359, -968,-1118,-1228,-1118},
7133 { -669,-1278,-1428,-1538,-1428},
7134 { -549,-1158,-1308,-1418,-1308}},
7135 /* UG.GU..GC */
7136 {{ DEF, -659, -809, -919, -809},
7137 { -929,-1538,-1688,-1798,-1688},
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7141 /* UG.U@..GC */
7142 {{ DEF, -549, -439, -549, -359},
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7147 /* UG.UA..GC */
7148 {{ DEF, -549, -439, -549, -359},
7149 { -569,-1068, -958,-1068, -878},
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7153 /* UG.UC..GC */
7154 {{ DEF, -549, -439, -549, -359},
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7156 { -359, -858, -748, -858, -668},
7157 { -789,-1288,-1178,-1288,-1098},
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7159 /* UG.UG..GC */
7160 {{ DEF, -549, -439, -549, -359},
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7161 { -609,-1108, -998,-1108, -918},
7162 { -359, -858, -748, -858, -668},
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7164 { -549,-1048, -938,-1048, -858}},
7165 /* UG.UU..GC */
7166 {{ DEF, -549, -439, -549, -359},
7167 { -929,-1428,-1318,-1428,-1238},
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7172 {{{ 0, 0, 0, 0, 0},
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7174 { DEF, DEF, DEF, DEF, DEF},
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7181 { -339, -339, -339, -339, -339},
7182 { -329, -329, -329, -329, -329}},
7183 /* UG.@C..GU */
7184 {{ 0, 0, 0, 0, 0},
7185 { -599, -599, -599, -599, -599},
7186 { -239, -239, -239, -239, -239},
7187 { -689, -689, -689, -689, -689},
7188 { -329, -329, -329, -329, -329}},
7189 /* UG.@G..GU */
7190 {{ 0, 0, 0, 0, 0},
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7207 /* UG.AA..GU */
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7210 { -309, -978,-1048,-1218,-1068},
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7212 { -379,-1048,-1118,-1288,-1138}},
7213 /* UG.AC..GU */
7214 {{ DEF, -719, -789, -959, -809},
7215 { -649,-1318,-1388,-1558,-1408},
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7220 {{ DEF, -719, -789, -959, -809},
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7242 { -379, -808, -808, -688, -808}},
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7244 {{ DEF, -479, -479, -359, -479},
7245 { -649,-1078,-1078, -958,-1078},
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7248 { -379, -808, -808, -688, -808}},
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7252 { -289, -718, -718, -598, -718},
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7254 { -379, -808, -808, -688, -808}},
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7261 /* UG.G@..GU */
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7284 { -379, -988,-1138,-1248,-1138}},
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7291 /* UG.U@..GU */
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7310 {{ DEF, -549, -439, -549, -359},
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7333 /* UG.@C..UG */
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7509 { -479,-1148,-1218,-1388,-1238},
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7552 { -289, -718, -718, -598, -718},
7553 { -739,-1168,-1168,-1048,-1168},
7554 { -379, -808, -808, -688, -808}},
7555 /* UG.CU..AU */
7556 {{ DEF, -479, -479, -359, -479},
7557 { -649,-1078,-1078, -958,-1078},
7558 { -289, -718, -718, -598, -718},
7559 { -739,-1168,-1168,-1048,-1168},
7560 { -379, -808, -808, -688, -808}}},
7561 /* UG.G@..AU */
7562 {{{ DEF, -659, -809, -919, -809},
7563 { -100, -709, -859, -969, -859},
7564 { -100, -709, -859, -969, -859},
7565 { -100, -709, -859, -969, -859},
7566 { -100, -709, -859, -969, -859}}},
7567 /* UG.GA..AU */
7568 {{ DEF, -659, -809, -919, -809},
7569 { -479,-1088,-1238,-1348,-1238},
7570 { -309, -918,-1068,-1178,-1068},
7571 { -389, -998,-1148,-1258,-1148},
7572 { -379, -988,-1138,-1248,-1138}},
7573 /* UG.GC..AU */
7574 {{ DEF, -659, -809, -919, -809},
7575 { -649,-1258,-1408,-1518,-1408},
7576 { -289, -898,-1048,-1158,-1048},
7577 { -739,-1348,-1498,-1608,-1498},
7578 { -379, -988,-1138,-1248,-1138}},
7579 /* UG.GG..AU */
7580 {{ DEF, -659, -809, -919, -809},
7581 { -649,-1258,-1408,-1518,-1408},
7582 { -289, -898,-1048,-1158,-1048},
7583 { -739,-1348,-1498,-1608,-1498},
7584 { -379, -988,-1138,-1248,-1138}},
7585 /* UG.GU..AU */
7586 {{ DEF, -659, -809, -919, -809},
7587 { -649,-1258,-1408,-1518,-1408},
7588 { -289, -898,-1048,-1158,-1048},
7589 { -739,-1348,-1498,-1608,-1498},
7590 { -379, -988,-1138,-1248,-1138}}},
7591 /* UG.U@..AU */
7592 {{{ DEF, -549, -439, -549, -359},
7593 { -100, -599, -489, -599, -409},
7594 { -100, -599, -489, -599, -409},
7595 { -100, -599, -489, -599, -409},

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7596 { -100, -599, -489, -599, -409}},
7597 /* UG.UA..AU */
7598 {{ DEF, -549, -439, -549, -359},
7599 { -479, -978, -868, -978, -788},
7600 { -309, -808, -698, -808, -618},
7601 { -389, -888, -778, -888, -698},
7602 { -379, -878, -768, -878, -688}},
7603 /* UG.UC..AU */
7604 {{ DEF, -549, -439, -549, -359},
7605 { -649, -1148, -1038, -1148, -958},
7606 { -289, -788, -678, -788, -598},
7607 { -739, -1238, -1128, -1238, -1048},
7608 { -379, -878, -768, -878, -688}},
7609 /* UG.UG..AU */
7610 {{ DEF, -549, -439, -549, -359},
7611 { -649, -1148, -1038, -1148, -958},
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7613 { -739, -1238, -1128, -1238, -1048},
7614 { -379, -878, -768, -878, -688}},
7615 /* UG.UU..AU */
7616 {{ DEF, -549, -439, -549, -359},
7617 { -649, -1148, -1038, -1148, -958},
7618 { -289, -788, -678, -788, -598},
7619 { -739, -1238, -1128, -1238, -1048},
7620 { -379, -878, -768, -878, -688}}}},
7621 /* UG.@@..UA */
7622 {{{ 0, 0, 0, 0, 0},
7623 { DEF, DEF, DEF, DEF, DEF},
7624 { DEF, DEF, DEF, DEF, DEF},
7625 { DEF, DEF, DEF, DEF, DEF},
7626 { DEF, DEF, DEF, DEF, DEF}},
7627 /* UG.@A..UA */
7628 {{ 0, 0, 0, 0, 0},
7629 { -399, -399, -399, -399, -399},
7630 { -429, -429, -429, -429, -429},
7631 { -379, -379, -379, -379, -379},
7632 { -279, -279, -279, -279, -279}},
7633 /* UG.@C..UA */
7634 {{ 0, 0, 0, 0, 0},
7635 { -629, -629, -629, -629, -629},
7636 { -509, -509, -509, -509, -509},
7637 { -679, -679, -679, -679, -679},
7638 { -139, -139, -139, -139, -139}},
7639 /* UG.@G..UA */
7640 {{ 0, 0, 0, 0, 0},
7641 { -889, -889, -889, -889, -889},
7642 { -199, -199, -199, -199, -199},
7643 { -889, -889, -889, -889, -889},
7644 { -279, -279, -279, -279, -279}},
7645 /* UG.@U..UA */
7646 {{ 0, 0, 0, 0, 0},
7647 { -589, -589, -589, -589, -589},
7648 { -179, -179, -179, -179, -179},
7649 { -679, -679, -679, -679, -679},
7650 { -140, -140, -140, -140, -140}}}},
7651 /* UG.A@..UA */
7652 {{{ DEF, -719, -789, -959, -809},
7653 { -100, -769, -839, -1009, -859},
7654 { -100, -769, -839, -1009, -859},
7655 { -100, -769, -839, -1009, -859},
7656 { -100, -769, -839, -1009, -859}}}},
7657 /* UG.AA..UA */
7658 {{ DEF, -719, -789, -959, -809},
7659 { -449, -1118, -1188, -1358, -1208},
7660 { -479, -1148, -1218, -1388, -1238},
7661 { -429, -1098, -1168, -1338, -1188},
7662 { -329, -998, -1068, -1238, -1088}},
7663 /* UG.AC..UA */
7664 {{ DEF, -719, -789, -959, -809},
7665 { -679, -1348, -1418, -1588, -1438},
7666 { -559, -1228, -1298, -1468, -1318},
7667 { -729, -1398, -1468, -1638, -1488},
7668 { -189, -858, -928, -1098, -948}},
7669 /* UG.AG..UA */
7670 {{ DEF, -719, -789, -959, -809},
7671 { -939, -1608, -1678, -1848, -1698},
7672 { -249, -918, -988, -1158, -1008},
7673 { -939, -1608, -1678, -1848, -1698},
7674 { -329, -998, -1068, -1238, -1088}},
7675 /* UG.AU..UA */
7676 {{ DEF, -719, -789, -959, -809},
7677 { -639, -1308, -1378, -1548, -1398},
7678 { -229, -898, -968, -1138, -988},
7679 { -729, -1398, -1468, -1638, -1488},
7680 { -190, -859, -929, -1099, -949}}}},
7681 /* UG.C@..UA */
7682 {{{ DEF, -479, -479, -359, -479},

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7683 { -100, -529, -529, -409, -529},
7684 { -100, -529, -529, -409, -529},
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7686 { -100, -529, -529, -409, -529}},
7687 /* UG.CA..UA */
7688 {{ DEF, -479, -479, -359, -479},
7689 { -449, -878, -878, -758, -878},
7690 { -479, -908, -908, -788, -908},
7691 { -429, -858, -858, -738, -858},
7692 { -329, -758, -758, -638, -758}},
7693 /* UG.CC..UA */
7694 {{ DEF, -479, -479, -359, -479},
7695 { -679, -1108, -1108, -988, -1108},
7696 { -559, -988, -988, -868, -988},
7697 { -729, -1158, -1158, -1038, -1158},
7698 { -189, -618, -618, -498, -618}},
7699 /* UG.CG..UA */
7700 {{ DEF, -479, -479, -359, -479},
7701 { -939, -1368, -1368, -1248, -1368},
7702 { -249, -678, -678, -558, -678},
7703 { -939, -1368, -1368, -1248, -1368},
7704 { -329, -758, -758, -638, -758}},
7705 /* UG.CU..UA */
7706 {{ DEF, -479, -479, -359, -479},
7707 { -639, -1068, -1068, -948, -1068},
7708 { -229, -658, -658, -538, -658},
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7710 { -190, -619, -619, -499, -619}}},
7711 /* UG.G@..UA */
7712 {{{ DEF, -659, -809, -919, -809},
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7716 { -100, -709, -859, -969, -859}},
7717 /* UG.GA..UA */
7718 {{ DEF, -659, -809, -919, -809},
7719 { -449, -1058, -1208, -1318, -1208},
7720 { -479, -1088, -1238, -1348, -1238},
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7722 { -329, -938, -1088, -1198, -1088}},
7723 /* UG.GC..UA */
7724 {{ DEF, -659, -809, -919, -809},
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7728 { -189, -798, -948, -1058, -948}},
7729 /* UG.GG..UA */
7730 {{ DEF, -659, -809, -919, -809},
7731 { -939, -1548, -1698, -1808, -1698},
7732 { -249, -858, -1008, -1118, -1008},
7733 { -939, -1548, -1698, -1808, -1698},
7734 { -329, -938, -1088, -1198, -1088}},
7735 /* UG.GU..UA */
7736 {{ DEF, -659, -809, -919, -809},
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7738 { -229, -838, -988, -1098, -988},
7739 { -729, -1338, -1488, -1598, -1488},
7740 { -190, -799, -949, -1059, -949}}},
7741 /* UG.U@..UA */
7742 {{{ DEF, -549, -439, -549, -359},
7743 { -100, -599, -489, -599, -409},
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7746 { -100, -599, -489, -599, -409}},
7747 /* UG.UA..UA */
7748 {{ DEF, -549, -439, -549, -359},
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7758 { -189, -688, -578, -688, -498}},
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7760 {{ DEF, -549, -439, -549, -359},
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7765 /* UG.UU..UA */
7766 {{ DEF, -549, -439, -549, -359},
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7769 { -729, -1228, -1118, -1228, -1038},

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7770 { -190, -689, -579, -689, -499}}},
7771 /* UG.@@.. @ */
7772 {{{ DEF, DEF, DEF, DEF, DEF},
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7774 { DEF, DEF, DEF, DEF, DEF},
7775 { DEF, DEF, DEF, DEF, DEF},
7776 { DEF, DEF, DEF, DEF, DEF}},
7777 /* UG.@A.. @ */
7778 {{ DEF, DEF, DEF, DEF, DEF},
7779 { DEF, DEF, DEF, DEF, DEF},
7780 { DEF, DEF, DEF, DEF, DEF},
7781 { DEF, DEF, DEF, DEF, DEF},
7782 { DEF, DEF, DEF, DEF, DEF}},
7783 /* UG.@C.. @ */
7784 {{ DEF, DEF, DEF, DEF, DEF},
7785 { DEF, DEF, DEF, DEF, DEF},
7786 { DEF, DEF, DEF, DEF, DEF},
7787 { DEF, DEF, DEF, DEF, DEF},
7788 { DEF, DEF, DEF, DEF, DEF}},
7789 /* UG.@G.. @ */
7790 {{ DEF, DEF, DEF, DEF, DEF},
7791 { DEF, DEF, DEF, DEF, DEF},
7792 { DEF, DEF, DEF, DEF, DEF},
7793 { DEF, DEF, DEF, DEF, DEF},
7794 { DEF, DEF, DEF, DEF, DEF}},
7795 /* UG.@U.. @ */
7796 {{ DEF, DEF, DEF, DEF, DEF},
7797 { DEF, DEF, DEF, DEF, DEF},
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7804 { -100, -769, -839,-1009, -859},
7805 { -100, -769, -839,-1009, -859},
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7808 {{{ -100, -769, -839,-1009, -859},
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7813 /* UG.AC.. @ */
7814 {{{ -100, -769, -839,-1009, -859},
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7817 { -100, -769, -839,-1009, -859},
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7819 /* UG.AG.. @ */
7820 {{{ -100, -769, -839,-1009, -859},
7821 { -100, -769, -839,-1009, -859},
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7825 /* UG.AU.. @ */
7826 {{{ -100, -769, -839,-1009, -859},
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7831 /* UG.C@.. @ */
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7834 { -100, -529, -529, -409, -529},
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7837 /* UG.CA.. @ */
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7843 /* UG.CC.. @ */
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7849 /* UG.CG.. @ */
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7853 { -100, -529, -529, -409, -529},
7854 { -100, -529, -529, -409, -529}},
7855 /* UG.CU.. @ */
7856 {{ -100, -529, -529, -409, -529},

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7857 { -100, -529, -529, -409, -529},
7858 { -100, -529, -529, -409, -529},
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7866 { -100, -709, -859, -969, -859}}},
7867 /* UG.GA... @ */
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7872 { -100, -709, -859, -969, -859}}},
7873 /* UG.GC... @ */
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7878 { -100, -709, -859, -969, -859}}},
7879 /* UG.GG... @ */
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7884 { -100, -709, -859, -969, -859}}},
7885 /* UG.GU... @ */
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7891 /* UG.U@... @ */
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7894 { -100, -599, -489, -599, -409},
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7897 /* UG.UA... @ */
7898 {{ { -100, -599, -489, -599, -409},
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7908 { -100, -599, -489, -599, -409}}},
7909 /* UG.UG... @ */
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7912 { -100, -599, -489, -599, -409},
7913 { -100, -599, -489, -599, -409},
7914 { -100, -599, -489, -599, -409}}},
7915 /* UG.UU... @ */
7916 {{ { -100, -599, -489, -599, -409},
7917 { -100, -599, -489, -599, -409},
7918 { -100, -599, -489, -599, -409},
7919 { -100, -599, -489, -599, -409},
7920 { -100, -599, -489, -599, -409}}}}},
7921 { /* noPair */ {{{{0}}}},
7922 /* AU.@...CG */
7923 {{{ { 0, 0, 0, 0, 0},
7924 { DEF, DEF, DEF, DEF, DEF},
7925 { DEF, DEF, DEF, DEF, DEF},
7926 { DEF, DEF, DEF, DEF, DEF},
7927 { DEF, DEF, DEF, DEF, DEF}}},
7928 /* AU.@A...CG */
7929 {{ { 0, 0, 0, 0, 0},
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7931 { -519, -519, -519, -519, -519},
7932 { -939, -939, -939, -939, -939},
7933 { -809, -809, -809, -809, -809}}},
7934 /* AU.@C...CG */
7935 {{ { 0, 0, 0, 0, 0},
7936 { -949, -949, -949, -949, -949},
7937 { -449, -449, -449, -449, -449},
7938 { -939, -939, -939, -939, -939},
7939 { -739, -739, -739, -739, -739}}},
7940 /* AU.@G...CG */
7941 {{ { 0, 0, 0, 0, 0},
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7943 { -519, -519, -519, -519, -519},

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7944 { -939, -939, -939, -939, -939},
7945 { -809, -809, -809, -809, -809}},
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7947 {{ 0, 0, 0, 0, 0},
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7952 /* AU.A@..CG */
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7955 { -100, -479, -649, -649, -649},
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7957 { -100, -479, -649, -649, -649}}},
7958 /* AU.AA..CG */
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7963 { -859,-1238,-1408,-1408,-1408}}},
7964 /* AU.AC..CG */
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7970 /* AU.AG..CG */
7971 {{ DEF, -429, -599, -599, -599},
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7975 { -859,-1238,-1408,-1408,-1408}}},
7976 /* AU.AU..CG */
7977 {{ DEF, -429, -599, -599, -599},
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7979 { -719,-1098,-1268,-1268,-1268},
7980 { -989,-1368,-1538,-1538,-1538},
7981 { -909,-1288,-1458,-1458,-1458}}},
7982 /* AU.C@..CG */
7983 {{{ DEF, -259, -239, -239, -239},
7984 { -100, -309, -289, -289, -289},
7985 { -100, -309, -289, -289, -289},
7986 { -100, -309, -289, -289, -289},
7987 { -100, -309, -289, -289, -289}}},
7988 /* AU.CA..CG */
7989 {{ DEF, -259, -239, -239, -239},
7990 {-1079,-1288,-1268,-1268,-1268},
7991 { -569, -778, -758, -758, -758},
7992 { -989,-1198,-1178,-1178,-1178},
7993 { -859,-1068,-1048,-1048,-1048}}},
7994 /* AU.CC..CG */
7995 {{ DEF, -259, -239, -239, -239},
7996 { -999,-1208,-1188,-1188,-1188},
7997 { -499, -708, -688, -688, -688},
7998 { -989,-1198,-1178,-1178,-1178},
7999 { -789, -998, -978, -978, -978}}},
8000 /* AU.CG..CG */
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8002 {-1079,-1288,-1268,-1268,-1268},
8003 { -569, -778, -758, -758, -758},
8004 { -989,-1198,-1178,-1178,-1178},
8005 { -859,-1068,-1048,-1048,-1048}}},
8006 /* AU.CU..CG */
8007 {{ DEF, -259, -239, -239, -239},
8008 {-1079,-1288,-1268,-1268,-1268},
8009 { -719, -928, -908, -908, -908},
8010 { -989,-1198,-1178,-1178,-1178},
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8012 /* AU.G@..CG */
8013 {{{ DEF, -339, -689, -689, -689},
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8018 /* AU.GA..CG */
8019 {{ DEF, -339, -689, -689, -689},
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8023 { -859,-1148,-1498,-1498,-1498}}},
8024 /* AU.GC..CG */
8025 {{ DEF, -339, -689, -689, -689},
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8028 { -989,-1278,-1628,-1628,-1628},
8029 { -789,-1078,-1428,-1428,-1428}}},
8030 /* AU.GG..CG */

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8031 {{ DEF, -339, -689, -689, -689},
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8035 { -859,-1148,-1498,-1498,-1498}},
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8042 /* AU.U@..CG */
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8045 { -100, -379, -379, -379, -379},
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8047 { -100, -379, -379, -379, -379}},
8048 /* AU.UA..CG */
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8059 { -789,-1068,-1068,-1068,-1068}},
8060 /* AU.UG..CG */
8061 {{ DEF, -329, -329, -329, -329},
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8065 { -859,-1138,-1138,-1138,-1138}},
8066 /* AU.UU..CG */
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8071 { -909,-1188,-1188,-1188,-1188}}},
8072 /* AU.@@..GC */
8073 {{{{ 0, 0, 0, 0, 0},
8074 { DEF, DEF, DEF, DEF, DEF},
8075 { DEF, DEF, DEF, DEF, DEF},
8076 { DEF, DEF, DEF, DEF, DEF},
8077 { DEF, DEF, DEF, DEF, DEF}},
8078 /* AU.@A..GC */
8079 {{ 0, 0, 0, 0, 0},
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8081 { -719, -719, -719, -719, -719},
8082 { -709, -709, -709, -709, -709},
8083 { -499, -499, -499, -499, -499}},
8084 /* AU.@C..GC */
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8089 { -499, -499, -499, -499, -499}},
8090 /* AU.@G..GC */
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8096 /* AU.@U..GC */
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8101 { -569, -569, -569, -569, -569}}},
8102 /* AU.A@..GC */
8103 {{{ DEF, -429, -599, -599, -599},
8104 { -100, -479, -649, -649, -649},
8105 { -100, -479, -649, -649, -649},
8106 { -100, -479, -649, -649, -649},
8107 { -100, -479, -649, -649, -649}},
8108 /* AU.AA..GC */
8109 {{ DEF, -429, -599, -599, -599},
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8113 { -549, -928,-1098,-1098,-1098}},
8114 /* AU.AC..GC */
8115 {{ DEF, -429, -599, -599, -599},
8116 { -929,-1308,-1478,-1478,-1478},
8117 { -359, -738, -908, -908, -908},

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8118 { -789,-1168,-1338,-1338,-1338},
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8120 /* AU.AG..GC */
8121 {{ DEF, -429, -599, -599, -599},
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8123 { -359, -738, -908, -908, -908},
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8125 { -549, -928,-1098,-1098,-1098}},
8126 /* AU.AU..GC */
8127 {{ DEF, -429, -599, -599, -599},
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8132 /* AU.C@..GC */
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8135 { -100, -309, -289, -289, -289},
8136 { -100, -309, -289, -289, -289},
8137 { -100, -309, -289, -289, -289}},
8138 /* AU.CA..GC */
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8143 { -549, -758, -738, -738, -738}},
8144 /* AU.CC..GC */
8145 {{ DEF, -259, -239, -239, -239},
8146 { -929,-1138,-1118,-1118,-1118},
8147 { -359, -568, -548, -548, -548},
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8150 /* AU.CG..GC */
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8156 /* AU.CU..GC */
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8162 /* AU.G@..GC */
8163 {{{ DEF, -339, -689, -689, -689},
8164 { -100, -389, -739, -739, -739},
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8174 /* AU.GC..GC */
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8192 /* AU.U@..GC */
8193 {{{ DEF, -329, -329, -329, -329},
8194 { -100, -379, -379, -379, -379},
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8197 { -100, -379, -379, -379, -379}},
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8204 /* AU.UC..GC */
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8216 /* AU.UU..GC */
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8222 /* AU.@@..GU */
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8226 { DEF, DEF, DEF, DEF, DEF},
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8240 /* AU.@G..GU */
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8287 { -100, -309, -289, -289, -289}},
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8365 { -379, -658, -658, -658, -658}},
8366 /* AU.UU..GU */
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8370 { -739, -1018, -1018, -1018, -1018},
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8378 /* AU.@A..UG */

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8390 /* AU.@G..UG */
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8405 { -100, -479, -649, -649, -649},
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8415 {{ { DEF, -429, -599, -599, -599},
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8427 {{ { DEF, -429, -599, -599, -599},
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8840 /* AU.@G.. @ */
8841 {{ DEF, DEF, DEF, DEF, DEF},
8842 { DEF, DEF, DEF, DEF, DEF},
8843 { DEF, DEF, DEF, DEF, DEF},
8844 { DEF, DEF, DEF, DEF, DEF},
8845 { DEF, DEF, DEF, DEF, DEF}}},
8846 /* AU.@U.. @ */
8847 {{ DEF, DEF, DEF, DEF, DEF},
8848 { DEF, DEF, DEF, DEF, DEF},
8849 { DEF, DEF, DEF, DEF, DEF},
8850 { DEF, DEF, DEF, DEF, DEF},
8851 { DEF, DEF, DEF, DEF, DEF}}}},
8852 /* AU.A@.. @ */
8853 {{{ -100, -479, -649, -649, -649},
8854 { -100, -479, -649, -649, -649},
8855 { -100, -479, -649, -649, -649},
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8857 { -100, -479, -649, -649, -649}}},
8858 /* AU.AA.. @ */
8859 {{ -100, -479, -649, -649, -649},
8860 { -100, -479, -649, -649, -649},
8861 { -100, -479, -649, -649, -649},
8862 { -100, -479, -649, -649, -649},
8863 { -100, -479, -649, -649, -649}}},
8864 /* AU.AC.. @ */
8865 {{{ -100, -479, -649, -649, -649},
8866 { -100, -479, -649, -649, -649},
8867 { -100, -479, -649, -649, -649},
8868 { -100, -479, -649, -649, -649},
8869 { -100, -479, -649, -649, -649}}},
8870 /* AU.AG.. @ */
8871 {{ -100, -479, -649, -649, -649},
8872 { -100, -479, -649, -649, -649},
8873 { -100, -479, -649, -649, -649},
8874 { -100, -479, -649, -649, -649},
8875 { -100, -479, -649, -649, -649}}},
8876 /* AU.AU.. @ */
8877 {{ -100, -479, -649, -649, -649},
8878 { -100, -479, -649, -649, -649},
8879 { -100, -479, -649, -649, -649},
8880 { -100, -479, -649, -649, -649},
8881 { -100, -479, -649, -649, -649}}}},
8882 /* AU.C@.. @ */
8883 {{{ -100, -309, -289, -289, -289},
8884 { -100, -309, -289, -289, -289},
8885 { -100, -309, -289, -289, -289},
8886 { -100, -309, -289, -289, -289},
8887 { -100, -309, -289, -289, -289}}},
8888 /* AU.CA.. @ */
8889 {{ -100, -309, -289, -289, -289},
8890 { -100, -309, -289, -289, -289},
8891 { -100, -309, -289, -289, -289},
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8893 { -100, -309, -289, -289, -289}}},
8894 /* AU.CC.. @ */
8895 {{ -100, -309, -289, -289, -289},
8896 { -100, -309, -289, -289, -289},
8897 { -100, -309, -289, -289, -289},
8898 { -100, -309, -289, -289, -289},
8899 { -100, -309, -289, -289, -289}}},
8900 /* AU.CG.. @ */

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8901 {{ -100, -309, -289, -289, -289},
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8903 { -100, -309, -289, -289, -289},
8904 { -100, -309, -289, -289, -289},
8905 { -100, -309, -289, -289, -289}},
8906 /* AU.CU.. @ */
8907 {{ -100, -309, -289, -289, -289},
8908 { -100, -309, -289, -289, -289},
8909 { -100, -309, -289, -289, -289},
8910 { -100, -309, -289, -289, -289},
8911 { -100, -309, -289, -289, -289}},
8912 /* AU.G@.. @ */
8913 {{{ -100, -389, -739, -739, -739},
8914 { -100, -389, -739, -739, -739},
8915 { -100, -389, -739, -739, -739},
8916 { -100, -389, -739, -739, -739},
8917 { -100, -389, -739, -739, -739}},
8918 /* AU.GA.. @ */
8919 {{ -100, -389, -739, -739, -739},
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8921 { -100, -389, -739, -739, -739},
8922 { -100, -389, -739, -739, -739},
8923 { -100, -389, -739, -739, -739}},
8924 /* AU.GC.. @ */
8925 {{ -100, -389, -739, -739, -739},
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8927 { -100, -389, -739, -739, -739},
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8929 { -100, -389, -739, -739, -739}},
8930 /* AU.GG.. @ */
8931 {{ -100, -389, -739, -739, -739},
8932 { -100, -389, -739, -739, -739},
8933 { -100, -389, -739, -739, -739},
8934 { -100, -389, -739, -739, -739},
8935 { -100, -389, -739, -739, -739}},
8936 /* AU.GU.. @ */
8937 {{ -100, -389, -739, -739, -739},
8938 { -100, -389, -739, -739, -739},
8939 { -100, -389, -739, -739, -739},
8940 { -100, -389, -739, -739, -739},
8941 { -100, -389, -739, -739, -739}},
8942 /* AU.U@.. @ */
8943 {{{ -100, -379, -379, -379, -379},
8944 { -100, -379, -379, -379, -379},
8945 { -100, -379, -379, -379, -379},
8946 { -100, -379, -379, -379, -379},
8947 { -100, -379, -379, -379, -379}},
8948 /* AU.UA.. @ */
8949 {{ -100, -379, -379, -379, -379},
8950 { -100, -379, -379, -379, -379},
8951 { -100, -379, -379, -379, -379},
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8954 /* AU.UC.. @ */
8955 {{ -100, -379, -379, -379, -379},
8956 { -100, -379, -379, -379, -379},
8957 { -100, -379, -379, -379, -379},
8958 { -100, -379, -379, -379, -379},
8959 { -100, -379, -379, -379, -379}},
8960 /* AU.UG.. @ */
8961 {{ -100, -379, -379, -379, -379},
8962 { -100, -379, -379, -379, -379},
8963 { -100, -379, -379, -379, -379},
8964 { -100, -379, -379, -379, -379},
8965 { -100, -379, -379, -379, -379}},
8966 /* AU.UU.. @ */
8967 {{{ -100, -379, -379, -379, -379},
8968 { -100, -379, -379, -379, -379},
8969 { -100, -379, -379, -379, -379},
8970 { -100, -379, -379, -379, -379},
8971 { -100, -379, -379, -379, -379}}}},
8972 { /* noPair */ {{{{0}}}},
8973 /* UA.@A..CG */
8974 {{{{ 0, 0, 0, 0, 0},
8975 { DEF, DEF, DEF, DEF, DEF},
8976 { DEF, DEF, DEF, DEF, DEF},
8977 { DEF, DEF, DEF, DEF, DEF},
8978 { DEF, DEF, DEF, DEF, DEF}}},
8979 /* UA.@A..CG */
8980 {{ 0, 0, 0, 0, 0},
8981 {-1029, -1029, -1029, -1029, -1029},
8982 {-519, -519, -519, -519, -519},
8983 {-939, -939, -939, -939, -939},
8984 {-809, -809, -809, -809, -809}},
8985 /* UA.@C..CG */
8986 {{ 0, 0, 0, 0, 0},
8987 {-949, -949, -949, -949, -949},

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```
8988 { -449, -449, -449, -449, -449},
8989 { -939, -939, -939, -939, -939},
8990 { -739, -739, -739, -739, -739}},
8991 /* UA.EG..CG */
8992 {{ 0, 0, 0, 0, 0},
8993 {-1029,-1029,-1029,-1029,-1029},
8994 { -519, -519, -519, -519, -519},
8995 { -939, -939, -939, -939, -939},
8996 { -809, -809, -809, -809, -809}},
8997 /* UA.UU..CG */
8998 {{ 0, 0, 0, 0, 0},
8999 {-1029,-1029,-1029,-1029,-1029},
9000 { -669, -669, -669, -669, -669},
9001 { -939, -939, -939, -939, -939},
9002 { -859, -859, -859, -859, -859}},
9003 /* UA.A@..CG */
9004 {{{ DEF, -399, -629, -889, -589},
9005 { -100, -449, -679, -939, -639},
9006 { -100, -449, -679, -939, -639},
9007 { -100, -449, -679, -939, -639},
9008 { -100, -449, -679, -939, -639}},
9009 /* UA.AA..CG */
9010 {{ DEF, -399, -629, -889, -589},
9011 {-1079,-1428,-1658,-1918,-1618},
9012 { -569, -918, -1148, -1408, -1108},
9013 { -989, -1338, -1568, -1828, -1528},
9014 { -859, -1208, -1438, -1698, -1398}},
9015 /* UA.AC..CG */
9016 {{ DEF, -399, -629, -889, -589},
9017 { -999, -1348, -1578, -1838, -1538},
9018 { -499, -848, -1078, -1338, -1038},
9019 { -989, -1338, -1568, -1828, -1528},
9020 { -789, -1138, -1368, -1628, -1328}},
9021 /* UA.AG..CG */
9022 {{ DEF, -399, -629, -889, -589},
9023 {-1079,-1428,-1658,-1918,-1618},
9024 { -569, -918, -1148, -1408, -1108},
9025 { -989, -1338, -1568, -1828, -1528},
9026 { -859, -1208, -1438, -1698, -1398}},
9027 /* UA.AU..CG */
9028 {{ DEF, -399, -629, -889, -589},
9029 {-1079,-1428,-1658,-1918,-1618},
9030 { -719, -1068, -1298, -1558, -1258},
9031 { -989, -1338, -1568, -1828, -1528},
9032 { -909, -1258, -1488, -1748, -1448}},
9033 /* UA.C@..CG */
9034 {{{ DEF, -429, -509, -199, -179},
9035 { -100, -479, -559, -249, -229},
9036 { -100, -479, -559, -249, -229},
9037 { -100, -479, -559, -249, -229},
9038 { -100, -479, -559, -249, -229}},
9039 /* UA.CA..CG */
9040 {{ DEF, -429, -509, -199, -179},
9041 {-1079,-1458,-1538,-1228,-1208},
9042 { -569, -948, -1028, -718, -698},
9043 { -989, -1368, -1448, -1138, -1118},
9044 { -859, -1238, -1318, -1008, -988}},
9045 /* UA.CC..CG */
9046 {{ DEF, -429, -509, -199, -179},
9047 { -999, -1378, -1458, -1148, -1128},
9048 { -499, -878, -958, -648, -628},
9049 { -989, -1368, -1448, -1138, -1118},
9050 { -789, -1168, -1248, -938, -918}},
9051 /* UA.CG..CG */
9052 {{ DEF, -429, -509, -199, -179},
9053 {-1079,-1458,-1538,-1228,-1208},
9054 { -569, -948, -1028, -718, -698},
9055 { -989, -1368, -1448, -1138, -1118},
9056 { -859, -1238, -1318, -1008, -988}},
9057 /* UA.CU..CG */
9058 {{ DEF, -429, -509, -199, -179},
9059 {-1079,-1458,-1538,-1228,-1208},
9060 { -719, -1098, -1178, -868, -848},
9061 { -989, -1368, -1448, -1138, -1118},
9062 { -909, -1288, -1368, -1058, -1038}},
9063 /* UA.G@..CG */
9064 {{{ DEF, -379, -679, -889, -679},
9065 { -100, -429, -729, -939, -729},
9066 { -100, -429, -729, -939, -729},
9067 { -100, -429, -729, -939, -729},
9068 { -100, -429, -729, -939, -729}},
9069 /* UA.GA..CG */
9070 {{ DEF, -379, -679, -889, -679},
9071 {-1079,-1408,-1708,-1918,-1708},
9072 { -569, -898, -1198, -1408, -1198},
9073 { -989, -1318, -1618, -1828, -1618},
9074 { -859, -1188, -1488, -1698, -1488}},
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9075 /* UA.GC..CG */
9076 {{ DEF, -379, -679, -889, -679},
9077 { -999,-1328,-1628,-1838,-1628},
9078 { -499, -828,-1128,-1338,-1128},
9079 { -989,-1318,-1618,-1828,-1618},
9080 { -789,-1118,-1418,-1628,-1418}},
9081 /* UA.GG..CG */
9082 {{ DEF, -379, -679, -889, -679},
9083 {-1079,-1408,-1708,-1918,-1708},
9084 { -569, -898,-1198,-1408,-1198},
9085 { -989,-1318,-1618,-1828,-1618},
9086 { -859,-1188,-1488,-1698,-1488}},
9087 /* UA.GU..CG */
9088 {{ DEF, -379, -679, -889, -679},
9089 {-1079,-1408,-1708,-1918,-1708},
9090 { -719,-1048,-1348,-1558,-1348},
9091 { -989,-1318,-1618,-1828,-1618},
9092 { -909,-1238,-1538,-1748,-1538}}},
9093 /* UA.U@..CG */
9094 {{{ DEF, -279, -139, -279, -140},
9095 { -100, -329, -189, -329, -190},
9096 { -100, -329, -189, -329, -190},
9097 { -100, -329, -189, -329, -190},
9098 { -100, -329, -189, -329, -190}}},
9099 /* UA.UA..CG */
9100 {{ DEF, -279, -139, -279, -140},
9101 {-1079,-1308,-1168,-1308,-1169},
9102 { -569, -798, -658, -798, -659},
9103 { -989,-1218,-1078,-1218,-1079},
9104 { -859,-1088, -948,-1088, -949}},
9105 /* UA.UC..CG */
9106 {{ DEF, -279, -139, -279, -140},
9107 { -999,-1228,-1088,-1228,-1089},
9108 { -499, -728, -588, -728, -589},
9109 { -989,-1218,-1078,-1218,-1079},
9110 { -789,-1018, -878,-1018, -879}},
9111 /* UA.UG..CG */
9112 {{ DEF, -279, -139, -279, -140},
9113 {-1079,-1308,-1168,-1308,-1169},
9114 { -569, -798, -658, -798, -659},
9115 { -989,-1218,-1078,-1218,-1079},
9116 { -859,-1088, -948,-1088, -949}},
9117 /* UA.UU..CG */
9118 {{ DEF, -279, -139, -279, -140},
9119 {-1079,-1308,-1168,-1308,-1169},
9120 { -719, -948, -808, -948, -809},
9121 { -989,-1218,-1078,-1218,-1079},
9122 { -909,-1138, -998,-1138, -999}}}},
9123 /* UA.@@..GC */
9124 {{{{ 0, 0, 0, 0, 0},
9125 { DEF, DEF, DEF, DEF, DEF},
9126 { DEF, DEF, DEF, DEF, DEF},
9127 { DEF, DEF, DEF, DEF, DEF},
9128 { DEF, DEF, DEF, DEF, DEF}}}},
9129 /* UA.@A..GC */
9130 {{ 0, 0, 0, 0, 0},
9131 { -519, -519, -519, -519, -519},
9132 { -719, -719, -719, -719, -719},
9133 { -709, -709, -709, -709, -709},
9134 { -499, -499, -499, -499, -499}},
9135 /* UA.@C..GC */
9136 {{ 0, 0, 0, 0, 0},
9137 { -879, -879, -879, -879, -879},
9138 { -309, -309, -309, -309, -309},
9139 { -739, -739, -739, -739, -739},
9140 { -499, -499, -499, -499, -499}},
9141 /* UA.@G..GC */
9142 {{ 0, 0, 0, 0, 0},
9143 { -559, -559, -559, -559, -559},
9144 { -309, -309, -309, -309, -309},
9145 { -619, -619, -619, -619, -619},
9146 { -499, -499, -499, -499, -499}},
9147 /* UA.@U..GC */
9148 {{{ 0, 0, 0, 0, 0},
9149 { -879, -879, -879, -879, -879},
9150 { -389, -389, -389, -389, -389},
9151 { -739, -739, -739, -739, -739},
9152 { -569, -569, -569, -569, -569}}}},
9153 /* UA.A@..GC */
9154 {{{ DEF, -399, -629, -889, -589},
9155 { -100, -449, -679, -939, -639},
9156 { -100, -449, -679, -939, -639},
9157 { -100, -449, -679, -939, -639},
9158 { -100, -449, -679, -939, -639}},
9159 /* UA.AA..GC */
9160 {{ DEF, -399, -629, -889, -589},
9161 { -569, -918,-1148,-1408,-1108},

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9162 { -769,-1118,-1348,-1608,-1308},
9163 { -759,-1108,-1338,-1598,-1298},
9164 { -549, -898,-1128,-1388,-1088}},
9165 /* UA.AC..GC */
9166 {{ DEF, -399, -629, -889, -589},
9167 { -929,-1278,-1508,-1768,-1468},
9168 { -359, -708, -938,-1198, -898},
9169 { -789,-1138,-1368,-1628,-1328},
9170 { -549, -898,-1128,-1388,-1088}},
9171 /* UA.AG..GC */
9172 {{ DEF, -399, -629, -889, -589},
9173 { -609, -958,-1188,-1448,-1148},
9174 { -359, -708, -938,-1198, -898},
9175 { -669,-1018,-1248,-1508,-1208},
9176 { -549, -898,-1128,-1388,-1088}},
9177 /* UA.AU..GC */
9178 {{ DEF, -399, -629, -889, -589},
9179 { -929,-1278,-1508,-1768,-1468},
9180 { -439, -788,-1018,-1278, -978},
9181 { -789,-1138,-1368,-1628,-1328},
9182 { -619, -968,-1198,-1458,-1158}},
9183 /* UA.C@..GC */
9184 {{{ DEF, -429, -509, -199, -179},
9185 { -100, -479, -559, -249, -229},
9186 { -100, -479, -559, -249, -229},
9187 { -100, -479, -559, -249, -229},
9188 { -100, -479, -559, -249, -229}},
9189 /* UA.CA..GC */
9190 {{ DEF, -429, -509, -199, -179},
9191 { -569, -948,-1028, -718, -698},
9192 { -769,-1148,-1228, -918, -898},
9193 { -759,-1138,-1218, -908, -888},
9194 { -549, -928,-1008, -698, -678}},
9195 /* UA.CC..GC */
9196 {{ DEF, -429, -509, -199, -179},
9197 { -929,-1308,-1388,-1078,-1058},
9198 { -359, -738, -818, -508, -488},
9199 { -789,-1168,-1248, -938, -918},
9200 { -549, -928,-1008, -698, -678}},
9201 /* UA.CG..GC */
9202 {{ DEF, -429, -509, -199, -179},
9203 { -609, -988,-1068, -758, -738},
9204 { -359, -738, -818, -508, -488},
9205 { -669,-1048,-1128, -818, -798},
9206 { -549, -928,-1008, -698, -678}},
9207 /* UA.CU..GC */
9208 {{ DEF, -429, -509, -199, -179},
9209 { -929,-1308,-1388,-1078,-1058},
9210 { -439, -818, -898, -588, -568},
9211 { -789,-1168,-1248, -938, -918},
9212 { -619, -998,-1078, -768, -748}},
9213 /* UA.G@..GC */
9214 {{{ DEF, -379, -679, -889, -679},
9215 { -100, -429, -729, -939, -729},
9216 { -100, -429, -729, -939, -729},
9217 { -100, -429, -729, -939, -729},
9218 { -100, -429, -729, -939, -729}},
9219 /* UA.GA..GC */
9220 {{ DEF, -379, -679, -889, -679},
9221 { -569, -898,-1198,-1408,-1198},
9222 { -769,-1098,-1398,-1608,-1398},
9223 { -759,-1088,-1388,-1598,-1388},
9224 { -549, -878,-1178,-1388,-1178}},
9225 /* UA.GC..GC */
9226 {{ DEF, -379, -679, -889, -679},
9227 { -929,-1258,-1558,-1768,-1558},
9228 { -359, -688, -988,-1198, -988},
9229 { -789,-1118,-1418,-1628,-1418},
9230 { -549, -878,-1178,-1388,-1178}},
9231 /* UA.GG..GC */
9232 {{ DEF, -379, -679, -889, -679},
9233 { -609, -938,-1238,-1448,-1238},
9234 { -359, -688, -988,-1198, -988},
9235 { -669, -998,-1298,-1508,-1298},
9236 { -549, -878,-1178,-1388,-1178}},
9237 /* UA.GU..GC */
9238 {{ DEF, -379, -679, -889, -679},
9239 { -929,-1258,-1558,-1768,-1558},
9240 { -439, -768,-1068,-1278,-1068},
9241 { -789,-1118,-1418,-1628,-1418},
9242 { -619, -948,-1248,-1458,-1248}},
9243 /* UA.U@..GC */
9244 {{{ DEF, -279, -139, -279, -140},
9245 { -100, -329, -189, -329, -190},
9246 { -100, -329, -189, -329, -190},
9247 { -100, -329, -189, -329, -190},
9248 { -100, -329, -189, -329, -190}},
```

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9249 /* UA.UA..GC */
9250 {{ DEF, -279, -139, -279, -140},
9251 { -569, -798, -658, -798, -659},
9252 { -769, -998, -858, -998, -859},
9253 { -759, -988, -848, -988, -849},
9254 { -549, -778, -638, -778, -639}},
9255 /* UA.UC..GC */
9256 {{ DEF, -279, -139, -279, -140},
9257 { -929, -1158, -1018, -1158, -1019},
9258 { -359, -588, -448, -588, -449},
9259 { -789, -1018, -878, -1018, -879},
9260 { -549, -778, -638, -778, -639}},
9261 /* UA.UG..GC */
9262 {{ DEF, -279, -139, -279, -140},
9263 { -609, -838, -698, -838, -699},
9264 { -359, -588, -448, -588, -449},
9265 { -669, -898, -758, -898, -759},
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9691 { -739, -1068, -1368, -1578, -1368},
9692 { -379, -708, -1008, -1218, -1008}}},
9693 /* UA.U@..AU */
9694 {{{ DEF, -279, -139, -279, -140},
9695 { -100, -329, -189, -329, -190},
9696 { -100, -329, -189, -329, -190},
9697 { -100, -329, -189, -329, -190},
9698 { -100, -329, -189, -329, -190}}},
9699 /* UA.UA..AU */
9700 {{ DEF, -279, -139, -279, -140},
9701 { -479, -708, -568, -708, -569},
9702 { -309, -538, -398, -538, -399},
9703 { -389, -618, -478, -618, -479},
9704 { -379, -608, -468, -608, -469}},
9705 /* UA.UC..AU */
9706 {{ DEF, -279, -139, -279, -140},
9707 { -649, -878, -738, -878, -739},
9708 { -289, -518, -378, -518, -379},
9709 { -739, -968, -828, -968, -829},
9710 { -379, -608, -468, -608, -469}}},
9711 /* UA.UG..AU */
9712 {{ DEF, -279, -139, -279, -140},
9713 { -649, -878, -738, -878, -739},
9714 { -289, -518, -378, -518, -379},
9715 { -739, -968, -828, -968, -829},
9716 { -379, -608, -468, -608, -469}}},
9717 /* UA.UU..AU */
9718 {{ DEF, -279, -139, -279, -140},
9719 { -649, -878, -738, -878, -739},
9720 { -289, -518, -378, -518, -379},
9721 { -739, -968, -828, -968, -829},
9722 { -379, -608, -468, -608, -469}}}},
9723 /* UA.@@..UA */
9724 {{{{ 0, 0, 0, 0, 0},
9725 { DEF, DEF, DEF, DEF, DEF},
9726 { DEF, DEF, DEF, DEF, DEF},
9727 { DEF, DEF, DEF, DEF, DEF},
9728 { DEF, DEF, DEF, DEF, DEF}}}},
9729 /* UA.@A..UA */
9730 {{ 0, 0, 0, 0, 0},
9731 { -399, -399, -399, -399, -399},
9732 { -429, -429, -429, -429, -429},
9733 { -379, -379, -379, -379, -379},
9734 { -279, -279, -279, -279, -279}}},
9735 /* UA.@C..UA */
9736 {{ 0, 0, 0, 0, 0},
9737 { -629, -629, -629, -629, -629},
9738 { -509, -509, -509, -509, -509},
9739 { -679, -679, -679, -679, -679},
9740 { -139, -139, -139, -139, -139}}},
9741 /* UA.@G..UA */
9742 {{ 0, 0, 0, 0, 0},
9743 { -889, -889, -889, -889, -889},
9744 { -199, -199, -199, -199, -199},
9745 { -889, -889, -889, -889, -889},
9746 { -279, -279, -279, -279, -279}}},
9747 /* UA.@U..UA */
9748 {{ 0, 0, 0, 0, 0},
9749 { -589, -589, -589, -589, -589},
9750 { -179, -179, -179, -179, -179},
9751 { -679, -679, -679, -679, -679},
9752 { -140, -140, -140, -140, -140}}}},
9753 /* UA.A@..UA */
9754 {{{ DEF, -399, -629, -889, -589},
9755 { -100, -449, -679, -939, -639},
9756 { -100, -449, -679, -939, -639},
9757 { -100, -449, -679, -939, -639},
9758 { -100, -449, -679, -939, -639}}},
9759 /* UA.AA..UA */
9760 {{ DEF, -399, -629, -889, -589},
9761 { -449, -798, -1028, -1288, -988},
9762 { -479, -828, -1058, -1318, -1018},
9763 { -429, -778, -1008, -1268, -968},
9764 { -329, -678, -908, -1168, -868}}},
9765 /* UA.AC..UA */
9766 {{ DEF, -399, -629, -889, -589},
9767 { -679, -1028, -1258, -1518, -1218},
9768 { -559, -908, -1138, -1398, -1098},
9769 { -729, -1078, -1308, -1568, -1268},
9770 { -189, -538, -768, -1028, -728}}},

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9771 /* UA.AG..UA */
9772 {{ DEF, -399, -629, -889, -589},
9773 { -939,-1288,-1518,-1778,-1478},
9774 { -249, -598, -828,-1088, -788},
9775 { -939,-1288,-1518,-1778,-1478},
9776 { -329, -678, -908,-1168, -868}},
9777 /* UA.AU..UA */
9778 {{ DEF, -399, -629, -889, -589},
9779 { -639, -988,-1218,-1478,-1178},
9780 { -229, -578, -808,-1068, -768},
9781 { -729,-1078,-1308,-1568,-1268},
9782 { -190, -539, -769,-1029, -729}}},
9783 /* UA.C@..UA */
9784 {{{ DEF, -429, -509, -199, -179},
9785 { -100, -479, -559, -249, -229},
9786 { -100, -479, -559, -249, -229},
9787 { -100, -479, -559, -249, -229},
9788 { -100, -479, -559, -249, -229}}},
9789 /* UA.CA..UA */
9790 {{ DEF, -429, -509, -199, -179},
9791 { -449, -828, -908, -598, -578},
9792 { -479, -858, -938, -628, -608},
9793 { -429, -808, -888, -578, -558},
9794 { -329, -708, -788, -478, -458}},
9795 /* UA.CC..UA */
9796 {{ DEF, -429, -509, -199, -179},
9797 { -679,-1058,-1138, -828, -808},
9798 { -559, -938,-1018, -708, -688},
9799 { -729,-1108,-1188, -878, -858},
9800 { -189, -568, -648, -338, -318}},
9801 /* UA.CG..UA */
9802 {{ DEF, -429, -509, -199, -179},
9803 { -939,-1318,-1398,-1088,-1068},
9804 { -249, -628, -708, -398, -378},
9805 { -939,-1318,-1398,-1088,-1068},
9806 { -329, -708, -788, -478, -458}},
9807 /* UA.CU..UA */
9808 {{ DEF, -429, -509, -199, -179},
9809 { -639,-1018,-1098, -788, -768},
9810 { -229, -608, -688, -378, -358},
9811 { -729,-1108,-1188, -878, -858},
9812 { -190, -569, -649, -339, -319}}},
9813 /* UA.G@..UA */
9814 {{{ DEF, -379, -679, -889, -679},
9815 { -100, -429, -729, -939, -729},
9816 { -100, -429, -729, -939, -729},
9817 { -100, -429, -729, -939, -729},
9818 { -100, -429, -729, -939, -729}}},
9819 /* UA.GA..UA */
9820 {{ DEF, -379, -679, -889, -679},
9821 { -449, -778,-1078,-1288,-1078},
9822 { -479, -808,-1108,-1318,-1108},
9823 { -429, -758,-1058,-1268,-1058},
9824 { -329, -658, -958,-1168, -958}},
9825 /* UA.GC..UA */
9826 {{ DEF, -379, -679, -889, -679},
9827 { -679,-1008,-1308,-1518,-1308},
9828 { -559, -888,-1188,-1398,-1188},
9829 { -729,-1058,-1358,-1568,-1358},
9830 { -189, -518, -818,-1028, -818}},
9831 /* UA.GG..UA */
9832 {{ DEF, -379, -679, -889, -679},
9833 { -939,-1268,-1568,-1778,-1568},
9834 { -249, -578, -878,-1088, -878},
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9836 { -329, -658, -958,-1168, -958}},
9837 /* UA.GU..UA */
9838 {{ DEF, -379, -679, -889, -679},
9839 { -639, -968,-1268,-1478,-1268},
9840 { -229, -558, -858,-1068, -858},
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9842 { -190, -519, -819,-1029, -819}}},
9843 /* UA.U@..UA */
9844 {{{ DEF, -279, -139, -279, -140},
9845 { -100, -329, -189, -329, -190},
9846 { -100, -329, -189, -329, -190},
9847 { -100, -329, -189, -329, -190},
9848 { -100, -329, -189, -329, -190}}},
9849 /* UA.UA..UA */
9850 {{ DEF, -279, -139, -279, -140},
9851 { -449, -678, -538, -678, -539},
9852 { -479, -708, -568, -708, -569},
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9854 { -329, -558, -418, -558, -419}},
9855 /* UA.UC..UA */
9856 {{ DEF, -279, -139, -279, -140},
9857 { -679, -908, -768, -908, -769},
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9858 { -559, -788, -648, -788, -649},
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9860 { -189, -418, -278, -418, -279}},
9861 /* UA.UG..UA */
9862 {{ DEF, -279, -139, -279, -140},
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9866 { -329, -558, -418, -558, -419}},
9867 /* UA.UU..UA */
9868 {{ DEF, -279, -139, -279, -140},
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9870 { -229, -458, -318, -458, -319},
9871 { -729, -958, -818, -958, -819},
9872 { -190, -419, -279, -419, -280}}}},
9873 /* UA.@@.. @ */
9874 {{{ DEF, DEF, DEF, DEF, DEF},
9875 { DEF, DEF, DEF, DEF, DEF},
9876 { DEF, DEF, DEF, DEF, DEF},
9877 { DEF, DEF, DEF, DEF, DEF},
9878 { DEF, DEF, DEF, DEF, DEF}}},
9879 /* UA.@A.. @ */
9880 {{ DEF, DEF, DEF, DEF, DEF},
9881 { DEF, DEF, DEF, DEF, DEF},
9882 { DEF, DEF, DEF, DEF, DEF},
9883 { DEF, DEF, DEF, DEF, DEF},
9884 { DEF, DEF, DEF, DEF, DEF}}},
9885 /* UA.@C.. @ */
9886 {{ DEF, DEF, DEF, DEF, DEF},
9887 { DEF, DEF, DEF, DEF, DEF},
9888 { DEF, DEF, DEF, DEF, DEF},
9889 { DEF, DEF, DEF, DEF, DEF},
9890 { DEF, DEF, DEF, DEF, DEF}}},
9891 /* UA.@G.. @ */
9892 {{ DEF, DEF, DEF, DEF, DEF},
9893 { DEF, DEF, DEF, DEF, DEF},
9894 { DEF, DEF, DEF, DEF, DEF},
9895 { DEF, DEF, DEF, DEF, DEF},
9896 { DEF, DEF, DEF, DEF, DEF}}},
9897 /* UA.@U.. @ */
9898 {{ DEF, DEF, DEF, DEF, DEF},
9899 { DEF, DEF, DEF, DEF, DEF},
9900 { DEF, DEF, DEF, DEF, DEF},
9901 { DEF, DEF, DEF, DEF, DEF},
9902 { DEF, DEF, DEF, DEF, DEF}}},
9903 /* UA.A@.. @ */
9904 {{{ -100, -449, -679, -939, -639},
9905 { -100, -449, -679, -939, -639},
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9907 { -100, -449, -679, -939, -639},
9908 { -100, -449, -679, -939, -639}}},
9909 /* UA.AA.. @ */
9910 {{ -100, -449, -679, -939, -639},
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9913 { -100, -449, -679, -939, -639},
9914 { -100, -449, -679, -939, -639}}},
9915 /* UA.AC.. @ */
9916 {{ -100, -449, -679, -939, -639},
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9920 { -100, -449, -679, -939, -639}}},
9921 /* UA.AG.. @ */
9922 {{ -100, -449, -679, -939, -639},
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9927 /* UA.AU.. @ */
9928 {{ -100, -449, -679, -939, -639},
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9933 /* UA.C@.. @ */
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9938 { -100, -479, -559, -249, -229}}},
9939 /* UA.CA.. @ */
9940 {{ -100, -479, -559, -249, -229},
9941 { -100, -479, -559, -249, -229},
9942 { -100, -479, -559, -249, -229},
9943 { -100, -479, -559, -249, -229},
9944 { -100, -479, -559, -249, -229}}},
```

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9945 /* UA.CC.. @ */
9946 {{ -100, -479, -559, -249, -229},
9947 { -100, -479, -559, -249, -229},
9948 { -100, -479, -559, -249, -229},
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9951 /* UA.CG.. @ */
9952 {{ -100, -479, -559, -249, -229},
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9954 { -100, -479, -559, -249, -229},
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9957 /* UA.CU.. @ */
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9963 /* UA.G@.. @ */
9964 {{{ -100, -429, -729, -939, -729},
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9969 /* UA.GA.. @ */
9970 {{ -100, -429, -729, -939, -729},
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9972 { -100, -429, -729, -939, -729},
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9974 { -100, -429, -729, -939, -729}},
9975 /* UA.GC.. @ */
9976 {{ -100, -429, -729, -939, -729},
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9980 { -100, -429, -729, -939, -729}},
9981 /* UA.GG.. @ */
9982 {{ -100, -429, -729, -939, -729},
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9987 /* UA.GU.. @ */
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9990 { -100, -429, -729, -939, -729},
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9993 /* UA.U@.. @ */
9994 {{{ -100, -329, -189, -329, -190},
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9996 { -100, -329, -189, -329, -190},
9997 { -100, -329, -189, -329, -190},
9998 { -100, -329, -189, -329, -190}},
9999 /* UA.UA.. @ */
10000 {{ -100, -329, -189, -329, -190},
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10002 { -100, -329, -189, -329, -190},
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10005 /* UA.UC.. @ */
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10007 { -100, -329, -189, -329, -190},
10008 { -100, -329, -189, -329, -190},
10009 { -100, -329, -189, -329, -190},
10010 { -100, -329, -189, -329, -190}},
10011 /* UA.UG.. @ */
10012 {{ -100, -329, -189, -329, -190},
10013 { -100, -329, -189, -329, -190},
10014 { -100, -329, -189, -329, -190},
10015 { -100, -329, -189, -329, -190},
10016 { -100, -329, -189, -329, -190}},
10017 /* UA.UU.. @ */
10018 {{ -100, -329, -189, -329, -190},
10019 { -100, -329, -189, -329, -190},
10020 { -100, -329, -189, -329, -190},
10021 { -100, -329, -189, -329, -190},
10022 { -100, -329, -189, -329, -190}}}},
10023 { /* noPair */ {{{0}}}},
10024 /* @.@@..CG */
10025 {{{ DEF, DEF, DEF, DEF, DEF},
10026 { -100, -100, -100, -100, -100},
10027 { -100, -100, -100, -100, -100},
10028 { -100, -100, -100, -100, -100},
10029 { -100, -100, -100, -100, -100}},
10030 /* @.@A..CG */
10031 {{ DEF, DEF, DEF, DEF, DEF},

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10032 {-1079,-1079,-1079,-1079,-1079},
10033 {-569,-569,-569,-569,-569},
10034 {-989,-989,-989,-989,-989},
10035 {-859,-859,-859,-859,-859}},
10036 /* @.C..CG */
10037 {{ DEF, DEF, DEF, DEF, DEF},
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10039 {-499,-499,-499,-499,-499},
10040 {-989,-989,-989,-989,-989},
10041 {-789,-789,-789,-789,-789}},
10042 /* @.G..CG */
10043 {{ DEF, DEF, DEF, DEF, DEF},
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10046 {-989,-989,-989,-989,-989},
10047 {-859,-859,-859,-859,-859}},
10048 /* @.U..CG */
10049 {{ DEF, DEF, DEF, DEF, DEF},
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10052 {-989,-989,-989,-989,-989},
10053 {-909,-909,-909,-909,-909}}},
10054 /* @.A@..CG */
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10057 {-100,-100,-100,-100,-100},
10058 {-100,-100,-100,-100,-100},
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10061 {{ DEF, DEF, DEF, DEF, DEF},
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10063 {-569,-569,-569,-569,-569},
10064 {-989,-989,-989,-989,-989},
10065 {-859,-859,-859,-859,-859}},
10066 /* @.AC..CG */
10067 {{ DEF, DEF, DEF, DEF, DEF},
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10069 {-499,-499,-499,-499,-499},
10070 {-989,-989,-989,-989,-989},
10071 {-789,-789,-789,-789,-789}},
10072 /* @.AG..CG */
10073 {{ DEF, DEF, DEF, DEF, DEF},
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10075 {-569,-569,-569,-569,-569},
10076 {-989,-989,-989,-989,-989},
10077 {-859,-859,-859,-859,-859}},
10078 /* @.AU..CG */
10079 {{ DEF, DEF, DEF, DEF, DEF},
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10081 {-719,-719,-719,-719,-719},
10082 {-989,-989,-989,-989,-989},
10083 {-909,-909,-909,-909,-909}}},
10084 /* @.C@..CG */
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10087 {-100,-100,-100,-100,-100},
10088 {-100,-100,-100,-100,-100},
10089 {-100,-100,-100,-100,-100}},
10090 /* @.CA..CG */
10091 {{ DEF, DEF, DEF, DEF, DEF},
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10094 {-989,-989,-989,-989,-989},
10095 {-859,-859,-859,-859,-859}},
10096 /* @.CC..CG */
10097 {{ DEF, DEF, DEF, DEF, DEF},
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10099 {-499,-499,-499,-499,-499},
10100 {-989,-989,-989,-989,-989},
10101 {-789,-789,-789,-789,-789}},
10102 /* @.CG..CG */
10103 {{ DEF, DEF, DEF, DEF, DEF},
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10105 {-569,-569,-569,-569,-569},
10106 {-989,-989,-989,-989,-989},
10107 {-859,-859,-859,-859,-859}},
10108 /* @.CU..CG */
10109 {{ DEF, DEF, DEF, DEF, DEF},
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10111 {-719,-719,-719,-719,-719},
10112 {-989,-989,-989,-989,-989},
10113 {-909,-909,-909,-909,-909}}},
10114 /* @.G@..CG */
10115 {{{ DEF, DEF, DEF, DEF, DEF},
10116 {-100,-100,-100,-100,-100},
10117 {-100,-100,-100,-100,-100},
10118 {-100,-100,-100,-100,-100},
```

```

10119 { -100, -100, -100, -100, -100}},
10120 /* @.GA..CG */
10121 {{ DEF, DEF, DEF, DEF, DEF}},
10122 {-1079,-1079,-1079,-1079,-1079}},
10123 { -569, -569, -569, -569, -569}},
10124 { -989, -989, -989, -989, -989}},
10125 { -859, -859, -859, -859, -859}},
10126 /* @.GC..CG */
10127 {{ DEF, DEF, DEF, DEF, DEF}},
10128 { -999, -999, -999, -999, -999}},
10129 { -499, -499, -499, -499, -499}},
10130 { -989, -989, -989, -989, -989}},
10131 { -789, -789, -789, -789, -789}},
10132 /* @.GG..CG */
10133 {{ DEF, DEF, DEF, DEF, DEF}},
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10135 { -569, -569, -569, -569, -569}},
10136 { -989, -989, -989, -989, -989}},
10137 { -859, -859, -859, -859, -859}},
10138 /* @.GU..CG */
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10552 /* @.CG..UG */
10553 {{ DEF, DEF, DEF, DEF, DEF},
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11035 { -100, -100, -100, -100, -100},
11036 { -100, -100, -100, -100, -100},
11037 { -100, -100, -100, -100, -100}},
11038 /* @.GU.. @ */
11039 {{ -100, -100, -100, -100, -100},
11040 { -100, -100, -100, -100, -100},
11041 { -100, -100, -100, -100, -100},
11042 { -100, -100, -100, -100, -100},
11043 { -100, -100, -100, -100, -100}}},
11044 /* @.U@.. @ */
11045 {{{ -100, -100, -100, -100, -100},
11046 { -100, -100, -100, -100, -100},
11047 { -100, -100, -100, -100, -100},
11048 { -100, -100, -100, -100, -100},
11049 { -100, -100, -100, -100, -100}},
11050 /* @.UA.. @ */
11051 {{ -100, -100, -100, -100, -100},
11052 { -100, -100, -100, -100, -100},
11053 { -100, -100, -100, -100, -100},
11054 { -100, -100, -100, -100, -100},
11055 { -100, -100, -100, -100, -100}},
11056 /* @.UC.. @ */
11057 {{ -100, -100, -100, -100, -100},
11058 { -100, -100, -100, -100, -100},
11059 { -100, -100, -100, -100, -100},
11060 { -100, -100, -100, -100, -100},
11061 { -100, -100, -100, -100, -100}},
11062 /* @.UG.. @ */
11063 {{ -100, -100, -100, -100, -100},
11064 { -100, -100, -100, -100, -100},
11065 { -100, -100, -100, -100, -100},
11066 { -100, -100, -100, -100, -100},
11067 { -100, -100, -100, -100, -100}},
11068 /* @.UU.. @ */
11069 {{ -100, -100, -100, -100, -100},
11070 { -100, -100, -100, -100, -100},
11071 { -100, -100, -100, -100, -100},
11072 { -100, -100, -100, -100, -100},
11073 { -100, -100, -100, -100, -100}}}}};
11074
11075

```

## 18.151 ViennaRNA/constraints/basic.h File Reference

Functions and data structures for constraining secondary structure predictions and evaluation.

Include dependency graph for basic.h: This graph shows which files directly or indirectly include this file:

### Macros

- `#define VRNA_CONSTRAINT_FILE 0`  
*Flag for `vrna_constraints_add()` to indicate that constraints are present in a text file.*
- `#define VRNA_CONSTRAINT_SOFT_MFE 0`  
*Indicate generation of constraints for MFE folding.*
- `#define VRNA_CONSTRAINT_SOFT_PF VRNA_OPTION_PF`  
*Indicate generation of constraints for partition function computation.*
- `#define VRNA_DECOMP_PAIR_HP (unsigned char)1`  
*Flag passed to generic softt constraints callback to indicate hairpin loop decomposition step.*
- `#define VRNA_DECOMP_PAIR_IL (unsigned char)2`  
*Indicator for interior loop decomposition step.*
- `#define VRNA_DECOMP_PAIR_ML (unsigned char)3`  
*Indicator for multibranch loop decomposition step.*
- `#define VRNA_DECOMP_ML_ML_ML (unsigned char)5`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_STEM (unsigned char)6`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_ML (unsigned char)7`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_UP (unsigned char)8`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_ML_STEM (unsigned char)9`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_COAXIAL (unsigned char)10`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_ML_COAXIAL_ENC (unsigned char)11`  
*Indicator for decomposition of multibranch loop part.*
- `#define VRNA_DECOMP_EXT_EXT (unsigned char)12`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_UP (unsigned char)13`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_STEM (unsigned char)14`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_EXT_EXT (unsigned char)15`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_STEM_EXT (unsigned char)16`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_STEM_OUTSIDE (unsigned char)17`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_EXT_STEM (unsigned char)18`  
*Indicator for decomposition of exterior loop part.*
- `#define VRNA_DECOMP_EXT_EXT_STEM1 (unsigned char)19`  
*Indicator for decomposition of exterior loop part.*

## Functions

- void [vrna\\_constraints\\_add](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*constraint, unsigned int options)

Add constraints to a [vrna\\_fold\\_compound\\_t](#) data structure.

### 18.151.1 Detailed Description

Functions and data structures for constraining secondary structure predictions and evaluation.

## 18.152 basic.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_CONSTRAINTS_H
2 #define VIENNA_RNA_PACKAGE_CONSTRAINTS_H
3
4 #include <ViennaRNA/fold_compound.h>
5
99 #define VRNA_CONSTRAINT_FILE      0
100
107 #define VRNA_CONSTRAINT_SOFT_MFE  0
108
115 #define VRNA_CONSTRAINT_SOFT_PF   VRNA_OPTION_PF
116
129 #define VRNA_DECOMP_PAIR_HP       (unsigned char)1
130
144 #define VRNA_DECOMP_PAIR_IL       (unsigned char)2
145
159 #define VRNA_DECOMP_PAIR_ML       (unsigned char)3
160 #define VRNA_DECOMP_PAIR_ML_EXT   (unsigned char)23
161
162 #define VRNA_DECOMP_PAIR_ML_OUTSIDE (unsigned char)4
176 #define VRNA_DECOMP_ML_ML_ML      (unsigned char)5
177
191 #define VRNA_DECOMP_ML_STEM       (unsigned char)6
192
206 #define VRNA_DECOMP_ML_ML         (unsigned char)7
207
222 #define VRNA_DECOMP_ML_UP         (unsigned char)8
223
238 #define VRNA_DECOMP_ML_ML_STEM    (unsigned char)9
239
254 #define VRNA_DECOMP_ML_COAXIAL     (unsigned char)10
255
270 #define VRNA_DECOMP_ML_COAXIAL_ENC (unsigned char)11
271
286 #define VRNA_DECOMP_EXT_EXT       (unsigned char)12
287
302 #define VRNA_DECOMP_EXT_UP        (unsigned char)13
303
317 #define VRNA_DECOMP_EXT_STEM      (unsigned char)14
318
332 #define VRNA_DECOMP_EXT_EXT_EXT   (unsigned char)15
333
348 #define VRNA_DECOMP_EXT_STEM_EXT  (unsigned char)16
349
356 #define VRNA_DECOMP_EXT_STEM_OUTSIDE (unsigned char)17
357
372 #define VRNA_DECOMP_EXT_EXT_STEM  (unsigned char)18
373
389 #define VRNA_DECOMP_EXT_EXT_STEM1 (unsigned char)19
390
391 #define VRNA_DECOMP_EXT_STEM_EXT1  (unsigned char)20
392
393 #define VRNA_DECOMP_EXT_L          (unsigned char)21
394 #define VRNA_DECOMP_EXT_EXT_L      (unsigned char)22
395
439 void vrna_constraints_add(vrna_fold_compound_t *vc,
440                          const char *constraint,
441                          unsigned int options);
442
443
444 #endif
```

## 18.153 ViennaRNA/datastructures/basic.h File Reference

Various data structures and pre-processor macros.

Include dependency graph for basic.h: This graph shows which files directly or indirectly include this file:

## Data Structures

- struct [vrna\\_basepair\\_s](#)  
*Base pair data structure used in subopt.c. [More...](#)*
- struct [vrna\\_cpair\\_s](#)  
*this datastructure is used as input parameter in functions of PS\_dot.c [More...](#)*
- struct [vrna\\_color\\_s](#)
- struct [vrna\\_data\\_linear\\_s](#)
- struct [vrna\\_sect\\_s](#)  
*Stack of partial structures for backtracking. [More...](#)*
- struct [vrna\\_bp\\_stack\\_s](#)  
*Base pair stack element. [More...](#)*
- struct [pu\\_contrib](#)  
*contributions to p\_u [More...](#)*
- struct [interact](#)  
*interaction data structure for RNAup [More...](#)*
- struct [pu\\_out](#)  
*Collection of all free\_energy of beeing unpaired values for output. [More...](#)*
- struct [constrain](#)  
*constraints for cofolding [More...](#)*
- struct [duplexT](#)  
*Data structure for RNAduplex. [More...](#)*
- struct [node](#)  
*Data structure for RNAsnoop (fold energy list) [More...](#)*
- struct [snoopT](#)  
*Data structure for RNAsnoop. [More...](#)*
- struct [dupVar](#)  
*Data structure used in RNApkplex. [More...](#)*

## Typedefs

- typedef struct [vrna\\_basepair\\_s](#) [vrna\\_basepair\\_t](#)  
*Typename for the base pair representing data structure [vrna\\_basepair\\_s](#).*
- typedef struct [vrna\\_elem\\_prob\\_s](#) [vrna\\_plist\\_t](#)  
*Typename for the base pair list representing data structure [vrna\\_elem\\_prob\\_s](#).*
- typedef struct [vrna\\_bp\\_stack\\_s](#) [vrna\\_bp\\_stack\\_t](#)  
*Typename for the base pair stack representing data structure [vrna\\_bp\\_stack\\_s](#).*
- typedef struct [vrna\\_cpair\\_s](#) [vrna\\_cpair\\_t](#)  
*Typename for data structure [vrna\\_cpair\\_s](#).*
- typedef struct [vrna\\_sect\\_s](#) [vrna\\_sect\\_t](#)  
*Typename for stack of partial structures [vrna\\_sect\\_s](#).*
- typedef double **FLT\_OR\_DBL**  
*Typename for floating point number in partition function computations.*
- typedef struct [vrna\\_basepair\\_s](#) PAIR  
*Old typename of [vrna\\_basepair\\_s](#).*
- typedef struct [vrna\\_elem\\_prob\\_s](#) plist  
*Old typename of [vrna\\_elem\\_prob\\_s](#).*
- typedef struct [vrna\\_cpair\\_s](#) cpair  
*Old typename of [vrna\\_cpair\\_s](#).*
- typedef struct [vrna\\_sect\\_s](#) sect  
*Old typename of [vrna\\_sect\\_s](#).*
- typedef struct [vrna\\_bp\\_stack\\_s](#) bondT

- *Old typename of `vrna_bp_stack_s`.*
- typedef struct `pu_contrib` **pu\_contrib**  
*contributions to `p_u`*
- typedef struct `interact` **interact**  
*interaction data structure for `RNAup`*
- typedef struct `pu_out` **pu\_out**  
*Collection of all `free_energy` of beeing unpaired values for output.*
- typedef struct `constrain` **constrain**  
*constraints for cofolding*
- typedef struct `node` **folden**  
*Data structure for `RNAshoop` (fold energy list)*
- typedef struct `dupVar` **dupVar**  
*Data structure used in `RNApkplex`.*

## Functions

- void `vrna_C11_features` (void)  
*Dummy symbol to check whether the library was build using C11/C++11 features.*

### 18.153.1 Detailed Description

Various data structures and pre-processor macros.

## 18.154 basic.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_DATA_STRUCTURES_H
2 #define VIENNA_RNA_PACKAGE_DATA_STRUCTURES_H
3
18 /* below are several convenience typedef's we use throughout the ViennaRNA library */
19
21 typedef struct vrna_basepair_s vrna_basepair_t;
22
24 typedef struct vrna_elem_prob_s vrna_plist_t;
25
27 typedef struct vrna_bp_stack_s vrna_bp_stack_t;
28
30 typedef struct vrna_cpair_s vrna_cpair_t;
31
33 typedef struct vrna_sect_s vrna_sect_t;
34
35 typedef struct vrna_data_linear_s vrna_data_lin_t;
36
37 typedef struct vrna_color_s vrna_color_t;
38
40 #ifdef USE_FLOAT_PF
41 typedef float FLT_OR_DBL;
42 #else
43 typedef double FLT_OR_DBL;
44 #endif
45
46
47 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
48
49 /* the following typedefs are for backward compatibility only */
50
55 typedef struct vrna_basepair_s PAIR;
56
61 typedef struct vrna_elem_prob_s plist;
66 typedef struct vrna_cpair_s cpair;
67
72 typedef struct vrna_sect_s sect;
73
78 typedef struct vrna_bp_stack_s bondT;
79
80 #endif
81
82 #include <ViennaRNA/params/constants.h>
83 #include <ViennaRNA/fold_compound.h>
84 #include <ViennaRNA/model.h>

```

```

85 #include <ViennaRNA/params/basic.h>
86 #include <ViennaRNA/dp_matrices.h>
87 #include <ViennaRNA/constraints/hard.h>
88 #include <ViennaRNA/constraints/soft.h>
89 #include <ViennaRNA/grammar.h>
90 #include "ViennaRNA/structured_domains.h"
91 #include "ViennaRNA/unstructured_domains.h"
92 #include "ViennaRNA/utils/structures.h"
93
94 /*
95  * #####
96  * Here are the type definitions of various datastructures
97  * shared among the Vienna RNA Package
98  * #####
99  */
100
101 struct vrna_basepair_s {
102     int i;
103     int j;
104 };
105
106 struct vrna_cpair_s {
107     int i, j, mfe;
108     float p, hue, sat;
109     int type;
110 };
111
112 struct vrna_color_s {
113     float hue;
114     float sat;
115     float bri;
116 };
117
118 struct vrna_data_linear_s {
119     unsigned int position;
120     float value;
121     vrna_color_t color;
122 };
123
124 struct vrna_sect_s {
125     int i;
126     int j;
127     int ml;
128 };
129
130 struct vrna_bp_stack_s {
131     unsigned int i;
132     unsigned int j;
133 };
134
135 /*
136  * #####
137  * RNAUp data structures
138  * #####
139  */
140
141 typedef struct pu_contrib {
142     double **H;
143     double **I;
144     double **M;
145     double **E;
146     int length;
147     int w;
148 } pu_contrib;
149
150 typedef struct interact {
151     double *Pi;
152     double *Gi;
153     double Gikjl;
154     double Gikjl_wo;
155     int i;
156     int k;
157     int j;
158     int l;
159     int length;
160 } interact;
161
162 typedef struct pu_out {
163     int len;
164     int u_vals;
165     int contribs;
166     char **header;
167     double **u_values;
168 } pu_out;
169
170
171

```

```

197 typedef struct constrain {
198     int    *indx;
199     char   *ptype;
200 } constrain;
201
202 /*
203  * #####
204  * RNA duplex data structures
205  * #####
206  */
207
208 typedef struct {
209     int    i;
210     int    j;
211     int    end;
212     char   *structure;
213     double energy;
214     double energy_backtrack;
215     double opening_backtrack_x;
216     double opening_backtrack_y;
217     int    offset;
218     double dG1;
219     double dG2;
220     double ddG;
221     int    tb;
222     int    te;
223     int    qb;
224     int    qe;
225 } duplexT;
226
227 /*
228  * #####
229  * RNAsnoop data structures
230  * #####
231  */
232
233 typedef struct node {
234     int    k;
235     int    energy;
236     struct node *next;
237 } folden;
238
239 typedef struct {
240     int    i;
241     int    j;
242     int    u;
243     char   *structure;
244     float  energy;
245     float  Duplex_El;
246     float  Duplex_Er;
247     float  Loop_E;
248     float  Loop_D;
249     float  pscd;
250     float  psct;
251     float  pscg;
252     float  Duplex_Ol;
253     float  Duplex_Or;
254     float  Duplex_Ot;
255     float  fullStemEnergy;
256 } snoopT;
257
258 /*
259  * #####
260  * PKplex data structures
261  * #####
262  */
263
264 typedef struct dupVar {
265     int    i;
266     int    j;
267     int    end;
268     char   *pk_helix;
269     char   *structure;
270     double energy;
271     int    offset;
272     double dG1;
273     double dG2;
274     double ddG;
275     int    tb;
276     int    te;
277     int    qb;
278     int    qe;
279     int    inactive;
280     int    processed;
281 } dupVar;
282
283

```

```

326 #ifndef VRNA_DISABLE_C11_FEATURES
327 void vrna_C11_features(void);
328
329
330 #endif
331
337 #endif

```

## 18.155 ViennaRNA/params/basic.h File Reference

Functions to deal with sets of energy parameters.

Include dependency graph for basic.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_param\\_s](#)  
The datastructure that contains temperature scaled energy parameters. [More...](#)
- struct [vrna\\_exp\\_param\\_s](#)  
The data structure that contains temperature scaled Boltzmann weights of the energy parameters. [More...](#)

### Typedefs

- typedef struct [vrna\\_param\\_s](#) [vrna\\_param\\_t](#)  
Typename for the free energy parameter data structure [vrna\\_params](#).
- typedef struct [vrna\\_exp\\_param\\_s](#) [vrna\\_exp\\_param\\_t](#)  
Typename for the Boltzmann factor data structure [vrna\\_exp\\_params](#).
- typedef struct [vrna\\_param\\_s](#) paramT  
Old typename of [vrna\\_param\\_s](#).
- typedef struct [vrna\\_exp\\_param\\_s](#) pf\_paramT  
Old typename of [vrna\\_exp\\_param\\_s](#).

### Functions

- [vrna\\_param\\_t](#) \* [vrna\\_params](#) ([vrna\\_md\\_t](#) \*md)  
Get a data structure containing prescaled free energy parameters.
- [vrna\\_param\\_t](#) \* [vrna\\_params\\_copy](#) ([vrna\\_param\\_t](#) \*par)  
Get a copy of the provided free energy parameters.
- [vrna\\_exp\\_param\\_t](#) \* [vrna\\_exp\\_params](#) ([vrna\\_md\\_t](#) \*md)  
Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors.
- [vrna\\_exp\\_param\\_t](#) \* [vrna\\_exp\\_params\\_comparative](#) (unsigned int n\_seq, [vrna\\_md\\_t](#) \*md)  
Get a data structure containing prescaled free energy parameters already transformed to Boltzmann factors (alifold version)
- [vrna\\_exp\\_param\\_t](#) \* [vrna\\_exp\\_params\\_copy](#) ([vrna\\_exp\\_param\\_t](#) \*par)  
Get a copy of the provided free energy parameters (provided as Boltzmann factors)
- void [vrna\\_params\\_subst](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_param\\_t](#) \*par)  
Update/Reset energy parameters data structure within a [vrna\\_fold\\_compound\\_t](#).
- void [vrna\\_exp\\_params\\_subst](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_exp\\_param\\_t](#) \*params)  
Update the energy parameters for subsequent partition function computations.
- void [vrna\\_exp\\_params\\_rescale](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double \*mfe)  
Rescale Boltzmann factors for partition function computations.
- void [vrna\\_params\\_reset](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_md\\_t](#) \*md\_p)  
Reset free energy parameters within a [vrna\\_fold\\_compound\\_t](#) according to provided, or default model details.
- void [vrna\\_exp\\_params\\_reset](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_md\\_t](#) \*md\_p)  
Reset Boltzmann factors for partition function computations within a [vrna\\_fold\\_compound\\_t](#) according to provided, or default model details.



- `vrna_exp_param_t * get_scaled_pf_parameters` (void)  
Get precomputed Boltzmann factors of the loop type dependent energy contributions with independent thermodynamic temperature.
- `vrna_exp_param_t * get_boltzmann_factors` (double `temperature`, double `betaScale`, `vrna_md_t` `md`, double `pf_scale`)  
Get a copy of already precomputed Boltzmann factors.
- `vrna_exp_param_t * get_scaled_alipf_parameters` (unsigned int `n_seq`)  
Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant)
- `vrna_exp_param_t * get_boltzmann_factors_ali` (unsigned int `n_seq`, double `temperature`, double `betaScale`, `vrna_md_t` `md`, double `pf_scale`)  
Get precomputed Boltzmann factors of the loop type dependent energy contributions (alifold variant) with independent thermodynamic temperature.
- `vrna_param_t * scale_parameters` (void)  
Get precomputed energy contributions for all the known loop types.
- `vrna_param_t * get_scaled_parameters` (double `temperature`, `vrna_md_t` `md`)  
Get precomputed energy contributions for all the known loop types.

## 18.155.1 Detailed Description

Functions to deal with sets of energy parameters.

## 18.156 basic.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 typedef struct vrna_param_s vrna_param_t;
17 typedef struct vrna_exp_param_s vrna_exp_param_t;
18
19 #include <ViennaRNA/params/constants.h>
20 #include <ViennaRNA/datastructures/basic.h>
21 #include <ViennaRNA/fold_compound.h>
22 #include <ViennaRNA/model.h>
23
24 #define VRNA_GQUAD_MAX_STACK_SIZE 7
25 #define VRNA_GQUAD_MIN_STACK_SIZE 2
26 #define VRNA_GQUAD_MAX_LINKER_LENGTH 15
27 #define VRNA_GQUAD_MIN_LINKER_LENGTH 1
28 #define VRNA_GQUAD_MIN_BOX_SIZE ((4 * VRNA_GQUAD_MIN_STACK_SIZE) + \
29                                   (3 * VRNA_GQUAD_MIN_LINKER_LENGTH))
30 #define VRNA_GQUAD_MAX_BOX_SIZE ((4 * VRNA_GQUAD_MAX_STACK_SIZE) + \
31                                   (3 * VRNA_GQUAD_MAX_LINKER_LENGTH))
32
33 struct vrna_param_s {
34     int id;
35     int stack[NBPAIRS + 1][NBPAIRS + 1];
36     int hairpin[31];
37     int bulge[MAXLOOP + 1];
38     int internal_loop[MAXLOOP + 1];
39     int mismatchExt[NBPAIRS + 1][5][5];
40     int mismatchI[NBPAIRS + 1][5][5];
41     int mismatchlnI[NBPAIRS + 1][5][5];
42     int mismatch23I[NBPAIRS + 1][5][5];
43     int mismatchH[NBPAIRS + 1][5][5];
44     int mismatchM[NBPAIRS + 1][5][5];
45     int dangle5[NBPAIRS + 1][5];
46     int dangle3[NBPAIRS + 1][5];
47 }
```

```

71  int      int11[NBPAIRS + 1][NBPAIRS + 1][5][5];
72  int      int21[NBPAIRS + 1][NBPAIRS + 1][5][5][5];
73  int      int22[NBPAIRS + 1][NBPAIRS + 1][5][5][5][5];
74  int      ninio[5];
75  double   lxc;
76  int      MLbase;
77  int      MLintern[NBPAIRS + 1];
78  int      MLclosing;
79  int      TerminalAU;
80  int      DuplexInit;
81  int      Tetraloop_E[200];
82  char     Tetraloops[1401];
83  int      Triloop_E[40];
84  char     Triloops[241];
85  int      Hexaloop_E[40];
86  char     Hexaloops[1801];
87  int      TripleC;
88  int      MultipleCA;
89  int      MultipleCB;
90  int      gquad[VRNA_GQUAD_MAX_STACK_SIZE + 1][3 * VRNA_GQUAD_MAX_LINKER_LENGTH + 1];
91  int      gquadLayerMismatch;
92  int      gquadLayerMismatchMax;
93
94  double   temperature;
96  vrna_md_t model_details;
97  char     param_file[256];
98 };
99
103 struct vrna_exp_param_s {
104     int      id;
107     double   expstack[NBPAIRS + 1][NBPAIRS + 1];
108     double   exphairpin[31];
109     double   expbulge[MAXLOOP + 1];
110     double   expinternal[MAXLOOP + 1];
111     double   expmismatchExt[NBPAIRS + 1][5][5];
112     double   expmismatchI[NBPAIRS + 1][5][5];
113     double   expmismatch23I[NBPAIRS + 1][5][5];
114     double   expmismatchlnI[NBPAIRS + 1][5][5];
115     double   expmismatchH[NBPAIRS + 1][5][5];
116     double   expmismatchM[NBPAIRS + 1][5][5];
117     double   expdangle5[NBPAIRS + 1][5];
118     double   expdangle3[NBPAIRS + 1][5];
119     double   expint11[NBPAIRS + 1][NBPAIRS + 1][5][5];
120     double   expint21[NBPAIRS + 1][NBPAIRS + 1][5][5][5];
121     double   expint22[NBPAIRS + 1][NBPAIRS + 1][5][5][5][5];
122     double   expninio[5][MAXLOOP + 1];
123     double   lxc;
124     double   expMLbase;
125     double   expMLintern[NBPAIRS + 1];
126     double   expMLclosing;
127     double   expTermAU;
128     double   expDuplexInit;
129     double   exptetra[40];
130     double   exptri[40];
131     double   exphex[40];
132     char     Tetraloops[1401];
133     double   expTriloop[40];
134     char     Triloops[241];
135     char     Hexaloops[1801];
136     double   expTripleC;
137     double   expMultipleCA;
138     double   expMultipleCB;
139     double   expgquad[VRNA_GQUAD_MAX_STACK_SIZE + 1][3 * VRNA_GQUAD_MAX_LINKER_LENGTH + 1];
140     double   expgquadLayerMismatch;
141     int      gquadLayerMismatchMax;
142
143     double   kT;
144     double   pf_scale;
146     double   temperature;
147     double   alpha;
154     vrna_md_t model_details;
155     char     param_file[256];
156 };
157
158
170 vrna_param_t *
171 vrna_params(vrna_md_t *md);
172
173
185 vrna_param_t *
186 vrna_params_copy(vrna_param_t *par);
187
188
211 vrna_exp_param_t *
212 vrna_exp_params(vrna_md_t *md);
213
214

```

```

228 vrna_exp_param_t *
229 vrna_exp_params_comparative(unsigned int n_seq,
230                             vrna_md_t    *md);
231
232
233 vrna_exp_param_t *
234 vrna_exp_params_copy(vrna_exp_param_t *par);
235
236
237 void
238 vrna_params_subst(vrna_fold_compound_t *vc,
239                  vrna_param_t          *par);
240
241
242 void
243 vrna_exp_params_subst(vrna_fold_compound_t *vc,
244                      vrna_exp_param_t     *params);
245
246
247 void
248 vrna_exp_params_rescale(vrna_fold_compound_t *vc,
249                        double                *mfe);
250
251
252 void
253 vrna_params_reset(vrna_fold_compound_t *vc,
254                  vrna_md_t             *md_p);
255
256
257 void
258 vrna_exp_params_reset(vrna_fold_compound_t *vc,
259                      vrna_md_t             *md_p);
260
261
262 void
263 vrna_params_prepare(vrna_fold_compound_t *vc,
264                    unsigned int          options);
265
266
267 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
268
269 typedef struct vrna_param_s paramT;
270
271 typedef struct vrna_exp_param_s pf_paramT;
272
273 DEPRECATED(vrna_param_t *get_parameter_copy(vrna_param_t *par),
274            "Use vrna_params_copy() instead");
275
276 DEPRECATED(vrna_exp_param_t *get_scaled_pf_parameters(void),
277            "Use vrna_params() instead");
278
279 DEPRECATED(vrna_exp_param_t *get_boltzmann_factors(double temperature,
280  double betaScale,
281  vrna_md_t md,
282  double pf_scale),
283            "Use vrna_exp_params() instead");
284
285 DEPRECATED(vrna_exp_param_t *get_boltzmann_factor_copy(vrna_exp_param_t *parameters),
286            "Use vrna_exp_params_copy() instead");
287
288 DEPRECATED(vrna_exp_param_t *get_scaled_alipf_parameters(unsigned int n_seq),
289            "Use vrna_exp_params_comparative() instead");
290
291 DEPRECATED(vrna_exp_param_t *get_boltzmann_factors_ali(unsigned int n_seq,
292   double temperature,
293   double betaScale,
294   vrna_md_t md,
295   double pf_scale),
296            "Use vrna_exp_params_comparative() instead");
297
298 DEPRECATED(vrna_param_t *scale_parameters(void),
299            "Use vrna_params() instead");
300
301 DEPRECATED(vrna_param_t *get_scaled_parameters(double temperature,
302  vrna_md_t md),
303            "Use vrna_params() instead");
304
305 DEPRECATED(vrna_param_t *copy_parameters(void), "Use vrna_params_copy() instead");
306 DEPRECATED(vrna_param_t *set_parameters(vrna_param_t *dest), "Use vrna_params_copy() instead");
307 DEPRECATED(vrna_exp_param_t *scale_pf_parameters(void), "Use vrna_exp_params() instead");
308 DEPRECATED(vrna_exp_param_t *copy_pf_param(void), "Use vrna_exp_params_copy() instead");
309 DEPRECATED(vrna_exp_param_t *set_pf_param(vrna_param_t *dest),
310            "Use vrna_exp_params_copy() instead");
311
312 #endif
313
314 #endif

```

## 18.157 ViennaRNA/utils/basic.h File Reference

General utility- and helper-functions used throughout the *ViennaRNA Package*.

Include dependency graph for basic.h: This graph shows which files directly or indirectly include this file:

### Macros

- **#define VRNA\_INPUT\_ERROR** 1U  
Output flag of `get_input_line()`: "An ERROR has occured, maybe EOF".
- **#define VRNA\_INPUT\_QUIT** 2U  
Output flag of `get_input_line()`: "the user requested quitting the program".
- **#define VRNA\_INPUT\_MISC** 4U  
Output flag of `get_input_line()`: "something was read".
- **#define VRNA\_INPUT\_FASTA\_HEADER** 8U  
Input/Output flag of `get_input_line()`:  
if used as input option this tells `get_input_line()` that the data to be read should comply with the FASTA format.
- **#define VRNA\_INPUT\_CONSTRAINT** 32U  
Input flag for `get_input_line()`:  
Tell `get_input_line()` that we assume to read a structure constraint.
- **#define VRNA\_INPUT\_NO\_TRUNCATION** 256U  
Input switch for `get_input_line()`: "do not truncate the line by eliminating white spaces at end of line".
- **#define VRNA\_INPUT\_NO\_REST** 512U  
Input switch for `vrna_file_fasta_read_record()`: "do fill rest array".
- **#define VRNA\_INPUT\_NO\_SPAN** 1024U  
Input switch for `vrna_file_fasta_read_record()`: "never allow data to span more than one line".
- **#define VRNA\_INPUT\_NOSKIP\_BLANK\_LINES** 2048U  
Input switch for `vrna_file_fasta_read_record()`: "do not skip empty lines".
- **#define VRNA\_INPUT\_BLANK\_LINE** 4096U  
Output flag for `vrna_file_fasta_read_record()`: "read an empty line".
- **#define VRNA\_INPUT\_NOSKIP\_COMMENTS** 128U  
Input switch for `get_input_line()`: "do not skip comment lines".
- **#define VRNA\_INPUT\_COMMENT** 8192U  
Output flag for `vrna_file_fasta_read_record()`: "read a comment".
- **#define MIN2(A, B)** ((A) < (B) ? (A) : (B))  
Get the minimum of two comparable values.
- **#define MAX2(A, B)** ((A) > (B) ? (A) : (B))  
Get the maximum of two comparable values.
- **#define MIN3(A, B, C)** (MIN2((MIN2((A), (B))), (C)))  
Get the minimum of three comparable values.
- **#define MAX3(A, B, C)** (MAX2((MAX2((A), (B))), (C)))  
Get the maximum of three comparable values.

### Functions

- void \* `vrna_alloc` (unsigned size)  
Allocate space safely.
- void \* `vrna_realloc` (void \*p, unsigned size)  
Reallocate space safely.
- void `vrna_init_rand` (void)  
Initialize seed for random number generator.
- void `vrna_init_rand_seed` (unsigned int seed)  
Initialize the random number generator with a pre-defined seed.

- double [vrna\\_urn](#) (void)  
*get a random number from [0..1]*
- int [vrna\\_int\\_urn](#) (int from, int to)  
*Generates a pseudo random integer in a specified range.*
- char \* [vrna\\_time\\_stamp](#) (void)  
*Get a timestamp.*
- unsigned int [get\\_input\\_line](#) (char \*\*string, unsigned int options)
- int \* [vrna\\_idx\\_row\\_wise](#) (unsigned int length)  
*Get an index mapper array (iindx) for accessing the energy matrices, e.g. in partition function related functions.*
- int \* [vrna\\_idx\\_col\\_wise](#) (unsigned int length)  
*Get an index mapper array (indx) for accessing the energy matrices, e.g. in MFE related functions.*
- void [vrna\\_message\\_error](#) (const char \*format,...)  
*Print an error message and die.*
- void [vrna\\_message\\_verror](#) (const char \*format, va\_list args)  
*Print an error message and die.*
- void [vrna\\_message\\_warning](#) (const char \*format,...)  
*Print a warning message.*
- void [vrna\\_message\\_vwarning](#) (const char \*format, va\_list args)  
*Print a warning message.*
- void [vrna\\_message\\_info](#) (FILE \*fp, const char \*format,...)  
*Print an info message.*
- void [vrna\\_message\\_vinfo](#) (FILE \*fp, const char \*format, va\_list args)  
*Print an info message.*
- void [vrna\\_message\\_input\\_seq\\_simple](#) (void)  
*Print a line to stdout that asks for an input sequence.*
- void [vrna\\_message\\_input\\_seq](#) (const char \*s)  
*Print a line with a user defined string and a ruler to stdout.*
- char \* [get\\_line](#) (FILE \*fp)  
*Read a line of arbitrary length from a stream.*
- void [print\\_tty\\_input\\_seq](#) (void)  
*Print a line to stdout that asks for an input sequence.*
- void [print\\_tty\\_input\\_seq\\_str](#) (const char \*s)  
*Print a line with a user defined string and a ruler to stdout.*
- void [warn\\_user](#) (const char message[ ])  
*Print a warning message.*
- void [nrerror](#) (const char message[ ])  
*Die with an error message.*
- void \* [space](#) (unsigned size)  
*Allocate space safely.*
- void \* [xrealloc](#) (void \*p, unsigned size)  
*Reallocate space safely.*
- void [init\\_rand](#) (void)  
*Make random number seeds.*
- double [urn](#) (void)  
*get a random number from [0..1]*
- int [int\\_urn](#) (int from, int to)  
*Generates a pseudo random integer in a specified range.*
- void [filecopy](#) (FILE \*from, FILE \*to)  
*Inefficient cp*
- char \* [time\\_stamp](#) (void)  
*Get a timestamp.*

## Variables

- unsigned short `xsubi` [3]  
Current 48 bit random number.

### 18.157.1 Detailed Description

General utility- and helper-functions used throughout the *ViennaRNA Package*.

### 18.157.2 Function Documentation

#### 18.157.2.1 `get_line()`

```
char * get_line (
    FILE * fp )
```

Read a line of arbitrary length from a stream.

Returns a pointer to the resulting string. The necessary memory is allocated and should be released using `free()` when the string is no longer needed.

**Deprecated** Use `vrna_read_line()` as a substitute!

#### Parameters

|                        |                                                                  |
|------------------------|------------------------------------------------------------------|
| <code><i>fp</i></code> | A file pointer to the stream where the function should read from |
|------------------------|------------------------------------------------------------------|

#### Returns

A pointer to the resulting string

#### 18.157.2.2 `print_tty_input_seq()`

```
void print_tty_input_seq (
    void )
```

Print a line to `stdout` that asks for an input sequence.

There will also be a ruler (scale line) printed that helps orientation of the sequence positions

**Deprecated** Use `vrna_message_input_seq_simple()` instead!

#### 18.157.2.3 `print_tty_input_seq_str()`

```
void print_tty_input_seq_str (
    const char * s )
```

Print a line with a user defined string and a ruler to `stdout`.

(usually this is used to ask for user input) There will also be a ruler (scale line) printed that helps orientation of the sequence positions

**Deprecated** Use `vrna_message_input_seq()` instead!

#### 18.157.2.4 `warn_user()`

```
void warn_user (
    const char message[] )
```

Print a warning message.  
Print a warning message to *stderr*

**Deprecated** Use `vrna_message_warning()` instead!

#### 18.157.2.5 `nrerror()`

```
void nrerror (
    const char message[ ] )
```

Die with an error message.

**Deprecated** Use `vrna_message_error()` instead!

#### 18.157.2.6 `space()`

```
void * space (
    unsigned size )
```

Allocate space safely.

**Deprecated** Use `vrna_alloc()` instead!

#### 18.157.2.7 `xrealloc()`

```
void * xrealloc (
    void * p,
    unsigned size )
```

Reallocate space safely.

**Deprecated** Use `vrna_realloc()` instead!

#### 18.157.2.8 `init_rand()`

```
void init_rand (
    void )
```

Make random number seeds.

**Deprecated** Use `vrna_init_rand()` instead!

#### 18.157.2.9 `urn()`

```
double urn (
    void )
```

get a random number from [0..1]

**Deprecated** Use `vrna_urn()` instead!

**18.157.2.10 int\_urn()**

```
int int_urn (
    int from,
    int to )
```

Generates a pseudo random integer in a specified range.

**Deprecated** Use [vrna\\_int\\_urn\(\)](#) instead!

**18.157.2.11 filecopy()**

```
void filecopy (
    FILE * from,
    FILE * to )
```

Inefficient `cp`

**Deprecated** Use [vrna\\_file\\_copy\(\)](#) instead!

**18.157.2.12 time\_stamp()**

```
char * time_stamp (
    void )
```

Get a timestamp.

**Deprecated** Use [vrna\\_time\\_stamp\(\)](#) instead!

**18.158 basic.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_UTILS_H
2 #define VIENNA_RNA_PACKAGE_UTILS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 /* two helper macros to indicate whether a function should be exported in
17  * the library or stays hidden */
18 #define PUBLIC
19 #define PRIVATE static
20
21 #define VRNA_INPUT_ERROR 1U
22 #define VRNA_INPUT_QUIT 2U
23 #define VRNA_INPUT_MISC 4U
24
25 #define VRNA_INPUT_FASTA_HEADER 8U
26
27 /*
28  * @brief Input flag for get_input_line():\n
29  * Tell get_input_line() that we assume to read a nucleotide sequence
30  */
31 #define VRNA_INPUT_SEQUENCE 16U
32
33 #define VRNA_INPUT_CONSTRAINT 32U
34
35 #define VRNA_INPUT_NO_TRUNCATION 256U
36
37 #define VRNA_INPUT_NO_REST 512U
38
39 #define VRNA_INPUT_NO_SPAN 1024U
```



```

82
86 #define VRNA_INPUT_NOSKIP_BLANK_LINES      2048U
87
91 #define VRNA_INPUT_BLANK_LINE              4096U
92
96 #define VRNA_INPUT_NOSKIP_COMMENTS        128U
97
101 #define VRNA_INPUT_COMMENT                 8192U
102
106 #define MIN2(A, B)      ((A) < (B) ? (A) : (B))
107
111 #define MAX2(A, B)      ((A) > (B) ? (A) : (B))
112
116 #define MIN3(A, B, C)   (MIN2((MIN2((A), (B))), (C)))
117
121 #define MAX3(A, B, C)   (MAX2((MAX2((A), (B))), (C)))
122
123 #include <stdio.h>
124 #include <stdarg.h>
125
126 #include <ViennaRNA/datastructures/basic.h>
127
128
129 #ifdef WITH_DMALLOC
130 /* use dmalloc library to check for memory management bugs */
131 #include "dmalloc.h"
132 #define vrna_alloc(S)      calloc(1, (S))
133 #define vrna_realloc(p, S) xrealloc(p, S)
134 #else
135
142 void *
143 vrna_alloc(unsigned size);
144
145
153 void *
154 vrna_realloc(void      *p,
155              unsigned size);
156
157
158 #endif
159
165 void
166 vrna_init_rand(void);
167
168
176 void
177 vrna_init_rand_seed(unsigned int seed);
178
179
188 extern unsigned short xsubi[3];
189
197 double
198 vrna_urn(void);
199
200
209 int
210 vrna_int_urn(int  from,
211             int  to);
212
213
222 char *
223 vrna_time_stamp(void);
224
225
246 unsigned int
247 get_input_line(char      **string,
248               unsigned int options);
249
250
264 int *
265 vrna_idx_row_wise(unsigned int length);
266
267
282 int *
283 vrna_idx_col_wise(unsigned int length);
284
285
308 void
309 vrna_message_error(const char *format,
310                  ...);
311
312
325 void
326 vrna_message_verror(const char *format,
327                   va_list     args);
328
329

```

```

341 void
342 vrna_message_warning(const char *format,
343                     ...);
344
345
346 void
347 vrna_message_vwarning(const char *format,
348                      va_list args);
349
350
351 void
352 vrna_message_info(FILE *fp,
353                  const char *format,
354                  ...);
355
356
357 void
358 vrna_message_vinfo(FILE *fp,
359                   const char *format,
360                   va_list args);
361
362
363 void
364 vrna_message_input_seq_simple(void);
365
366
367 void
368 vrna_message_input_seq(const char *s);
369
370
371 void
372 vrna_message_input_msa(const char *s);
373
374
375 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
376
377 DEPRECATED(int *get_idx(unsigned int length), "Use vrna_idx_col_wise() instead");
378
379 DEPRECATED(int *get_iidx(unsigned int length), "Use vrna_idx_row_wise() instead");
380
381 DEPRECATED(char *get_line(FILE *fp), "Use vrna_read_line() instead");
382
383 DEPRECATED(void print_tty_input_seq(void), "Use vrna_message_input_seq_simple() instead");
384
385 DEPRECATED(void print_tty_input_seq_str(const char *s), "Use vrna_message_input_seq() instead");
386
387 DEPRECATED(void warn_user(const char message[]), "Use vrna_message_warning() instead");
388
389 DEPRECATED(void nrerror(const char message[]), "Use vrna_message_error() instead()");
390
391 DEPRECATED(void *space(unsigned size), "Use vrna_alloc() instead");
392
393 DEPRECATED(void *xrealloc(void *p,
394                          unsigned size), "Use vrna_realloc() instead");
395
396 DEPRECATED(void init_rand(void), "Use vrna_init_rand() instead");
397
398 DEPRECATED(double urn(void), "Use vrna_urn() instead");
399
400 DEPRECATED(int int_urn(int from,
401                      int to), "Use vrna_int_urn() instead()");
402
403 DEPRECATED(void filecopy(FILE *from,
404                          FILE *to), "Use vrna_file_copy() instead");
405
406 DEPRECATED(char *time_stamp(void), "Use vrna_time_stamp() instead");
407
408 #endif
409
410 #endif

```

## 18.159 ViennaRNA/params/constants.h File Reference

Energy parameter constants.

Include dependency graph for constants.h: This graph shows which files directly or indirectly include this file:

### Macros

- #define **GASCONST** 1.98717 /\* in [cal/K] \*/
- #define **K0** 273.15
- #define **INF** 10000000 /\* (INT\_MAX/10) \*/

- `#define FORBIDDEN 9999`
- `#define BONUS 10000`
- `#define NBPAIRS 7`
- `#define TURN 3`
- `#define MAXLOOP 30`

### 18.159.1 Detailed Description

Energy parameter constants.

### 18.159.2 Macro Definition Documentation

#### 18.159.2.1 GASCONST

```
#define GASCONST 1.98717 /* in [cal/K] */
```

The gas constant

#### 18.159.2.2 K0

```
#define K0 273.15
```

0 deg Celsius in Kelvin

#### 18.159.2.3 INF

```
#define INF 10000000 /* (INT_MAX/10) */
```

Infinity as used in minimization routines

#### 18.159.2.4 FORBIDDEN

```
#define FORBIDDEN 9999
```

forbidden

#### 18.159.2.5 BONUS

```
#define BONUS 10000
```

bonus contribution

#### 18.159.2.6 NBPAIRS

```
#define NBPAIRS 7
```

The number of distinguishable base pairs

#### 18.159.2.7 TURN

```
#define TURN 3
```

The minimum loop length

#### 18.159.2.8 MAXLOOP

```
#define MAXLOOP 30
```

The maximum loop length

## 18.160 constants.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_CONSTANTS_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_CONSTANTS_H
3
4 #include <limits.h>
5
13 #define GASCONST 1.98717 /* in [cal/K] */
15 #define K0 273.15
17 #define INF 10000000 /* (INT_MAX/10) */
18
19 #define EMAX (INF/10)
21 #define FORBIDDEN 9999
23 #define BONUS 10000
25 #define NBPAIRS 7
27 #define TURN 3
29 #define MAXLOOP 30
30
31 #define UNIT 100
32
33 #define MINPScore -2 * UNIT
34
35 #endif
```

## 18.161 ViennaRNA/params/convert.h File Reference

Functions and definitions for energy parameter file format conversion.

This graph shows which files directly or indirectly include this file:

### Macros

- #define [VRNA\\_CONVERT\\_OUTPUT\\_ALL](#) 1U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_HP](#) 2U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_STACK](#) 4U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_HP](#) 8U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_INT](#) 16U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_INT\\_1N](#) 32U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_INT\\_23](#) 64U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_MULTI](#) 128U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MM\\_EXT](#) 256U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_DANGLE5](#) 512U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_DANGLE3](#) 1024U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_INT\\_11](#) 2048U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_INT\\_21](#) 4096U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_INT\\_22](#) 8192U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_BULGE](#) 16384U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_INT](#) 32768U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_ML](#) 65536U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_MISC](#) 131072U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_SPECIAL\\_HP](#) 262144U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_VANILLA](#) 524288U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_NINIO](#) 1048576U
- #define [VRNA\\_CONVERT\\_OUTPUT\\_DUMP](#) 2097152U

### Functions

- void [convert\\_parameter\\_file](#) (const char \*iname, const char \*oname, unsigned int options)

#### 18.161.1 Detailed Description

Functions and definitions for energy parameter file format conversion.

## 18.162 convert.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_CONVERT_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_CONVERT_H
3
23 #define VRNA_CONVERT_OUTPUT_ALL          1U
25 #define VRNA_CONVERT_OUTPUT_HP          2U
27 #define VRNA_CONVERT_OUTPUT_STACK        4U
29 #define VRNA_CONVERT_OUTPUT_MM_HP        8U
31 #define VRNA_CONVERT_OUTPUT_MM_INT       16U
33 #define VRNA_CONVERT_OUTPUT_MM_INT_1N    32U
35 #define VRNA_CONVERT_OUTPUT_MM_INT_23    64U
37 #define VRNA_CONVERT_OUTPUT_MM_MULTI     128U
39 #define VRNA_CONVERT_OUTPUT_MM_EXT       256U
41 #define VRNA_CONVERT_OUTPUT_DANGLE5      512U
43 #define VRNA_CONVERT_OUTPUT_DANGLE3      1024U
45 #define VRNA_CONVERT_OUTPUT_INT_11       2048U
47 #define VRNA_CONVERT_OUTPUT_INT_21       4096U
49 #define VRNA_CONVERT_OUTPUT_INT_22       8192U
51 #define VRNA_CONVERT_OUTPUT_BULGE        16384U
53 #define VRNA_CONVERT_OUTPUT_INT          32768U
55 #define VRNA_CONVERT_OUTPUT_ML           65536U
57 #define VRNA_CONVERT_OUTPUT_MISC         131072U
59 #define VRNA_CONVERT_OUTPUT_SPECIAL_HP    262144U
61 #define VRNA_CONVERT_OUTPUT_VANILLA      524288U
63 #define VRNA_CONVERT_OUTPUT_NINIO        1048576U
65 #define VRNA_CONVERT_OUTPUT_DUMP         2097152U
66
89 void convert_parameter_file(const char *iname,
90                             const char *oname,
91                             unsigned int options);
92
93
97 #endif

```

## 18.163 default.h

```

1 /*
2  * prototypes for energy_par.c
3  */
4
5 #ifndef VIENNA_RNA_PACKAGE_PARAMS_DEFAULT_H
6 #define VIENNA_RNA_PACKAGE_PARAMS_DEFAULT_H
7
8 #include <ViennaRNA/params/constants.h>
9
10 #define PUBLIC
11
12
13 extern double lxc37; /* parameter for logarithmic loop
14                    energy extrapolation */
15
16 extern int stack37[NBPAIRS+1][NBPAIRS+1];
17 extern int stackdH[NBPAIRS+1][NBPAIRS+1]; /* stack enthalpies */
18
19 extern int hairpin37[31];
20 extern int hairpindH[31];
21 extern int bulge37[31];
22 extern int bulgedH[31];
23 extern int internal_loop37[31];
24 extern int internal_loophH[31];
25 extern int mismatchI37[NBPAIRS+1][5][5]; /* interior loop mismatches */
26 extern int mismatchIdH[NBPAIRS+1][5][5]; /* interior loop mismatches */
27 extern int mismatchlnI37[NBPAIRS+1][5][5]; /* interior loop mismatches */
28 extern int mismatch23I37[NBPAIRS+1][5][5]; /* interior loop mismatches */
29 extern int mismatchlnIdH[NBPAIRS+1][5][5]; /* interior loop mismatches */
30 extern int mismatch23IdH[NBPAIRS+1][5][5]; /* interior loop mismatches */
31 extern int mismatchH37[NBPAIRS+1][5][5]; /* same for hairpins */
32 extern int mismatchM37[NBPAIRS+1][5][5]; /* same for multiloops */
33 extern int mismatchHdH[NBPAIRS+1][5][5]; /* same for hairpins */
34 extern int mismatchMdH[NBPAIRS+1][5][5]; /* same for multiloops */
35 extern int mismatchExt37[NBPAIRS+1][5][5];
36 extern int mismatchExtIdH[NBPAIRS+1][5][5];
37
38 extern int dangle5_37[NBPAIRS+1][5]; /* 5' dangle exterior of pair */
39 extern int dangle3_37[NBPAIRS+1][5]; /* 3' dangle */
40 extern int dangle3_dH[NBPAIRS+1][5]; /* corresponding enthalpies */
41 extern int dangle5_dH[NBPAIRS+1][5];
42
43 extern int int11_37[NBPAIRS+1][NBPAIRS+1][5][5]; /* 1x1 interior loops */
44 extern int int11_dH[NBPAIRS+1][NBPAIRS+1][5][5];
45
46 extern int int21_37[NBPAIRS+1][NBPAIRS+1][5][5][5]; /* 2x1 interior loops */

```

```

47 extern int int21_dH[NBPAIRS+1][NBPAIRS+1][5][5][5];
48
49 extern int int22_37[NBPAIRS+1][NBPAIRS+1][5][5][5][5]; /* 2x2 interior loops */
50 extern int int22_dH[NBPAIRS+1][NBPAIRS+1][5][5][5][5];
51
52 /* constants for linearly destabilizing contributions for multi-loops
53    F = ML_closing + ML_intern*(k-1) + ML_BASE*u */
54 extern int ML_BASE37;
55 extern int ML_BASEdH;
56 extern int ML_closing37;
57 extern int ML_closingdH;
58 extern int ML_intern37;
59 extern int ML_interndH;
60
61 extern int TripleC37;
62 extern int TripleCdH;
63 extern int MultipleCA37;
64 extern int MultipleCAdH;
65 extern int MultipleCB37;
66 extern int MultipleCBdH;
67
68 /* Ninio-correction for asymmetric internal loops with branches n1 and n2 */
69 /*    ninio_energy = min{max_ninio, |n1-n2|*F_ninio[min{4.0, n1, n2}] } */
70 extern int MAX_NINIO; /* maximum correction */
71 extern int ninio37;
72 extern int niniodH;
73 /* penalty for helices terminated by AU (actually not GC) */
74 extern int TerminalAU37;
75 extern int TerminalAUdH;
76 /* penalty for forming bi-molecular duplex */
77 extern int DuplexInit37;
78 extern int DuplexInitdH;
79 /* stabilizing contribution due to special hairpins of size 4 (tetraloops) */
80 extern char Tetraloops[281]; /* string containing the special tetraloops */
81 extern int Tetraloop37[40]; /* Bonus energy for special tetraloops */
82 extern int TetraloopdH[40];
83 extern char Triloops[241]; /* string containing the special triloops */
84 extern int Triloop37[40]; /* Bonus energy for special Triloops */
85 extern int TriloopdH[40]; /* Bonus energy for special Triloops */
86 extern char Hexaloops[361]; /* string containing the special triloops */
87 extern int Hexaloop37[40]; /* Bonus energy for special Triloops */
88 extern int HexaloopdH[40]; /* Bonus energy for special Triloops */
89
90 extern int GQuadAlpha37;
91 extern int GQuadAlphadH;
92 extern int GQuadBeta37;
93 extern int GQuadBetadH;
94 extern int GQuadLayerMismatch37; /* penalty per incompatible gquad layer in a sub-alignment (applied
    twice for inner layers) */
95 extern int GQuadLayerMismatchH;
96 extern int GQuadLayerMismatchMax; /* maximum number of mismatching sequences in the alignment when gquad
    should be formed */
97
98 extern double Tmeasure; /* temperature of param measurements */
99
100 #endif

```

## 18.164 intl11.h

```

1 PUBLIC int intl1_37[NBPAIRS+1][NBPAIRS+1][5][5] =
2 {{{{ INF, INF, INF, INF, INF }
3  ,{ INF, INF, INF, INF, INF }
4  ,{ INF, INF, INF, INF, INF }
5  ,{ INF, INF, INF, INF, INF }
6  ,{ INF, INF, INF, INF, INF }
7  }
8  ,{{{ INF, INF, INF, INF, INF }
9   ,{ INF, INF, INF, INF, INF }
10  ,{ INF, INF, INF, INF, INF }
11  ,{ INF, INF, INF, INF, INF }
12  ,{ INF, INF, INF, INF, INF }
13  }
14  ,{{{ INF, INF, INF, INF, INF }
15   ,{ INF, INF, INF, INF, INF }
16   ,{ INF, INF, INF, INF, INF }
17   ,{ INF, INF, INF, INF, INF }
18   ,{ INF, INF, INF, INF, INF }
19   }
20  ,{{{ INF, INF, INF, INF, INF }
21   ,{ INF, INF, INF, INF, INF }
22   ,{ INF, INF, INF, INF, INF }
23   ,{ INF, INF, INF, INF, INF }
24   ,{ INF, INF, INF, INF, INF }
25   }
26  ,{{{ INF, INF, INF, INF, INF }

```

```

27 , { INF, INF, INF, INF, INF }
28 , { INF, INF, INF, INF, INF }
29 , { INF, INF, INF, INF, INF }
30 , { INF, INF, INF, INF, INF }
31 }
32 , { { INF, INF, INF, INF, INF }
33 , { INF, INF, INF, INF, INF }
34 , { INF, INF, INF, INF, INF }
35 , { INF, INF, INF, INF, INF }
36 , { INF, INF, INF, INF, INF }
37 }
38 , { { INF, INF, INF, INF, INF }
39 , { INF, INF, INF, INF, INF }
40 , { INF, INF, INF, INF, INF }
41 , { INF, INF, INF, INF, INF }
42 , { INF, INF, INF, INF, INF }
43 }
44 , { { INF, INF, INF, INF, INF }
45 , { INF, INF, INF, INF, INF }
46 , { INF, INF, INF, INF, INF }
47 , { INF, INF, INF, INF, INF }
48 , { INF, INF, INF, INF, INF }
49 }
50 }
51 , { { { INF, INF, INF, INF, INF }
52 , { INF, INF, INF, INF, INF }
53 , { INF, INF, INF, INF, INF }
54 , { INF, INF, INF, INF, INF }
55 , { INF, INF, INF, INF, INF }
56 }
57 , { { 90, 90, 50, 50, 50 }
58 , { 90, 90, 50, 50, 50 }
59 , { 50, 50, 50, 50, 50 }
60 , { 50, 50, 50, -140, 50 }
61 , { 50, 50, 50, 50, 40 }
62 }
63 , { { 90, 90, 50, 50, 60 }
64 , { 90, 90, -40, 50, 50 }
65 , { 60, 30, 50, 50, 60 }
66 , { 50, -10, 50, -220, 50 }
67 , { 50, 50, 0, 50, -10 }
68 }
69 , { { 120, 120, 120, 120, 120 }
70 , { 120, 60, 50, 120, 120 }
71 , { 120, 120, 120, 120, 120 }
72 , { 120, -20, 120, -140, 120 }
73 , { 120, 120, 100, 120, 110 }
74 }
75 , { { 220, 220, 170, 120, 120 }
76 , { 220, 220, 130, 120, 120 }
77 , { 170, 120, 170, 120, 120 }
78 , { 120, 120, 120, -140, 120 }
79 , { 120, 120, 120, 120, 110 }
80 }
81 , { { 120, 120, 120, 120, 120 }
82 , { 120, 120, 120, 120, 120 }
83 , { 120, 120, 120, 120, 120 }
84 , { 120, 120, 120, -140, 120 }
85 , { 120, 120, 120, 120, 80 }
86 }
87 , { { 120, 120, 120, 120, 120 }
88 , { 120, 120, 120, 120, 120 }
89 , { 120, 120, 120, 120, 120 }
90 , { 120, 120, 120, -140, 120 }
91 , { 120, 120, 120, 120, 120 }
92 }
93 , { { 220, 220, 170, 120, 120 }
94 , { 220, 220, 130, 120, 120 }
95 , { 170, 120, 170, 120, 120 }
96 , { 120, 120, 120, -140, 120 }
97 , { 120, 120, 120, 120, 120 }
98 }
99 }
100 , { { { INF, INF, INF, INF, INF }
101 , { INF, INF, INF, INF, INF }
102 , { INF, INF, INF, INF, INF }
103 , { INF, INF, INF, INF, INF }
104 , { INF, INF, INF, INF, INF }
105 }
106 , { { 90, 90, 60, 50, 50 }
107 , { 90, 90, 30, -10, 50 }
108 , { 50, -40, 50, 50, 0 }
109 , { 50, 50, 50, -220, 50 }
110 , { 60, 50, 60, 50, -10 }
111 }
112 , { { 80, 80, 50, 50, 50 }
113 , { 80, 80, 50, 50, 50 }

```

```

114 , { 50, 50, 50, 50, 50}
115 , { 50, 50, 50, -230, 50}
116 , { 50, 50, 50, 50, -60}
117 }
118 , { { 190, 190, 120, 150, 150}
119 , { 190, 190, 120, 150, 120}
120 , { 120, 120, 120, 120, 120}
121 , { 120, 120, 120, -140, 120}
122 , { 150, 120, 120, 120, 150}
123 }
124 , { { 160, 160, 120, 120, 120}
125 , { 160, 160, 120, 100, 120}
126 , { 120, 120, 120, 120, 120}
127 , { 120, 120, 120, -140, 120}
128 , { 120, 120, 120, 120, 70}
129 }
130 , { { 120, 120, 120, 120, 120}
131 , { 120, 120, 120, 120, 120}
132 , { 120, 120, 120, 120, 120}
133 , { 120, 120, 120, -140, 120}
134 , { 120, 120, 120, 120, 80}
135 }
136 , { { 120, 120, 120, 120, 120}
137 , { 120, 120, 120, 120, 120}
138 , { 120, 120, 120, 120, 120}
139 , { 120, 120, 120, -140, 120}
140 , { 120, 120, 120, 120, 120}
141 }
142 , { { 190, 190, 120, 150, 150}
143 , { 190, 190, 120, 150, 120}
144 , { 120, 120, 120, 120, 120}
145 , { 120, 120, 120, -140, 120}
146 , { 150, 120, 120, 120, 150}
147 }
148 }
149 , { { { INF, INF, INF, INF, INF}
150 , { { INF, INF, INF, INF, INF}
151 , { { INF, INF, INF, INF, INF}
152 , { { INF, INF, INF, INF, INF}
153 , { { INF, INF, INF, INF, INF}
154 }
155 , { { 120, 120, 120, 120, 120}
156 , { 120, 60, 120, -20, 120}
157 , { 120, 50, 120, 120, 100}
158 , { 120, 120, 120, -140, 120}
159 , { 120, 120, 120, 120, 110}
160 }
161 , { { 190, 190, 120, 120, 150}
162 , { 190, 190, 120, 120, 120}
163 , { 120, 120, 120, 120, 120}
164 , { 150, 150, 120, -140, 120}
165 , { 150, 120, 120, 120, 150}
166 }
167 , { { 190, 190, 190, 190, 190}
168 , { 190, 190, 190, 190, 190}
169 , { 190, 190, 190, 190, 190}
170 , { 190, 190, 190, -70, 190}
171 , { 190, 190, 190, 190, 120}
172 }
173 , { { 190, 190, 190, 190, 190}
174 , { 190, 190, 190, 190, 190}
175 , { 190, 190, 190, 190, 190}
176 , { 190, 190, 190, -70, 190}
177 , { 190, 190, 190, 190, 160}
178 }
179 , { { 190, 190, 190, 190, 190}
180 , { 190, 190, 190, 190, 190}
181 , { 190, 190, 190, 190, 190}
182 , { 190, 190, 190, -70, 190}
183 , { 190, 190, 190, 190, 120}
184 }
185 , { { 190, 190, 190, 190, 190}
186 , { 190, 190, 190, 190, 190}
187 , { 190, 190, 190, 190, 190}
188 , { 190, 190, 190, -70, 190}
189 , { 190, 190, 190, 190, 160}
190 }
191 , { { 190, 190, 190, 190, 190}
192 , { 190, 190, 190, 190, 190}
193 , { 190, 190, 190, 190, 190}
194 , { 190, 190, 190, -70, 190}
195 , { 190, 190, 190, 190, 160}
196 }
197 }
198 , { { { INF, INF, INF, INF, INF}
199 , { { INF, INF, INF, INF, INF}
200 , { { INF, INF, INF, INF, INF}

```



```
201 , { INF, INF, INF, INF, INF }
202 , { INF, INF, INF, INF, INF }
203 }
204 , { { 220, 220, 170, 120, 120 }
205 , { 220, 220, 120, 120, 120 }
206 , { 170, 130, 170, 120, 120 }
207 , { 120, 120, 120, -140, 120 }
208 , { 120, 120, 120, 120, 110 }
209 }
210 , { { 160, 160, 120, 120, 120 }
211 , { 160, 160, 120, 120, 120 }
212 , { 120, 120, 120, 120, 120 }
213 , { 120, 100, 120, -140, 120 }
214 , { 120, 120, 120, 120, 70 }
215 }
216 , { { 190, 190, 190, 190, 190 }
217 , { 190, 190, 190, 190, 190 }
218 , { 190, 190, 190, 190, 190 }
219 , { 190, 190, 190, -70, 190 }
220 , { 190, 190, 190, 190, 160 }
221 }
222 , { { 190, 190, 190, 190, 190 }
223 , { 190, 190, 190, 190, 190 }
224 , { 190, 190, 190, 190, 190 }
225 , { 190, 190, 190, -70, 190 }
226 , { 190, 190, 190, 190, 190 }
227 }
228 , { { 190, 190, 190, 190, 190 }
229 , { 190, 190, 190, 190, 190 }
230 , { 190, 190, 190, 190, 190 }
231 , { 190, 190, 190, -70, 190 }
232 , { 190, 190, 190, 190, 160 }
233 }
234 , { { 190, 190, 190, 190, 190 }
235 , { 190, 190, 190, 190, 190 }
236 , { 190, 190, 190, 190, 190 }
237 , { 190, 190, 190, -70, 190 }
238 , { 190, 190, 190, 190, 190 }
239 }
240 , { { 220, 220, 190, 190, 190 }
241 , { 220, 220, 190, 190, 190 }
242 , { 190, 190, 190, 190, 190 }
243 , { 190, 190, 190, -70, 190 }
244 , { 190, 190, 190, 190, 190 }
245 }
246 }
247 , { { { INF, INF, INF, INF, INF }
248 , { INF, INF, INF, INF, INF }
249 , { INF, INF, INF, INF, INF }
250 , { INF, INF, INF, INF, INF }
251 , { INF, INF, INF, INF, INF }
252 }
253 , { { 120, 120, 120, 120, 120 }
254 , { 120, 120, 120, 120, 120 }
255 , { 120, 120, 120, 120, 120 }
256 , { 120, 120, 120, -140, 120 }
257 , { 120, 120, 120, 120, 80 }
258 }
259 , { { 120, 120, 120, 120, 120 }
260 , { 120, 120, 120, 120, 120 }
261 , { 120, 120, 120, 120, 120 }
262 , { 120, 120, 120, -140, 120 }
263 , { 120, 120, 120, 120, 80 }
264 }
265 , { { 190, 190, 190, 190, 190 }
266 , { 190, 190, 190, 190, 190 }
267 , { 190, 190, 190, 190, 190 }
268 , { 190, 190, 190, -70, 190 }
269 , { 190, 190, 190, 190, 120 }
270 }
271 , { { 190, 190, 190, 190, 190 }
272 , { 190, 190, 190, 190, 190 }
273 , { 190, 190, 190, 190, 190 }
274 , { 190, 190, 190, -70, 190 }
275 , { 190, 190, 190, 190, 160 }
276 }
277 , { { 190, 190, 190, 190, 190 }
278 , { 190, 190, 190, 190, 190 }
279 , { 190, 190, 190, 190, 190 }
280 , { 190, 190, 190, -70, 190 }
281 , { 190, 190, 190, 190, 120 }
282 }
283 , { { 190, 190, 190, 190, 190 }
284 , { 190, 190, 190, 190, 190 }
285 , { 190, 190, 190, 190, 190 }
286 , { 190, 190, 190, -70, 190 }
287 , { 190, 190, 190, 190, 150 }
```

```

288     }
289     ,{{ 190, 190, 190, 190, 190}
290     ,{ 190, 190, 190, 190, 190}
291     ,{ 190, 190, 190, 190, 190}
292     ,{ 190, 190, 190, -70, 190}
293     ,{ 190, 190, 190, 190, 160}
294     }
295     }
296     ,{{{ INF, INF, INF, INF, INF}
297     ,{ INF, INF, INF, INF, INF}
298     ,{ INF, INF, INF, INF, INF}
299     ,{ INF, INF, INF, INF, INF}
300     ,{ INF, INF, INF, INF, INF}
301     }
302     ,{{ 120, 120, 120, 120, 120}
303     ,{ 120, 120, 120, 120, 120}
304     ,{ 120, 120, 120, 120, 120}
305     ,{ 120, 120, 120, -140, 120}
306     ,{ 120, 120, 120, 120, 120}
307     }
308     ,{{ 120, 120, 120, 120, 120}
309     ,{ 120, 120, 120, 120, 120}
310     ,{ 120, 120, 120, 120, 120}
311     ,{ 120, 120, 120, -140, 120}
312     ,{ 120, 120, 120, 120, 120}
313     }
314     ,{{ 190, 190, 190, 190, 190}
315     ,{ 190, 190, 190, 190, 190}
316     ,{ 190, 190, 190, 190, 190}
317     ,{ 190, 190, 190, -70, 190}
318     ,{ 190, 190, 190, 190, 160}
319     }
320     ,{{ 190, 190, 190, 190, 190}
321     ,{ 190, 190, 190, 190, 190}
322     ,{ 190, 190, 190, 190, 190}
323     ,{ 190, 190, 190, -70, 190}
324     ,{ 190, 190, 190, 190, 190}
325     }
326     ,{{ 190, 190, 190, 190, 190}
327     ,{ 190, 190, 190, 190, 190}
328     ,{ 190, 190, 190, 190, 190}
329     ,{ 190, 190, 190, -70, 190}
330     ,{ 190, 190, 190, 190, 150}
331     }
332     ,{{ 190, 190, 190, 190, 190}
333     ,{ 190, 190, 190, 190, 190}
334     ,{ 190, 190, 190, 190, 190}
335     ,{ 190, 190, 190, -70, 190}
336     ,{ 190, 190, 190, 190, 170}
337     }
338     ,{{ 190, 190, 190, 190, 190}
339     ,{ 190, 190, 190, 190, 190}
340     ,{ 190, 190, 190, 190, 190}
341     ,{ 190, 190, 190, -70, 190}
342     ,{ 190, 190, 190, 190, 190}
343     }
344     }
345     ,{{{ INF, INF, INF, INF, INF}
346     ,{ INF, INF, INF, INF, INF}
347     ,{ INF, INF, INF, INF, INF}
348     ,{ INF, INF, INF, INF, INF}
349     ,{ INF, INF, INF, INF, INF}
350     }
351     ,{{ 220, 220, 170, 120, 120}
352     ,{ 220, 220, 120, 120, 120}
353     ,{ 170, 130, 170, 120, 120}
354     ,{ 120, 120, 120, -140, 120}
355     ,{ 120, 120, 120, 120, 120}
356     }
357     ,{{ 190, 190, 120, 120, 150}
358     ,{ 190, 190, 120, 120, 120}
359     ,{ 120, 120, 120, 120, 120}
360     ,{ 150, 150, 120, -140, 120}
361     ,{ 150, 120, 120, 120, 150}
362     }
363     ,{{ 190, 190, 190, 190, 190}
364     ,{ 190, 190, 190, 190, 190}
365     ,{ 190, 190, 190, 190, 190}
366     ,{ 190, 190, 190, -70, 190}
367     ,{ 190, 190, 190, 190, 160}
368     }
369     ,{{ 220, 220, 190, 190, 190}
370     ,{ 220, 220, 190, 190, 190}
371     ,{ 190, 190, 190, 190, 190}
372     ,{ 190, 190, 190, -70, 190}
373     ,{ 190, 190, 190, 190, 190}
374     }

```

```

375 ,{{ 190, 190, 190, 190, 190}
376 ,{ 190, 190, 190, 190, 190}
377 ,{ 190, 190, 190, 190, 190}
378 ,{ 190, 190, 190, -70, 190}
379 ,{ 190, 190, 190, 190, 160}
380 }
381 ,{{ 190, 190, 190, 190, 190}
382 ,{ 190, 190, 190, 190, 190}
383 ,{ 190, 190, 190, 190, 190}
384 ,{ 190, 190, 190, -70, 190}
385 ,{ 190, 190, 190, 190, 190}
386 }
387 ,{{ 220, 220, 190, 190, 190}
388 ,{ 220, 220, 190, 190, 190}
389 ,{ 190, 190, 190, 190, 190}
390 ,{ 190, 190, 190, -70, 190}
391 ,{ 190, 190, 190, 190, 190}
392 }
393 };
```

## 18.165 intl11dH.h

```

1 PUBLIC int intl1_dH[NBPAIRS+1][NBPAIRS+1][5][5] =
2 {{{{ INF, INF, INF, INF, INF}
3 ,{ INF, INF, INF, INF, INF}
4 ,{ INF, INF, INF, INF, INF}
5 ,{ INF, INF, INF, INF, INF}
6 ,{ INF, INF, INF, INF, INF}
7 }
8 ,{{ INF, INF, INF, INF, INF}
9 ,{ INF, INF, INF, INF, INF}
10 ,{ INF, INF, INF, INF, INF}
11 ,{ INF, INF, INF, INF, INF}
12 ,{ INF, INF, INF, INF, INF}
13 }
14 ,{{ INF, INF, INF, INF, INF}
15 ,{ INF, INF, INF, INF, INF}
16 ,{ INF, INF, INF, INF, INF}
17 ,{ INF, INF, INF, INF, INF}
18 ,{ INF, INF, INF, INF, INF}
19 }
20 ,{{ INF, INF, INF, INF, INF}
21 ,{ INF, INF, INF, INF, INF}
22 ,{ INF, INF, INF, INF, INF}
23 ,{ INF, INF, INF, INF, INF}
24 ,{ INF, INF, INF, INF, INF}
25 }
26 ,{{ INF, INF, INF, INF, INF}
27 ,{ INF, INF, INF, INF, INF}
28 ,{ INF, INF, INF, INF, INF}
29 ,{ INF, INF, INF, INF, INF}
30 ,{ INF, INF, INF, INF, INF}
31 }
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36 ,{ INF, INF, INF, INF, INF}
37 }
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41 ,{ INF, INF, INF, INF, INF}
42 ,{ INF, INF, INF, INF, INF}
43 }
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48 ,{ INF, INF, INF, INF, INF}
49 }
50 }
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61 ,{ -1050, -1050, -1050, -1050, -1050}
62 }
63 ,{{ -1050, -1050, -1050, -1050, -1050}
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139 , { -550, -550, -550, -1340, -550}
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150 , { INF, INF, INF, INF, INF}

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189 , { -50, -50, -50, -50, -390 }
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195 , { -50, -50, -50, -50, -390 }
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231 , { -50, -50, -50, -830, -50 }
232 , { -50, -50, -50, -50, -390 }
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237 , { -50, -50, -50, -830, -50 }
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275 , { -50, -50, -50, -50, -390}
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287 , { -50, -50, -50, -50, -390}
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293 , { -50, -50, -50, -50, -390}
294 }
295 }
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299 , { INF, INF, INF, INF, INF}
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325     }
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333     , { -50, -50, -50, -50, -50 }
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342     , { -50, -50, -50, -50, -50 }
343     }
344     }
345     , {{{ INF, INF, INF, INF, INF }
346     , { INF, INF, INF, INF, INF }
347     , { INF, INF, INF, INF, INF }
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349     , { INF, INF, INF, INF, INF }
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358     , { -550, -550, -550, -550, -550 }
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367     , { -50, -50, -50, -50, -390 }
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379     , { -50, -50, -50, -50, -390 }
380     }
381     , {{ -50, -50, -50, -50, -50 }
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386     }
387     , {{ -50, -50, -50, -50, -50 }
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392     }
393     }

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## 18.166 intl21.h

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6     , { INF, INF, INF, INF, INF }
7     }
8     , {{ INF, INF, INF, INF, INF }
9     , { INF, INF, INF, INF, INF }
10    , { INF, INF, INF, INF, INF }
11    , { INF, INF, INF, INF, INF }
12    , { INF, INF, INF, INF, INF }
13    }

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18 ,{ INF, INF, INF, INF, INF }
19 }
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38 }
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96 ,{ INF, INF, INF, INF, INF }
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2722     , { -650, -650, -870, -650, -1180 }
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2810 }
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3563     , {  870,    870,    650,    870,   -110 }
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9757 , { 1210, 1060, 1210, 1060, 970 }
9758 , { 1210, 1060, 1210, 1060, 970 }
9759 , { 1080, 930, 1080, 930, 840 }
9760 }
9761 , { { 1990, 1840, 1990, 1840, 1750 }
9762 , { -120, -510, -120, -510, -360 }
9763 , { 1060, 910, 1060, 910, 820 }
9764 , { 1990, 1840, 1990, 1840, 1750 }
9765 , { 1060, 910, 1060, 910, 820 }
9766 }
9767 , { { 1210, 1060, 1210, 1060, 970 }
9768 , { 1210, 1060, 1210, 1060, 970 }
9769 , { 770, 620, 770, 620, 530 }
9770 , { 1210, 1060, 1210, 1060, 970 }

```



```
9771 , { 270, 120, 270, 120, 30 }
9772 }
9773 }
9774 , { { { 2120, 400, 1990, 2120, 1990 }
9775 , { 2120, 290, 1340, 2120, 1340 }
9776 , { 1990, 400, 1210, 1990, 1210 }
9777 , { 1990, 160, 1990, 1990, 1990 }
9778 , { 1860, 270, 1080, 1860, 1080 }
9779 }
9780 , { { { 2120, 290, 1340, 2120, 1340 }
9781 , { 2120, 290, 1340, 2120, 1340 }
9782 , { 1840, 10, 1060, 1840, 1060 }
9783 , { -60, -1110, -60, -530, -60 }
9784 , { 1840, 10, 1060, 1840, 1060 }
9785 }
9786 , { { { 1990, 400, 1210, 1990, 1210 }
9787 , { 1990, 160, 1210, 1990, 1210 }
9788 , { 1990, 400, 1210, 1990, 1210 }
9789 , { 1990, 160, 1210, 1990, 1210 }
9790 , { 1860, 270, 1080, 1860, 1080 }
9791 }
9792 , { { { 1990, 10, 1990, 1840, 1990 }
9793 , { -360, -1410, -360, -830, -360 }
9794 , { 1840, 10, 1060, 1840, 1060 }
9795 , { 1990, -310, 1990, 270, 1990 }
9796 , { 1840, 10, 1060, 1840, 1060 }
9797 }
9798 , { { { 1990, 160, 1210, 1990, 1210 }
9799 , { 1990, 160, 1210, 1990, 1210 }
9800 , { 1550, -40, 770, 1550, 770 }
9801 , { 1990, 160, 1210, 1990, 1210 }
9802 , { 270, -780, 270, -200, 270 }
9803 }
9804 }
9805 , { { { { 1860, 1840, 1860, 1840, 640 }
9806 , { 1210, 1190, 1210, 1190, 640 }
9807 , { 1080, 1060, 1080, 1060, 270 }
9808 , { 1860, 1840, 1860, 1840, 270 }
9809 , { 950, 930, 950, 930, 140 }
9810 }
9811 , { { { 1210, 1190, 1210, 1190, 640 }
9812 , { 1210, 1190, 1210, 1190, 640 }
9813 , { 930, 910, 930, 910, 120 }
9814 , { 50, -210, 50, -210, -1000 }
9815 , { 930, 910, 930, 910, 120 }
9816 }
9817 , { { { 1080, 1060, 1080, 1060, 270 }
9818 , { 1080, 1060, 1080, 1060, 270 }
9819 , { 1080, 1060, 1080, 1060, 270 }
9820 , { 1080, 1060, 1080, 1060, 270 }
9821 , { 950, 930, 950, 930, 140 }
9822 }
9823 , { { { 1860, 1840, 1860, 1840, 120 }
9824 , { -250, -510, -250, -510, -1300 }
9825 , { 930, 910, 930, 910, 120 }
9826 , { 1860, 1840, 1860, 1840, -200 }
9827 , { 930, 910, 930, 910, 120 }
9828 }
9829 , { { { 1080, 1060, 1080, 1060, 270 }
9830 , { 1080, 1060, 1080, 1060, 270 }
9831 , { 640, 620, 640, 620, -170 }
9832 , { 1080, 1060, 1080, 1060, 270 }
9833 , { 140, 120, 140, 120, -670 }
9834 }
9835 }
9836 }
9837 , { { { { 2120, 2120, 1990, 2120, 1990 }
9838 , { 2120, 1470, 1340, 2120, 1340 }
9839 , { 1990, 1340, 1210, 1990, 1210 }
9840 , { 2120, 2120, 1990, 1990, 1990 }
9841 , { 1860, 1210, 1080, 1860, 1080 }
9842 }
9843 , { { { 2120, 1470, 1340, 2120, 1340 }
9844 , { 2120, 1470, 1340, 2120, 1340 }
9845 , { 1840, 1190, 1060, 1840, 1060 }
9846 , { 400, 290, 400, 10, 170 }
9847 , { 1840, 1190, 1060, 1840, 1060 }
9848 }
9849 , { { { 1990, 1340, 1210, 1990, 1210 }
9850 , { 1990, 1340, 1210, 1990, 1210 }
9851 , { 1990, 1340, 1210, 1990, 1210 }
9852 , { 1990, 1340, 1210, 1990, 1210 }
9853 , { 1860, 1210, 1080, 1860, 1080 }
9854 }
9855 , { { { 2120, 2120, 1990, 1840, 1990 }
9856 , { 540, 190, 540, -80, 70 }
9857 , { 1840, 1190, 1060, 1840, 1060 }
```

```

9858 , { 2120, 2120, 1990, 1840, 1990}
9859 , { 1840, 1190, 1060, 1840, 1060}
9860 }
9861 , { { 1990, 1340, 1210, 1990, 1210}
9862 , { 1990, 1340, 1210, 1990, 1210}
9863 , { 1750, 1100, 970, 1750, 970}
9864 , { 1990, 1340, 1210, 1990, 1210}
9865 , { 640, 640, 270, 120, 270}
9866 }
9867 }
9868 , { { { 2120, 2120, 1990, 540, 1990}
9869 , { 1470, 1470, 1340, 190, 1340}
9870 , { 1340, 1340, 1210, 540, 1210}
9871 , { 2120, 2120, 1990, 60, 1990}
9872 , { 1210, 1210, 1080, 180, 1080}
9873 }
9874 , { { 1470, 1470, 1340, 190, 1340}
9875 , { 1470, 1470, 1340, 190, 1340}
9876 , { 1190, 1190, 1060, -80, 1060}
9877 , { 290, 290, 160, -980, 160}
9878 , { 1190, 1190, 1060, -80, 1060}
9879 }
9880 , { { 1340, 1340, 1210, 540, 1210}
9881 , { 1340, 1340, 1210, 60, 1210}
9882 , { 1340, 1340, 1210, 540, 1210}
9883 , { 1340, 1340, 1210, 60, 1210}
9884 , { 1210, 1210, 1080, 180, 1080}
9885 }
9886 , { { 2120, 2120, 1990, -80, 1990}
9887 , { 190, 190, 60, -1080, 60}
9888 , { 1190, 1190, 1060, -80, 1060}
9889 , { 2120, 2120, 1990, -400, 1990}
9890 , { 1190, 1190, 1060, -80, 1060}
9891 }
9892 , { { 1340, 1340, 1210, 70, 1210}
9893 , { 1340, 1340, 1210, 60, 1210}
9894 , { 1100, 1100, 970, 70, 970}
9895 , { 1340, 1340, 1210, 60, 1210}
9896 , { 640, 640, 270, -810, 270}
9897 }
9898 }
9899 , { { { 1990, 1840, 1990, 1840, 1750}
9900 , { 1340, 1190, 1340, 1190, 1100}
9901 , { 1210, 1060, 1210, 1060, 970}
9902 , { 1990, 1840, 1990, 1840, 1750}
9903 , { 1080, 930, 1080, 930, 840}
9904 }
9905 , { { 1340, 1190, 1340, 1190, 1100}
9906 , { 1340, 1190, 1340, 1190, 1100}
9907 , { 1060, 910, 1060, 910, 820}
9908 , { 400, 10, 400, 10, 170}
9909 , { 1060, 910, 1060, 910, 820}
9910 }
9911 , { { 1210, 1060, 1210, 1060, 970}
9912 , { 1210, 1060, 1210, 1060, 970}
9913 , { 1210, 1060, 1210, 1060, 970}
9914 , { 1210, 1060, 1210, 1060, 970}
9915 , { 1080, 930, 1080, 930, 840}
9916 }
9917 , { { 1990, 1840, 1990, 1840, 1750}
9918 , { 540, -80, 540, -80, 70}
9919 , { 1060, 910, 1060, 910, 820}
9920 , { 1990, 1840, 1990, 1840, 1750}
9921 , { 1060, 910, 1060, 910, 820}
9922 }
9923 , { { 1210, 1060, 1210, 1060, 970}
9924 , { 1210, 1060, 1210, 1060, 970}
9925 , { 970, 820, 970, 820, 740}
9926 , { 1210, 1060, 1210, 1060, 970}
9927 , { 270, 120, 270, 120, 30}
9928 }
9929 }
9930 , { { { 2120, 400, 1990, 2120, 1990}
9931 , { 2120, 290, 1340, 2120, 1340}
9932 , { 1990, 400, 1210, 1990, 1210}
9933 , { 1990, 160, 1990, 1990, 1990}
9934 , { 1860, 270, 1080, 1860, 1080}
9935 }
9936 , { { 2120, 290, 1340, 2120, 1340}
9937 , { 2120, 290, 1340, 2120, 1340}
9938 , { 1840, 10, 1060, 1840, 1060}
9939 , { 160, -890, 160, -310, 160}
9940 , { 1840, 10, 1060, 1840, 1060}
9941 }
9942 , { { 1990, 400, 1210, 1990, 1210}
9943 , { 1990, 160, 1210, 1990, 1210}
9944 , { 1990, 400, 1210, 1990, 1210}

```

```

9945     , { 1990, 160, 1210, 1990, 1210 }
9946     , { 1860, 270, 1080, 1860, 1080 }
9947     }
9948     , { { 1990, 10, 1990, 1840, 1990 }
9949     , { 60, -980, 60, -400, 60 }
9950     , { 1840, 10, 1060, 1840, 1060 }
9951     , { 1990, -310, 1990, 270, 1990 }
9952     , { 1840, 10, 1060, 1840, 1060 }
9953     }
9954     , { { 1990, 170, 1210, 1990, 1210 }
9955     , { 1990, 160, 1210, 1990, 1210 }
9956     , { 1750, 170, 970, 1750, 970 }
9957     , { 1990, 160, 1210, 1990, 1210 }
9958     , { 270, -780, 270, -200, 270 }
9959     }
9960     }
9961     , { { { 1860, 1840, 1860, 1840, 640 }
9962     , { 1210, 1190, 1210, 1190, 640 }
9963     , { 1080, 1060, 1080, 1060, 270 }
9964     , { 1860, 1840, 1860, 1840, 270 }
9965     , { 950, 930, 950, 930, 140 }
9966     }
9967     , { { 1210, 1190, 1210, 1190, 640 }
9968     , { 1210, 1190, 1210, 1190, 640 }
9969     , { 930, 910, 930, 910, 120 }
9970     , { 270, 10, 270, 10, -780 }
9971     , { 930, 910, 930, 910, 120 }
9972     }
9973     , { { 1080, 1060, 1080, 1060, 270 }
9974     , { 1080, 1060, 1080, 1060, 270 }
9975     , { 1080, 1060, 1080, 1060, 270 }
9976     , { 1080, 1060, 1080, 1060, 270 }
9977     , { 950, 930, 950, 930, 140 }
9978     }
9979     , { { 1860, 1840, 1860, 1840, 120 }
9980     , { 180, -80, 180, -80, -810 }
9981     , { 930, 910, 930, 910, 120 }
9982     , { 1860, 1840, 1860, 1840, -200 }
9983     , { 930, 910, 930, 910, 120 }
9984     }
9985     , { { 1080, 1060, 1080, 1060, 270 }
9986     , { 1080, 1060, 1080, 1060, 270 }
9987     , { 840, 820, 840, 820, 30 }
9988     , { 1080, 1060, 1080, 1060, 270 }
9989     , { 140, 120, 140, 120, -670 }
9990     }
9991     }
9992     }
9993     } };
```

## 18.170 ViennaRNA/params/io.h File Reference

Read and write energy parameter files.

This graph shows which files directly or indirectly include this file:

### Macros

- `#define VRNA_PARAMETER_FORMAT_DEFAULT 0`

*Default Energy Parameter File format.*

### Functions

- `int vrna_params_load` (const char fname[], unsigned int options)  
*Load energy parameters from a file.*
- `int vrna_params_save` (const char fname[], unsigned int options)  
*Save energy parameters to a file.*
- `int vrna_params_load_from_string` (const char \*string, const char \*name, unsigned int options)  
*Load energy paramters from string.*
- `int vrna_params_load_defaults` (void)  
*Load default RNA energy parameter set.*
- `int vrna_params_load_RNA_Turner2004` (void)  
*Load Turner 2004 RNA energy parameter set.*

- `int vrna_params_load_RNA_Turner1999` (void)  
*Load Turner 1999 RNA energy parameter set.*
- `int vrna_params_load_RNA_Andronescu2007` (void)  
*Load Andronescu 2007 RNA energy parameter set.*
- `int vrna_params_load_RNA_Langdon2018` (void)  
*Load Langdon 2018 RNA energy parameter set.*
- `int vrna_params_load_RNA_misc_special_hairpins` (void)  
*Load Misc Special Hairpin RNA energy parameter set.*
- `int vrna_params_load_DNA_Mathews2004` (void)  
*Load Mathews 2004 DNA energy parameter set.*
- `int vrna_params_load_DNA_Mathews1999` (void)  
*Load Mathews 1999 DNA energy parameter set.*
- `const char * last_parameter_file` (void)  
*Get the file name of the parameter file that was most recently loaded.*
- `void read_parameter_file` (const char fname[])  
*Read energy parameters from a file.*
- `void write_parameter_file` (const char fname[])  
*Write energy parameters to a file.*

### 18.170.1 Detailed Description

Read and write energy parameter files.

## 18.171 io.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_IO_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_IO_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #define VRNA_PARAMETER_FORMAT_DEFAULT 0
17
18 int
19 vrna_params_load(const char  fname[],
20                 unsigned int options);
21
22 int
23 vrna_params_save(const char  fname[],
24                 unsigned int options);
25
26 int
27 vrna_params_load_from_string(const char  *string,
28                             const char  *name,
29                             unsigned int options);
30
31 int
32 vrna_params_load_defaults(void);
33
34 int
35 vrna_params_load_RNA_Turner2004(void);
36
37 int

```

```

143 vrna_params_load_RNA_Turner1999(void);
144
145
158 int
159 vrna_params_load_RNA_Andronescu2007(void);
160
161
174 int
175 vrna_params_load_RNA_Langdon2018(void);
176
177
190 int
191 vrna_params_load_RNA_misc_special_hairpins(void);
192
193
206 int
207 vrna_params_load_DNA_Mathews2004(void);
208
209
222 int
223 vrna_params_load_DNA_Mathews1999(void);
224
225
226 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
227
232 enum parset {
233     UNKNOWN= -1, QUIT,
234     S, S_H, HP, HP_H, B, B_H, IL, IL_H, MMH, MMH_H, MMI, MMI_H,
235     MMI1N, MMI1N_H, MMI23, MMI23_H, MMM, MMM_H, MME, MME_H, D5, D5_H, D3, D3_H,
236     INT11, INT11_H, INT21, INT21_H, INT22, INT22_H, ML, TL,
237     TRI, HEX, NIN, MISC
238 };
239
240
246 const char *
247 last_parameter_file(void);
248
249
256 DEPRECATED(void
257     read_parameter_file(const char fname[]),
258     "Use vrna_params_load() instead!");
259
260
267 DEPRECATED(void
268     write_parameter_file(const char fname[]),
269     "Use vrna_params_save() instead!");
270
271
276 enum parset
277 gettype(const char *ident);
278
279
284 char *
285 settype(enum parset s);
286
287
292 #endif
293
294 #endif

```

## 18.172 ViennaRNA/part\_func.h File Reference

Partition function implementations.

Include dependency graph for part\_func.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_dimer\\_pf\\_s](#)  
Data structure returned by [vrna\\_pf\\_dimer\(\)](#) [More...](#)
- struct [vrna\\_multimer\\_pf\\_s](#)

### Typedefs

- typedef struct [vrna\\_dimer\\_pf\\_s](#) [vrna\\_dimer\\_pf\\_t](#)  
Typename for the data structure that stores the dimer partition functions, [vrna\\_dimer\\_pf\\_s](#), as returned by [vrna\\_pf\\_dimer\(\)](#)

- typedef struct [vrna\\_dimer\\_pf\\_s](#) **cofoldF**

*Backward compatibility typedef for [vrna\\_dimer\\_pf\\_s](#).*

## Functions

- int [vrna\\_pf\\_float\\_precision](#) (void)  
*Find out whether partition function computations are using single precision floating points.*
- float [pf\\_fold\\_par](#) (const char \*sequence, char \*structure, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_bp, int is\_constrained, int is\_circular)  
*Compute the partition function  $Q$  for a given RNA sequence.*
- float [pf\\_fold](#) (const char \*sequence, char \*structure)  
*Compute the partition function  $Q$  of an RNA sequence.*
- float [pf\\_circ\\_fold](#) (const char \*sequence, char \*structure)  
*Compute the partition function of a circular RNA sequence.*
- char \* [pbacktrack](#) (char \*sequence)  
*Sample a secondary structure from the Boltzmann ensemble according its probability.*
- char \* [pbacktrack5](#) (char \*sequence, int length)  
*Sample a sub-structure from the Boltzmann ensemble according its probability.*
- char \* [pbacktrack\\_circ](#) (char \*sequence)  
*Sample a secondary structure of a circular RNA from the Boltzmann ensemble according its probability.*
- void [free\\_pf\\_arrays](#) (void)  
*Free arrays for the partition function recursions.*
- void [update\\_pf\\_params](#) (int length)  
*Recalculate energy parameters.*
- void [update\\_pf\\_params\\_par](#) (int length, [vrna\\_exp\\_param\\_t](#) \*parameters)  
*Recalculate energy parameters.*
- [FLT\\_OR\\_DBL](#) \* [export\\_bppm](#) (void)  
*Get a pointer to the base pair probability array.*
- int [get\\_pf\\_arrays](#) (short \*\*S\_p, short \*\*S1\_p, char \*\*ptype\_p, [FLT\\_OR\\_DBL](#) \*\*qb\_p, [FLT\\_OR\\_DBL](#) \*\*qm\_p, [FLT\\_OR\\_DBL](#) \*\*q1k\_p, [FLT\\_OR\\_DBL](#) \*\*qln\_p)  
*Get the pointers to (almost) all relevant computation arrays used in partition function computation.*
- double [get\\_subseq\\_F](#) (int i, int j)  
*Get the free energy of a subsequence from the  $q[]$  array.*
- double [mean\\_bp\\_distance](#) (int length)  
*Get the mean base pair distance of the last partition function computation.*
- double [mean\\_bp\\_distance\\_pr](#) (int length, [FLT\\_OR\\_DBL](#) \*pr)  
*Get the mean base pair distance in the thermodynamic ensemble.*
- [vrna\\_ep\\_t](#) \* [stackProb](#) (double cutoff)  
*Get the probability of stacks.*
- void [init\\_pf\\_fold](#) (int length)  
*Allocate space for [pf\\_fold\(\)](#)*
- char \* [centroid](#) (int length, double \*dist)
- char \* [get\\_centroid\\_struct\\_gquad\\_pr](#) (int length, double \*dist)
- double [mean\\_bp\\_dist](#) (int length)
- double [expLoopEnergy](#) (int u1, int u2, int type, int type2, short si1, short sj1, short sp1, short sq1)
- double [expHairpinEnergy](#) (int u, int type, short si1, short sj1, const char \*string)

## Basic global partition function interface

- [FLT\\_OR\\_DBL](#) [vrna\\_pf](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Compute the partition function  $Q$  for a given RNA sequence, or sequence alignment.*
- [vrna\\_dimer\\_pf\\_t](#) [vrna\\_pf\\_dimer](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, char \*structure)  
*Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.*

- [FLT\\_OR\\_DBL](#) \* [vrna\\_pf\\_substrands](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, [size\\_t](#) complex\_size)
- [FLT\\_OR\\_DBL](#) [vrna\\_pf\\_add](#) ([FLT\\_OR\\_DBL](#) dG1, [FLT\\_OR\\_DBL](#) dG2, [double](#) kT)

### Simplified global partition function computation using sequence(s) or multiple sequence alignment(s)

- [float](#) [vrna\\_pf\\_fold](#) ([const char](#) \*sequence, [char](#) \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence using a comparative method.*
- [float](#) [vrna\\_pf\\_circfold](#) ([const char](#) \*sequence, [char](#) \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for a circular RNA sequences using a comparative method.*
- [float](#) [vrna\\_pf\\_alifold](#) ([const char](#) \*\*sequences, [char](#) \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an RNA sequence alignment using a comparative method.*
- [float](#) [vrna\\_pf\\_circalifold](#) ([const char](#) \*\*sequences, [char](#) \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Compute Partition function  $Q$  (and base pair probabilities) for an alignment of circular RNA sequences using a comparative method.*
- [vrna\\_dimer\\_pf\\_t](#) [vrna\\_pf\\_co\\_fold](#) ([const char](#) \*seq, [char](#) \*structure, [vrna\\_ep\\_t](#) \*\*pl)  
*Calculate partition function and base pair probabilities of nucleic acid/nucleic acid dimers.*

## Variables

- [int](#) [st\\_back](#)  
*Flag indicating that auxiliary arrays are needed throughout the computations. This is essential for stochastic backtracking.*

### 18.172.1 Detailed Description

Partition function implementations.

This file includes (almost) all function declarations within the **RNAlib** that are related to Partition function computations

### 18.172.2 Function Documentation

#### 18.172.2.1 centroid()

```
char * centroid (
    int length,
    double * dist )
```

**Deprecated** This function is deprecated and should not be used anymore as it is not threadsafe!

See also

[get\\_centroid\\_struct\\_pl\(\)](#), [get\\_centroid\\_struct\\_pr\(\)](#)

#### 18.172.2.2 get\_centroid\_struct\_gquad\_pr()

```
char * get_centroid_struct_gquad_pr (
    int length,
    double * dist )
```

**Deprecated** This function is deprecated and should not be used anymore as it is not threadsafe!

See also

[vrna\\_centroid\(\)](#), [vrna\\_centroid\\_from\\_probs\(\)](#), [vrna\\_centroid\\_from\\_plist\(\)](#)

**18.172.2.3 mean\_bp\_dist()**

```
double mean_bp_dist (
    int length )
```

get the mean pair distance of ensemble

**Deprecated** This function is not threadsafe and should not be used anymore. Use [mean\\_bp\\_distance\(\)](#) instead!

**18.172.2.4 expLoopEnergy()**

```
double expLoopEnergy (
    int u1,
    int u2,
    int type,
    int type2,
    short sil,
    short sj1,
    short spl,
    short sql )
```

**Deprecated** Use [exp\\_E\\_IntLoop\(\)](#) from [loop\\_energies.h](#) instead

**18.172.2.5 expHairpinEnergy()**

```
double expHairpinEnergy (
    int u,
    int type,
    short sil,
    short sj1,
    const char * string )
```

**Deprecated** Use [exp\\_E\\_Hairpin\(\)](#) from [loop\\_energies.h](#) instead

**18.173 part\_func.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PART_FUNC_H
2 #define VIENNA_RNA_PACKAGE_PART_FUNC_H
3
4 typedef struct vrna_dimer_pf_s vrna_dimer_pf_t;
5
6 typedef struct vrna_multimer_pf_s vrna_multimer_pf_t;
7
8 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
9 typedef struct vrna_dimer_pf_s cofoldF;
10
11 #endif
12
13 #include <ViennaRNA/datastructures/basic.h>
14 #include <ViennaRNA/fold_compound.h>
15 #include <ViennaRNA/utils/structures.h>
16 #include <ViennaRNA/params/basic.h>
17 #include <ViennaRNA/centroid.h>
18 #include <ViennaRNA/equilibrium_probs.h>
19 #include <ViennaRNA/boltzmann_sampling.h>
20
21 #ifdef VRNA_WARN_DEPRECATED
22 # if defined(__clang__)
23 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
24 # elif defined(__GNUC__)
25 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
26 # else
27 #   define DEPRECATED(func, msg) func
28 # endif
29
```



```

38 # endif
39 #else
40 # define DEPRECATED(func, msg) func
41 #endif
42
43 /*
44 #####
45 # PARTITION FUNCTION COMPUTATION
46 #####
47 */
48
49 struct vrna_dimer_pf_s {
50     /* free energies for: */
51     double F0AB;
52     double FAB;
53     double FcAB;
54     double FA;
55     double FB;
56 };
57
58 struct vrna_multimer_pf_s {
59     /* free energies for: */
60     double F_connected;
61     double *F_monomers;
62     size_t num_monomers;
63 };
64
65 FLT_OR_DBL
66 vrna_pf(vrna_fold_compound_t *vc,
67         char *structure);
68
69 vrna_dimer_pf_t
70 vrna_pf_dimer(vrna_fold_compound_t *vc,
71               char *structure);
72
73 FLT_OR_DBL *
74 vrna_pf_substrands(vrna_fold_compound_t *fc,
75                    size_t complex_size);
76
77 FLT_OR_DBL
78 vrna_pf_add(FLT_OR_DBL dG1,
79             FLT_OR_DBL dG2,
80             double kT);
81
82 /* End basic global interface */
83
84 float
85 vrna_pf_fold(const char *sequence,
86              char *structure,
87              vrna_ep_t **pl);
88
89 float
90 vrna_pf_circfold(const char *sequence,
91                  char *structure,
92                  vrna_ep_t **pl);
93
94 float
95 vrna_pf_alifold(const char **sequences,
96                 char *structure,
97                 vrna_ep_t **pl);
98
99 float
100 vrna_pf_circalifold(const char **sequences,
101                     char *structure,
102                     vrna_ep_t **pl);
103
104 vrna_dimer_pf_t
105 vrna_pf_co_fold(const char *seq,
106                 char *structure,
107                 vrna_ep_t **pl);
108
109 /* End simplified global interface */
110
111 #####
112 # OTHER PARTITION FUNCTION RELATED DECLARATIONS #
113 #####
114
115 int
116 vrna_pf_float_precision(void);
117

```

```

361
362 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
363
364 /*
365 #####
366 # DEPRECATED FUNCTIONS #
367 #####
368 */
369
382 extern int st_back;
383
424 DEPRECATED(float
425     pf_fold_par(const char *sequence,
426                 char *structure,
427                 vrna_exp_param_t *parameters,
428                 int calculate_bppm,
429                 int is_constrained,
430                 int is_circular),
431     "Use the new API and vrna_pf() instead");
432
472 DEPRECATED(float
473     pf_fold(const char *sequence,
474             char *structure),
475     "Use vrna_pf_fold() or vrna_pf() instead");
476
503 DEPRECATED(float
504     pf_circ_fold(const char *sequence,
505                 char *structure),
506     "Use vrna_pf_circfold() or vrna_pf() instead");
507
519 DEPRECATED(char *pbacktrack(char *sequence), "Use vrna_pbacktrack() instead");
520
526 DEPRECATED(char *pbacktrack5(char *sequence,
527                               int length), "Use vrna_pbacktrack5() instead");
528
544 DEPRECATED(char *pbacktrack_circ(char *sequence), "Use vrna_pbacktrack() instead");
545
564 DEPRECATED(void
565     free_pf_arrays(void), "This function is obsolete");
566
578 DEPRECATED(void
579     update_pf_params(int length), "This function is obsolete");
580
589 DEPRECATED(void
590     update_pf_params_par(int length,
591                          vrna_exp_param_t *parameters),
592     "Use the new API with vrna_fold_compound_t instead");
593
611 DEPRECATED(FLT_OR_DBL * export_bppm(void),
612     "Use the new API with vrna_fold_compound_t instead");
613
614
631 DEPRECATED(int
632     get_pf_arrays(short **S_p,
633                  short **S1_p,
634                  char **ptype_p,
635                  FLT_OR_DBL **qb_p,
636                  FLT_OR_DBL **qm_p,
637                  FLT_OR_DBL **qlk_p,
638                  FLT_OR_DBL **qln_p),
639     "Use the new API with vrna_fold_compound_t instead");
640
646 DEPRECATED(double
647     get_subseq_F(int i,
648                 int j),
649     "Use the new API with vrna_fold_compound_t instead");
650
651
663 DEPRECATED(double
664     mean_bp_distance(int length),
665     "Use vrna_mean_bp_distance() or vrna_mean_bp_distance_pr() instead");
666
684 DEPRECATED(double
685     mean_bp_distance_pr(int length,
686                        FLT_OR_DBL *pr),
687     "Use vrna_mean_bp_distance() or vrna_mean_bp_distance_pr() instead");
688
696 DEPRECATED(vrna_ep_t * stackProb(double cutoff), "Use vrna_stack_prob() instead");
697
698
706 DEPRECATED(void
707     init_pf_fold(int length), "This function is obsolete");
708
713 DEPRECATED(char *centroid(int length,
714                           double *dist),
715     "Use vrna_centroid() instead");
716

```

```

721 DEPRECATED(char *get_centroid_struct_gquad_pr(int length,
722   double *dist),
723             "Use vrna_centroid() instead");
724
730 DEPRECATED(double
731             mean_bp_dist(int length),
732             "Use vrna_mean_bp_distance() or vrna_mean_bp_distance_pr() instead");
733
737 DEPRECATED(double
738             expLoopEnergy(int    u1,
739                           int    u2,
740                           int    type,
741                           int    type2,
742                           short  sil,
743                           short  sj1,
744                           short  spl,
745                           short  sql),
746             "");
747
751 DEPRECATED(double
752             expHairpinEnergy(int    u,
753                              int    type,
754                              short  sil,
755                              short  sj1,
756                              const char *string),
757             "");
758
759 /* this doesn't work if free_pf_arrays() is called before */
760 DEPRECATED(void
761             assign_plist_gquad_from_pr(vrna_ep_t **pl,
762   int    length,
763   double  cut_off),
764             "Use vrna_plist_from_probs() instead");
765
766 #endif
767
768 #endif

```

## 18.174 ViennaRNA/part\_func\_co.h File Reference

Partition function for two RNA sequences.

Include dependency graph for part\_func\_co.h:

### Functions

- [vrna\\_dimer\\_pf\\_t\\_co\\_pf\\_fold](#) (char \*sequence, char \*structure)  
*Calculate partition function and base pair probabilities.*
- [vrna\\_dimer\\_pf\\_t\\_co\\_pf\\_fold\\_par](#) (char \*sequence, char \*structure, [vrna\\_exp\\_param\\_t](#) \*parameters, int calculate\_bppm, int is\_constrained)  
*Calculate partition function and base pair probabilities.*
- [vrna\\_ep\\_t](#) \* [get\\_plist](#) ([vrna\\_ep\\_t](#) \*pl, int length, double cut\_off)
- void [compute\\_probabilities](#) (double FAB, double FEA, double FEB, [vrna\\_ep\\_t](#) \*prAB, [vrna\\_ep\\_t](#) \*prA, [vrna\\_ep\\_t](#) \*prB, int Alength)  
*Compute Boltzmann probabilities of dimerization without homodimers.*
- void [init\\_co\\_pf\\_fold](#) (int length)
- [FLT\\_OR\\_DBL](#) \* [export\\_co\\_bppm](#) (void)  
*Get a pointer to the base pair probability array.*
- void [free\\_co\\_pf\\_arrays](#) (void)  
*Free the memory occupied by [co\\_pf\\_fold\(\)](#)*
- void [update\\_co\\_pf\\_params](#) (int length)  
*Recalculate energy parameters.*
- void [update\\_co\\_pf\\_params\\_par](#) (int length, [vrna\\_exp\\_param\\_t](#) \*parameters)  
*Recalculate energy parameters.*

## Variables

- int **mirnatog**  
*Toggles no intrabp in 2nd mol.*
- double **F\_monomer** [2]  
*Free energies of the two monomers.*

### 18.174.1 Detailed Description

Partition function for two RNA sequences.

### 18.174.2 Function Documentation

#### 18.174.2.1 get\_plist()

```
vrna_ep_t * get_plist (
    vrna_ep_t * pl,
    int length,
    double cut_off )
```

DO NOT USE THIS FUNCTION ANYMORE

**Deprecated** { This function is deprecated and will be removed soon!} use [assign\\_plist\\_from\\_pr\(\)](#) instead!

## 18.175 part\_func\_co.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PART_FUNC_CO_H
2 #define VIENNA_RNA_PACKAGE_PART_FUNC_CO_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <ViennaRNA/datastructures/basic.h>
17 #include <ViennaRNA/params/basic.h>
18 #include <ViennaRNA/part_func.h>
19 #include <ViennaRNA/equilibrium_probs.h>
20 #include <ViennaRNA/concentrations.h>
21 #include <ViennaRNA/utils/structures.h>
22
23 extern int    mirnatog;
24
25 extern double F_monomer[2];
26
27 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
28
29 /*
30  * DEPRECATED FUNCTIONS
31  */
32
33 DEPRECATED(vrna_dimer_pf_t co_pf_fold(char *sequence,
34                                     char *structure),
35 "Use vrna_pf_co_fold() or vrna_pf_dimer() instead");
36
37 DEPRECATED(vrna_dimer_pf_t co_pf_fold_par(char *sequence,
38                                     char *structure,
39                                     vrna_exp_param_t *parameters,
40                                     int calculate_bppm,
41                                     int is_constrained),
42 "Use the new API and vrna_pf_dimer() instead");
43
44 #endif
```

```

138 DEPRECATED(vrna_ep_t *get_plist(vrna_ep_t *pl,
139                                int      length,
140                                double   cut_off),
141 "Use vrna_plist() and vrna_plist_from_probs() instead");
142
143 DEPRECATED(void compute_probabilities(double   FAB,
144                                     double   FEA,
145                                     double   FEB,
146                                     vrna_ep_t *prAB,
147                                     vrna_ep_t *prA,
148                                     vrna_ep_t *prB,
149                                     int      Alength),
150 "Use vrna_pf_dimer_probs() instead");
151
152 DEPRECATED(void init_co_pf_fold(int length),
153 "This function is obsolete");
154
155 DEPRECATED(FLT_OR_DBL *export_co_bppm(void),
156 "Use the new API with vrna_fold_compound_t instead");
157
158 DEPRECATED(void free_co_pf_arrays(void),
159 "This function is obsolete");
160
161 DEPRECATED(void update_co_pf_params(int length),
162 "This function is obsolete");
163
164 DEPRECATED(void update_co_pf_params_par(int      length,
165   vrna_exp_param_t *parameters),
166 "Use the new API with vrna_fold_compound_t instead");
167
168 #endif
169
170 #endif

```

## 18.176 ViennaRNA/part\_func\_up.h File Reference

Implementations for accessibility and RNA-RNA interaction as a stepwise process.  
Include dependency graph for part\_func\_up.h:

### Functions

- [pu\\_contrib](#) \* [pf\\_unstru](#) (char \*sequence, int max\_w)  
*Calculate the partition function over all unpaired regions of a maximal length.*
- [interact](#) \* [pf\\_interact](#) (const char \*s1, const char \*s2, [pu\\_contrib](#) \*p\_c, [pu\\_contrib](#) \*p\_c2, int max\_w, char \*cstruc, int incr3, int incr5)  
*Calculates the probability of a local interaction between two sequences.*
- void [free\\_interact](#) ([interact](#) \*pin)  
*Frees the output of function [pf\\_interact\(\)](#).*
- void [free\\_pu\\_contrib\\_struct](#) ([pu\\_contrib](#) \*pu)  
*Frees the output of function [pf\\_unstru\(\)](#).*

### 18.176.1 Detailed Description

Implementations for accessibility and RNA-RNA interaction as a stepwise process.

## 18.177 part\_func\_up.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PART_FUNC_UP_H
2 #define VIENNA_RNA_PACKAGE_PART_FUNC_UP_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5
6 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
7
8 #define RNA_UP_MODE_1 1U
9 #define RNA_UP_MODE_2 2U
10 #define RNA_UP_MODE_3 4U
11
12 pu\_contrib *pf\_unstru(char *sequence,
13                     int max_w);

```

```

63
106 interact *pf_interact(const char *s1,
107                       const char *s2,
108                       pu_contrib *p_c,
109                       pu_contrib *p_c2,
110                       int max_w,
111                       char *cstruc,
112                       int incr3,
113                       int incr5);
114
118 void free_interact(interact *pin);
119
123 int Up_plot(pu_contrib *p_c,
124            pu_contrib *p_c_sh,
125            interact *pint,
126            char *ofile,
127            int **unpaired_values,
128            char *select_contrib,
129            char *head,
130            unsigned int mode);
131
135 pu_contrib *get_pu_contrib_struct( unsigned int n,
136                                   unsigned int w);
137
141 void free_pu_contrib_struct(pu_contrib *pu);
142
143 void free_pu_contrib(pu_contrib *pu);
144
150 #endif
151
152 #endif

```

## 18.178 ViennaRNA/part\_func\_window.h File Reference

Partition function and equilibrium probability implementation for the sliding window algorithm.

Include dependency graph for part\_func\_window.h: This graph shows which files directly or indirectly include this file:

### Macros

- **#define VRNA\_EXT\_LOOP** 1U  
*Exterior loop.*
- **#define VRNA\_HP\_LOOP** 2U  
*Hairpin loop.*
- **#define VRNA\_INT\_LOOP** 4U  
*Internal loop.*
- **#define VRNA\_MB\_LOOP** 8U  
*Multibranch loop.*
- **#define VRNA\_ANY\_LOOP** (VRNA\_EXT\_LOOP | VRNA\_HP\_LOOP | VRNA\_INT\_LOOP | VRNA\_MB\_LOOP)  
*Any loop.*
- **#define VRNA\_PROBS\_WINDOW\_BPP** 4096U  
*Trigger base pairing probabilities.*
- **#define VRNA\_PROBS\_WINDOW\_UP** 8192U  
*Trigger unpaired probabilities.*
- **#define VRNA\_PROBS\_WINDOW\_STACKP** 16384U  
*Trigger base pair stack probabilities.*
- **#define VRNA\_PROBS\_WINDOW\_UP\_SPLIT** 32768U  
*Trigger detailed unpaired probabilities split up into different loop type contexts.*
- **#define VRNA\_PROBS\_WINDOW\_PF** 65536U  
*Trigger partition function.*

## Typedefs

- typedef void() [vrna\\_probs\\_window\\_callback](#)([FLT\\_OR\\_DBL](#) \*pr, int pr\_size, int i, int max, unsigned int type, void \*data)

*Sliding window probability computation callback.*

## Functions

### Basic local partition function interface

- int [vrna\\_probs\\_window](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int ulength, unsigned int options, [vrna\\_probs\\_window\\_callback](#) \*cb, void \*data)

*Compute various equilibrium probabilities under a sliding window approach.*

### Simplified global partition function computation using sequence(s) or multiple sequence alignment(s)

- [vrna\\_ep\\_t](#) \* [vrna\\_pfl\\_fold](#) (const char \*sequence, int window\_size, int [max\\_bp\\_span](#), float cutoff)  
*Compute base pair probabilities using a sliding-window approach.*
- int [vrna\\_pfl\\_fold\\_cb](#) (const char \*sequence, int window\_size, int [max\\_bp\\_span](#), [vrna\\_probs\\_window\\_callback](#) \*cb, void \*data)  
*Compute base pair probabilities using a sliding-window approach (callback version)*
- double \*\* [vrna\\_pfl\\_fold\\_up](#) (const char \*sequence, int ulength, int window\_size, int [max\\_bp\\_span](#))  
*Compute probability of contiguous unpaired segments.*
- int [vrna\\_pfl\\_fold\\_up\\_cb](#) (const char \*sequence, int ulength, int window\_size, int [max\\_bp\\_span](#), [vrna\\_probs\\_window\\_callback](#) \*cb, void \*data)  
*Compute probability of contiguous unpaired segments.*

## 18.178.1 Detailed Description

Partition function and equilibrium probability implementation for the sliding window algorithm.

This file contains the implementation for sliding window partition function and equilibrium probabilities. It also provides the unpaired probability implementation from Bernhart et al. 2011 [4]

## 18.179 part\_func\_window.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PART_FUNC_WINDOW_H
2 #define VIENNA_RNA_PACKAGE_PART_FUNC_WINDOW_H
3
15 #include <ViennaRNA/datastructures/basic.h>
16
63 typedef void (vrna_probs_window_callback) (FLT_OR_DBL      *pr,
64   int              pr_size,
65   int              i,
66   int              max,
67   unsigned int    type,
68   void             *data);
69
70 #include <ViennaRNA/fold_compound.h>
71 #include <ViennaRNA/utils/structures.h>
72
76 #define VRNA_EXT_LOOP    1U
77
81 #define VRNA_HP_LOOP     2U
82
86 #define VRNA_INT_LOOP    4U
87
91 #define VRNA_MB_LOOP     8U
92
96 #define VRNA_ANY_LOOP    (VRNA_EXT_LOOP | VRNA_HP_LOOP | VRNA_INT_LOOP | VRNA_MB_LOOP)
97
98
111 #define VRNA_PROBS_WINDOW_BPP    4096U
112
125 #define VRNA_PROBS_WINDOW_UP     8192U
126
139 #define VRNA_PROBS_WINDOW_STACKP 16384U
140
```

```

158 #define VRNA_PROBS_WINDOW_UP_SPLIT    32768U
159
160
174 #define VRNA_PROBS_WINDOW_PF          65536U
175
207 int
208 vrna_probs_window(vrna_fold_compound_t      *fc,
209                  int                        ulength,
210                  unsigned int               options,
211                  vrna_probs_window_callback *cb,
212                  void                      *data);
213
214 /* End basic interface */
243 vrna_ep_t *
244 vrna_pfl_fold(const char *sequence,
245              int         window_size,
246              int         max_bp_span,
247              float       cutoff);
248
249
272 int
273 vrna_pfl_fold_cb(const char *sequence,
274                 int         window_size,
275                 int         max_bp_span,
276                 vrna_probs_window_callback *cb,
277                 void         *data);
278
279
302 double **
303 vrna_pfl_fold_up(const char *sequence,
304                 int         ulength,
305                 int         window_size,
306                 int         max_bp_span);
307
308
332 int
333 vrna_pfl_fold_up_cb(const char *sequence,
334                    int         ulength,
335                    int         window_size,
336                    int         max_bp_span,
337                    vrna_probs_window_callback *cb,
338                    void         *data);
339
340
341 /* End simplified interface */
347 #endif

```

## 18.180 ViennaRNA/perturbation\_fold.h File Reference

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

Include dependency graph for perturbation\_fold.h:

### Macros

- #define **VRNA\_OBJECTIVE\_FUNCTION\_QUADRATIC** 0  
*Use the sum of squared aberrations as objective function.*
- #define **VRNA\_OBJECTIVE\_FUNCTION\_ABSOLUTE** 1  
*Use the sum of absolute aberrations as objective function.*
- #define **VRNA\_MINIMIZER\_DEFAULT** 0  
*Use a custom implementation of the gradient descent algorithm to minimize the objective function.*
- #define **VRNA\_MINIMIZER\_CONJUGATE\_FR** 1  
*Use the GNU Scientific Library implementation of the Fletcher-Reeves conjugate gradient algorithm to minimize the objective function.*
- #define **VRNA\_MINIMIZER\_CONJUGATE\_PR** 2  
*Use the GNU Scientific Library implementation of the Polak-Ribiere conjugate gradient algorithm to minimize the objective function.*
- #define **VRNA\_MINIMIZER\_VECTOR\_BFGS** 3  
*Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.*
- #define **VRNA\_MINIMIZER\_VECTOR\_BFGS2** 4



Use the GNU Scientific Library implementation of the vector Broyden-Fletcher-Goldfarb-Shanno algorithm to minimize the objective function.

- `#define VRNA_MINIMIZER_STEEPEST_DESCENT 5`

Use the GNU Scientific Library implementation of the steepest descent algorithm to minimize the objective function.

## Typedefs

- `typedef void(* progress_callback) (int iteration, double score, double *epsilon)`

Callback for following the progress of the minimization process.

## Functions

- `void vrna_sc_minimize_pertubation (vrna_fold_compound_t *vc, const double *q_prob_unpaired, int objective_function, double sigma_squared, double tau_squared, int algorithm, int sample_size, double *epsilon, double initialStepSize, double minStepSize, double minImprovement, double minimizerTolerance, progress_callback callback)`

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

### 18.180.1 Detailed Description

Find a vector of perturbation energies that minimizes the discrepancies between predicted and observed pairing probabilities and the amount of necessary adjustments.

## 18.181 perturbation\_fold.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PERTURBATION_FOLD_H
2 #define VIENNA_RNA_PACKAGE_PERTURBATION_FOLD_H
3
4 #include <ViennaRNA/fold_compound.h>
5
24 #define VRNA_OBJECTIVE_FUNCTION_QUADRATIC 0
25
33 #define VRNA_OBJECTIVE_FUNCTION_ABSOLUTE 1
34
40 #define VRNA_MINIMIZER_DEFAULT 0
41
49 #define VRNA_MINIMIZER_CONJUGATE_FR 1
50
58 #define VRNA_MINIMIZER_CONJUGATE_PR 2
59
67 #define VRNA_MINIMIZER_VECTOR_BFGS 3
68
76 #define VRNA_MINIMIZER_VECTOR_BFGS2 4
77
85 #define VRNA_MINIMIZER_STEEPEST_DESCENT 5
86
96 typedef void (*progress_callback) (int    iteration,
97                                   double  score,
98                                   double  *epsilon);
99
139 void vrna_sc_minimize_pertubation (vrna_fold_compound_t *vc,
140                                   const double
141                                   int
142                                   double
143                                   double
144                                   int
145                                   int
146                                   double
147                                   double
148                                   double
149                                   double
150                                   double
151                                   progress_callback
152                                   callback);
153
154 #endif
```

## 18.182 pf\_multifold.h

```

1 #ifndef VIENNA_RNA_PACKAGE_PART_FUNC_MULTIFOLD_H
2 #define VIENNA_RNA_PACKAGE_PART_FUNC_MULTIFOLD_H
3
4 #include "ViennaRNA/fold_compound.h"
5
6 int
7 vrna_pf_multifold_prepare(vrna_fold_compound_t *fc);
8
9
10 #endif

```

## 18.183 ViennaRNA/pk\_plex.h File Reference

Heuristics for two-step pseudoknot forming interaction predictions.

Include dependency graph for pk\_plex.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_pk\\_plex\\_result\\_s](#)  
*A result of the RNA PKplex interaction prediction. [More...](#)*

### Typedefs

- typedef int() [vrna\\_callback\\_pk\\_plex\\_score](#)(const short \*pt, int start\_5, int end\_5, int start\_3, int end\_3, void \*data)  
*Pseudoknot loop scoring function prototype.*
- typedef struct vrna\_pk\_plex\_option\_s \* [vrna\\_pk\\_plex\\_opt\\_t](#)  
*RNA PKplex options object.*
- typedef struct [vrna\\_pk\\_plex\\_result\\_s](#) [vrna\\_pk\\_plex\\_t](#)  
*Convenience typedef for results of the RNA PKplex prediction.*

### Functions

- [vrna\\_pk\\_plex\\_t](#) \* [vrna\\_pk\\_plex](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const int \*\*accessibility, [vrna\\_pk\\_plex\\_opt\\_t](#) options)  
*Predict Pseudoknot interactions in terms of a two-step folding process.*
- int \*\* [vrna\\_pk\\_plex\\_accessibility](#) (const char \*sequence, unsigned int [unpaired](#), double cutoff)  
*Obtain a list of opening energies suitable for PKplex computations.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt\\_defaults](#) (void)  
*Default options for PKplex algorithm.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt](#) (unsigned int delta, unsigned int max\_interaction\_length, int pk\_↔ penalty)  
*Simple options for PKplex algorithm.*
- [vrna\\_pk\\_plex\\_opt\\_t](#) [vrna\\_pk\\_plex\\_opt\\_fun](#) (unsigned int delta, unsigned int max\_interaction\_length, [vrna\\_callback\\_pk\\_plex\\_score](#) \*scoring\_function, void \*scoring\_data)  
*Simple options for PKplex algorithm.*

### 18.183.1 Detailed Description

Heuristics for two-step pseudoknot forming interaction predictions.

## 18.184 pk\_plex.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PK_PLEX_H
2 #define VIENNA_RNA_PACKAGE_PK_PLEX_H
3
45 typedef int (vrna_callback_pk_plex_score)(const short *pt,
46   int          start_5,
47   int          end_5,
48   int          start_3,
49   int          end_3,
50   void          *data);
51
58 typedef struct vrna_pk_plex_option_s *vrna_pk_plex_opt_t;
59
65 typedef struct vrna_pk_plex_result_s vrna_pk_plex_t;
66
67 #include <ViennaRNA/fold_compound.h>
68
74 struct vrna_pk_plex_result_s {
75     char          *structure;
76     double         energy;
77     double         dGpk;
78     double         dGint;
79     double         dG1;
80     double         dG2;
81     unsigned int    start_5;
82     unsigned int    end_5;
83     unsigned int    start_3;
84     unsigned int    end_3;
85 };
86
116 vrna_pk_plex_t *
117 vrna_pk_plex(vrna_fold_compound_t *fc,
118              const int              **accessibility,
119              vrna_pk_plex_opt_t    options);
120
121
132 int **
133 vrna_pk_plex_accessibility(const char *sequence,
134                            unsigned int unpaired,
135                            double      cutoff);
136
137
145 vrna_pk_plex_opt_t
146 vrna_pk_plex_opt_defaults(void);
147
148
159 vrna_pk_plex_opt_t
160 vrna_pk_plex_opt(unsigned int delta,
161                  unsigned int max_interaction_length,
162                  int          pk_penalty);
163
164
176 vrna_pk_plex_opt_t
177 vrna_pk_plex_opt_fun(unsigned int          delta,
178                      unsigned int          max_interaction_length,
179                      vrna_callback_pk_plex_score *scoring_function,
180                      void                    *scoring_data);
181
182
187 #endif

```

## 18.185 PKplex.h

```

1 #ifndef VIENNA_RNA_PACKAGE_PKPLEX_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PKPLEX_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/PKplex.h>! Use <ViennaRNA/pk_plex.h> instead!"
13 # endif
14
15 #ifdef VRNA_WARN_DEPRECATED
16 # if defined(__clang__)
17 #   define DEPRECATED(func, msg) func __attribute__((deprecated(" ", msg)))
18 # elif defined(__GNUC__)
19 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
20 # else
21 #   define DEPRECATED(func, msg) func
22 # endif
23 #else
24 # define DEPRECATED(func, msg) func
25 #endif

```

```

26
27 #include <ViennaRNA/datastructures/basic.h>
28
29
30 DEPRECATED(dupVar *
31 PKLduplexfold_XS(const char *s1,
32                  const int **access_s1,
33                  int penalty,
34                  int max_interaction_length,
35                  int delta),
36          "Use vrna_pk_plex() instead!");
37
38 #include <ViennaRNA/pk_plex.h>
39
40 #endif
41
42 #endif

```

## 18.186 plex.h

```

1 #ifndef VIENNA_RNA_PACKAGE_PLEX_H
2 #define VIENNA_RNA_PACKAGE_PLEX_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5
6 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
7
8 extern int subopt_sorted;
9
13 duplexT** Lduplexfold(const char *s1,
14                      const char *s2,
15                      const int threshold,
16                      const int extension_cost,
17                      const int alignment_length,
18                      const int delta,
19                      const int fast,
20                      const int il_a,
21                      const int il_b,
22                      const int b_a,
23                      const int b_b);
24
28 duplexT** Lduplexfold_XS( const char*s1,
29                          const char* s2,
30                          const int **access_s1,
31                          const int **access_s2,
32                          const int threshold,
33                          const int delta,
34                          const int alignment_length,
35                          const int fast,
36                          const int il_a,
37                          const int il_b,
38                          const int b_a,
39                          const int b_b); /* , const int target_dead, const int query_dead); */
40
44 duplexT** Lduplexfold_C(const char *s1,
45                        const char *s2,
46                        const int threshold,
47                        const int extension_cost,
48                        const int alignment_length,
49                        const int delta,
50                        const int fast,
51                        const char* structure,
52                        const int il_a,
53                        const int il_b,
54                        const int b_a,
55                        const int b_b);
56
61 duplexT** Lduplexfold_CXS(const char*s1,
62                          const char* s2,
63                          const int **access_s1,
64                          const int **access_s2,
65                          const int threshold,
66                          const int delta,
67                          const int alignment_length,
68                          const int fast,
69                          const char* structure,
70                          const int il_a,
71                          const int il_b,
72                          const int b_a,
73                          const int b_b); /* , const int target_dead, const int query_dead); */
74
75
76
77
78 int      arraySize(duplexT** array);

```

```
79 void      freeDuplexT(duplexT** array);
80
81 #endif
82
83 #endif
```

## 18.187 ViennaRNA/plot\_aln.h File Reference

Use [ViennaRNA/plotting/alignments.h](#) instead.

Include dependency graph for plot\_aln.h:

### 18.187.1 Detailed Description

Use [ViennaRNA/plotting/alignments.h](#) instead.

**Deprecated** Use [ViennaRNA/plotting/alignments.h](#) instead

## 18.188 plot\_aln.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_ALN_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_ALN_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/plot_aln.h>! Use <ViennaRNA/plotting/alignments.h>
    instead!"
13 # endif
14 #include <ViennaRNA/plotting/alignments.h>
15 #endif
16
17 #endif
```

## 18.189 ViennaRNA/plot\_layouts.h File Reference

Use [ViennaRNA/plotting/layouts.h](#) instead.

Include dependency graph for plot\_layouts.h:

### 18.189.1 Detailed Description

Use [ViennaRNA/plotting/layouts.h](#) instead.

**Deprecated** Use [ViennaRNA/plotting/layouts.h](#) instead

## 18.190 plot\_layouts.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_LAYOUTS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_LAYOUTS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/plot_layouts.h>! Use <ViennaRNA/plotting/layouts.h>
    instead!"
13 # endif
14 #include <ViennaRNA/plotting/layouts.h>
15 #endif
16
17 #endif
```

## 18.191 ViennaRNA/plot\_structure.h File Reference

Use [ViennaRNA/plotting/structures.h](#) instead.

Include dependency graph for plot\_structure.h:

### 18.191.1 Detailed Description

Use [ViennaRNA/plotting/structures.h](#) instead.

**Deprecated** Use [ViennaRNA/plotting/structures.h](#) instead

### 18.192 plot\_structure.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_STRUCTURE_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_STRUCTURE_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/plot_structure.h>! Use
    <ViennaRNA/plotting/structures.h> instead!"
13 # endif
14 #include <ViennaRNA/plotting/structures.h>
15 #endif
16
17 #endif
```

### 18.193 ViennaRNA/plot\_utils.h File Reference

Use [ViennaRNA/plotting/utlis.h](#) instead.

Include dependency graph for plot\_utils.h:

#### 18.193.1 Detailed Description

Use [ViennaRNA/plotting/utlis.h](#) instead.

**Deprecated** Use [ViennaRNA/plotting/utlis.h](#) instead

### 18.194 plot\_utils.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/plot_utils.h>! Use <ViennaRNA/plotting/utlis.h>
    instead!"
13 # endif
14 #include <ViennaRNA/plotting/utlis.h>
15 #endif
16
17 #endif
```

### 18.195 ViennaRNA/plotting/alignments.h File Reference

Various functions for plotting Sequence / Structure Alignments.

This graph shows which files directly or indirectly include this file:

#### Functions

- int [vrna\\_file\\_PS\\_aln](#) (const char \*filename, const char \*\*seqs, const char \*\*names, const char \*structure, unsigned int columns)  
*Create an annotated PostScript alignment plot.*
- int [vrna\\_file\\_PS\\_aln\\_slice](#) (const char \*filename, const char \*\*seqs, const char \*\*names, const char \*structure, unsigned int start, unsigned int end, int offset, unsigned int columns)  
*Create an annotated PostScript alignment plot.*
- int [PS\\_color\\_aln](#) (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])

*Produce PostScript sequence alignment color-annotated by consensus structure.*

- int `aliPS_color_aln` (const char \*structure, const char \*filename, const char \*seqs[], const char \*names[])  
*PS\_color\_aln for duplexes.*

### 18.195.1 Detailed Description

Various functions for plotting Sequence / Structure Alignments.

## 18.196 alignments.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_ALN_H
2 #define VIENNA_RNA_PACKAGE_PLOT_ALN_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 int
17 vrna_file_PS_aln(const char *filename,
18                 const char **seqs,
19                 const char **names,
20                 const char *structure,
21                 unsigned int columns);
22
23 int
24 vrna_file_PS_aln_slice(const char *filename,
25                       const char **seqs,
26                       const char **names,
27                       const char *structure,
28                       unsigned int start,
29                       unsigned int end,
30                       int offset,
31                       unsigned int columns);
32
33 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
34
35 DEPRECATED(int PS_color_aln(const char *structure,
36                             const char *filename,
37                             const char *seqs[],
38                             const char *names[]),
39            "Use vrna_file_PS_aln() instead!");
40
41 DEPRECATED(int aliPS_color_aln(const char *structure,
42                                const char *filename,
43                                const char *seqs[],
44                                const char *names[]),
45            "Use vrna_file_PS_aln() instead!");
46
47 #endif
48 #endif
```

## 18.197 ViennaRNA/utils/alignments.h File Reference

Various utility- and helper-functions for sequence alignments and comparative structure prediction.

Include dependency graph for alignments.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct `vrna_pinfo_s`  
*A base pair info structure. [More...](#)*

## Macros

- `#define VRNA_ALN_DEFAULT 0U`  
*Use default alignment settings.*
- `#define VRNA_ALN_RNA 1U`  
*Convert to RNA alphabet.*
- `#define VRNA_ALN_DNA 2U`  
*Convert to DNA alphabet.*
- `#define VRNA_ALN_UPPERCASE 4U`  
*Convert to uppercase nucleotide letters.*
- `#define VRNA_ALN_LOWERCASE 8U`  
*Convert to lowercase nucleotide letters.*
- `#define VRNA_MEASURE_SHANNON_ENTROPY 1U`  
*Flag indicating Shannon Entropy measure.*

## Typedefs

- `typedef struct vrna_pinfo_s vrna_pinfo_t`  
*Typename for the base pair info representing data structure `vrna_pinfo_s`.*
- `typedef struct vrna_pinfo_s pair_info`  
*Old typename of `vrna_pinfo_s`.*

## Functions

- `int vrna_aln_mpi (const char **alignment)`  
*Get the mean pairwise identity in steps from ?to?(ident)*
- `vrna_pinfo_t * vrna_aln_pinfo (vrna_fold_compound_t *vc, const char *structure, double threshold)`  
*Retrieve an array of `vrna_pinfo_t` structures from precomputed pair probabilities.*
- `char ** vrna_aln_slice (const char **alignment, unsigned int i, unsigned int j)`  
*Slice out a subalignment from a larger alignment.*
- `void vrna_aln_free (char **alignment)`  
*Free memory occupied by a set of aligned sequences.*
- `char ** vrna_aln_uppercase (const char **alignment)`  
*Create a copy of an alignment with only uppercase letters in the sequences.*
- `char ** vrna_aln_toRNA (const char **alignment)`  
*Create a copy of an alignment where DNA alphabet is replaced by RNA alphabet.*
- `char ** vrna_aln_copy (const char **alignment, unsigned int options)`  
*Make a copy of a multiple sequence alignment.*
- `float * vrna_aln_conservation_struct (const char **alignment, const char *structure, const vrna_md_t *md)`  
*Compute base pair conservation of a consensus structure.*
- `float * vrna_aln_conservation_col (const char **alignment, const vrna_md_t *md_p, unsigned int options)`  
*Compute nucleotide conservation in an alignment.*
- `char * vrna_aln_consensus_sequence (const char **alignment, const vrna_md_t *md_p)`  
*Compute the consensus sequence for a given multiple sequence alignment.*
- `char * vrna_aln_consensus_mis (const char **alignment, const vrna_md_t *md_p)`  
*Compute the Most Informative Sequence (MIS) for a given multiple sequence alignment.*
- `int get_mpi (char *Aseq[], int n_seq, int length, int *mini)`  
*Get the mean pairwise identity in steps from ?to?(ident)*
- `void encode_aln_sequence (const char *sequence, short *S, short *s5, short *s3, char *ss, unsigned short *as, int circ)`  
*Get arrays with encoded sequence of the alignment.*



- void [alloc\\_sequence\\_arrays](#) (const char \*\*sequences, short \*\*\*S, short \*\*\*S5, short \*\*\*S3, unsigned short \*\*\*a2s, char \*\*\*Ss, int circ)

*Allocate memory for sequence array used to deal with aligned sequences.*

- void [free\\_sequence\\_arrays](#) (unsigned int n\_seq, short \*\*\*S, short \*\*\*S5, short \*\*\*S3, unsigned short \*\*\*a2s, char \*\*\*Ss)

*Free the memory of the sequence arrays used to deal with aligned sequences.*

### 18.197.1 Detailed Description

Various utility- and helper-functions for sequence alignments and comparative structure prediction.

## 18.198 alignments.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_ALN_UTIL_H
2 #define VIENNA_RNA_PACKAGE_ALN_UTIL_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated("'" msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
29 typedef struct vrna_pinfo_s vrna_pinfo_t;
30
31
35 #define VRNA_ALN_DEFAULT      0U
36
37
41 #define VRNA_ALN_RNA          1U
42
43
47 #define VRNA_ALN_DNA          2U
48
49
53 #define VRNA_ALN_UPPERCASE    4U
54
55
59 #define VRNA_ALN_LOWERCASE    8U
60
66 #define VRNA_MEASURE_SHANNON_ENTROPY 1U
67
68 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
69
70 /* the following typedefs are for backward compatibility only */
71
77 typedef struct vrna_pinfo_s pair_info;
78
79 #endif
80
81 #include <ViennaRNA/fold_compound.h>
82 #include <ViennaRNA/model.h>
83
94 struct vrna_pinfo_s {
95     unsigned i;
96     unsigned j;
97     float p;
98     float ent;
99     short bp[8];
100    char comp;
101 };
102
103
110 int
111 vrna_aln_mpi(const char **alignment);
112
113
127 vrna_pinfo_t *
128 vrna_aln_pinfo(vrna_fold_compound_t *vc,
129                const char *structure,
130                double threshold);
```

```

131
132
133 int *
134 vrna_aln_pscore(const char **alignment,
135                 vrna_md_t *md);
136
137
138 int
139 vrna_pscore(vrna_fold_compound_t *fc,
140             unsigned int i,
141             unsigned int j);
142
143
144 int
145 vrna_pscore_freq(vrna_fold_compound_t *fc,
146                  const unsigned int *frequencies,
147                  unsigned int pairs);
148
149
150 char **
151 vrna_aln_slice(const char **alignment,
152               unsigned int i,
153               unsigned int j);
154
155
156 void
157 vrna_aln_free(char **alignment);
158
159
160 char **
161 vrna_aln_uppercase(const char **alignment);
162
163
164 char **
165 vrna_aln_toRNA(const char **alignment);
166
167
168 char **
169 vrna_aln_copy(const char **alignment,
170              unsigned int options);
171
172
173 float *
174 vrna_aln_conservation_struct(const char **alignment,
175                             const char *structure,
176                             const vrna_md_t *md);
177
178
179 float *
180 vrna_aln_conservation_col(const char **alignment,
181                          const vrna_md_t *md_p,
182                          unsigned int options);
183
184
185 char *
186 vrna_aln_consensus_sequence(const char **alignment,
187                             const vrna_md_t *md_p);
188
189
190 char *
191 vrna_aln_consensus_mis(const char **alignment,
192                       const vrna_md_t *md_p);
193
194
195 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
196
197 #include <stdio.h>
198 DEPRECATED(int read_clustal(FILE *clust,
199                           char *AlignedSeqs[],
200                           char *names[]),
201            "Use vrna_file_msa_read() and vrna_file_msa_read_record() instead");
202
203
204 DEPRECATED(char *consensus(const char *AS[]),
205            "Use vrna_aln_consensus_sequence() instead!");
206
207
208 DEPRECATED(char *consens_mis(const char *AS[]),
209            "Use vrna_aln_consensus_mis() instead!");
210
211
212 DEPRECATED(char *get_ungapped_sequence(const char *seq),
213            "Use vrna_seq_ungapped() instead!");
214
215
216 DEPRECATED(int get_mpi(char *Alseq[],
217                      int n_seq,
218                      int length,
219                      int *mini),

```

```

337         "Use vrna_aln_mpi() instead");
338
339  /*
340  #####
341  # some helper functions that might be useful in the library #
342  #####
343  */
344
360 DEPRECATED(void encode_ali_sequence(const char      *sequence,
361                                     short            *S,
362                                     short            *s5,
363                                     short            *s3,
364                                     char             *ss,
365                                     unsigned short  *as,
366                                     int              circ),
367         "This function is obsolete");
368
369
386 DEPRECATED(void alloc_sequence_arrays(const char      **sequences,
387                                       short            ***S,
388                                       short            ***s5,
389                                       short            ***s3,
390                                       unsigned short  ***a2s,
391                                       char             ***ss,
392                                       int              circ),
393         "This function is obsolete");
394
395
411 DEPRECATED(void free_sequence_arrays(unsigned int      n_seq,
412                                       short            ***S,
413                                       short            ***s5,
414                                       short            ***s3,
415                                       unsigned short  ***a2s,
416                                       char             ***ss),
417         "This fuction is obsolete");
418
419 #endif
420
426 #endif

```

## 18.199 ViennaRNA/plotting/layouts.h File Reference

Secondary structure plot layout algorithms.

Include dependency graph for layouts.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_plot\\_layout\\_s](#)
- struct [COORDINATE](#)

*this is a workaround for the SWIG Perl Wrapper RNA plot function that returns an array of type [COORDINATE](#) [More...](#)*

### Macros

- `#define VRNA\_PLOT\_TYPE\_SIMPLE 0`  
*Definition of Plot type simple*
- `#define VRNA\_PLOT\_TYPE\_NAVIEW 1`  
*Definition of Plot type Naview*
- `#define VRNA\_PLOT\_TYPE\_CIRCULAR 2`  
*Definition of Plot type Circular*
- `#define VRNA\_PLOT\_TYPE\_TURTLE 3`  
*Definition of Plot type Turtle [\[24\]](#).*
- `#define VRNA\_PLOT\_TYPE\_PUZZLER 4`  
*Definition of Plot type RNApuzzler [\[24\]](#).*

### Typedefs

- typedef struct [vrna\\_plot\\_layout\\_s](#) [vrna\\_plot\\_layout\\_t](#)  
*RNA secondary structure figure layout.*

## Functions

- `vrna_plot_layout_t * vrna_plot_layout` (const char \*structure, unsigned int plot\_type)  
*Create a layout (coordinates, etc.) for a secondary structure plot.*
- `vrna_plot_layout_t * vrna_plot_layout_simple` (const char \*structure)  
*Create a layout (coordinates, etc.) for a simple secondary structure plot.*
- `vrna_plot_layout_t * vrna_plot_layout_circular` (const char \*structure)  
*Create a layout (coordinates, etc.) for a circular secondary structure plot.*
- `vrna_plot_layout_t * vrna_plot_layout_turtle` (const char \*structure)  
*Create a layout (coordinates, etc.) for a secondary structure plot using the Turtle Algorithm [24].*
- `vrna_plot_layout_t * vrna_plot_layout_puzzler` (const char \*structure, `vrna_plot_options_puzzler_t` \*options)  
*Create a layout (coordinates, etc.) for a secondary structure plot using the RNApuzzler Algorithm [24].*
- void `vrna_plot_layout_free` (`vrna_plot_layout_t` \*layout)  
*Free memory occupied by a figure layout data structure.*
- int `vrna_plot_coords` (const char \*structure, float \*\*x, float \*\*y, int plot\_type)  
*Compute nucleotide coordinates for secondary structure plot.*
- int `vrna_plot_coords_pt` (const short \*pt, float \*\*x, float \*\*y, int plot\_type)  
*Compute nucleotide coordinates for secondary structure plot.*
- int `vrna_plot_coords_simple` (const char \*structure, float \*\*x, float \*\*y)  
*Compute nucleotide coordinates for secondary structure plot the Simple way*
- int `vrna_plot_coords_simple_pt` (const short \*pt, float \*\*x, float \*\*y)  
*Compute nucleotide coordinates for secondary structure plot the Simple way*
- int `vrna_plot_coords_circular` (const char \*structure, float \*\*x, float \*\*y)  
*Compute coordinates of nucleotides mapped in equal distances onto a unit circle.*
- int `vrna_plot_coords_circular_pt` (const short \*pt, float \*\*x, float \*\*y)  
*Compute nucleotide coordinates for a Circular Plot*
- int `simple_xy_coordinates` (short \*pair\_table, float \*X, float \*Y)  
*Calculate nucleotide coordinates for secondary structure plot the Simple way*
- int `simple_circplot_coordinates` (short \*pair\_table, float \*x, float \*y)  
*Calculate nucleotide coordinates for Circular Plot*

## Variables

- int `rna_plot_type`  
*Switch for changing the secondary structure layout algorithm.*

### 18.199.1 Detailed Description

Secondary structure plot layout algorithms.

## 18.200 layouts.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PLOT_LAYOUTS_H
2 #define VIENNA_RNA_PACKAGE_PLOT_LAYOUTS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #  define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
36 typedef struct vrna_plot_layout_s vrna_plot_layout_t;
```

```

37
38
39 #include <ViennaRNA/datastructures/basic.h>
40
41 #ifndef VRNA_WITH_NAVIEW_LAYOUT
42 #include <ViennaRNA/plotting/naview/naview.h>
43 #endif
44
45 #include "ViennaRNA/plotting/RNApuzzler/RNAturtle.h"
46 #include "ViennaRNA/plotting/RNApuzzler/RNApuzzler.h"
47
48
49 #define VRNA_PLOT_TYPE_SIMPLE      0
50
51 #define VRNA_PLOT_TYPE_NAVIEW      1
52
53 #define VRNA_PLOT_TYPE_CIRCULAR    2
54
55 #define VRNA_PLOT_TYPE_TURTLE      3
56
57 #define VRNA_PLOT_TYPE_PUZZLER     4
58
59 #ifndef VRNA_WITH_NAVIEW_LAYOUT
60 # define VRNA_PLOT_TYPE_DEFAULT    VRNA_PLOT_TYPE_NAVIEW
61 #else
62 # define VRNA_PLOT_TYPE_DEFAULT    VRNA_PLOT_TYPE_PUZZLER
63 #endif
64
65
66 struct vrna_plot_layout_s {
67     unsigned int  length;
68     float         *x;
69     float         *y;
70     double        *arcs;
71     int           bbox[4];
72 };
73
74 vrna_plot_layout_t *
75 vrna_plot_layout(const char *structure,
76                 unsigned int plot_type);
77
78 vrna_plot_layout_t *
79 vrna_plot_layout_simple(const char *structure);
80
81 #ifndef VRNA_WITH_NAVIEW_LAYOUT
82 vrna_plot_layout_t *
83 vrna_plot_layout_naview(const char *structure);
84 #endif
85
86 vrna_plot_layout_t *
87 vrna_plot_layout_circular(const char *structure);
88
89 vrna_plot_layout_t *
90 vrna_plot_layout_turtle(const char *structure);
91
92 vrna_plot_layout_t *
93 vrna_plot_layout_puzzler(const char *structure,
94                          vrna_plot_options_puzzler_t *options);
95
96 void
97 vrna_plot_layout_free(vrna_plot_layout_t *layout);
98
99 int
100 vrna_plot_coords(const char *structure,
101                 float **x,
102                 float **y,
103                 int plot_type);
104
105 int
106 vrna_plot_coords_pt(const short *pt,
107                   float **x,
108                   float **y,
109                   int plot_type);
110
111 int
112 vrna_plot_coords_simple(const char *structure,
113                       float **x,
114                       float **y);

```

```

360
361
380 int
381 vrna_plot_coords_simple_pt(const short *pt,
382                             float      **x,
383                             float      **y);
384
385
416 int
417 vrna_plot_coords_circular(const char *structure,
418                           float      **x,
419                           float      **y);
420
421
440 int
441 vrna_plot_coords_circular_pt(const short *pt,
442                              float      **x,
443                              float      **y);
444
445
451 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
452
463 typedef struct {
464     float X; /* X coords */
465     float Y; /* Y coords */
466 } COORDINATE;
467
468
481 extern int rna_plot_type;
482
483
497 DEPRECATED(int
498             simple_xy_coordinates(short *pair_table,
499                                   float *X,
500                                   float *Y),
501             "Use vrna_plot_coords_simple_pt() instead!");
502
503
526 DEPRECATED(int
527             simple_circplot_coordinates(short *pair_table,
528   float *X,
529   float *Y),
530             "Use vrna_plot_coords_circular_pt() instead!");
531
532
537 #endif
538
539
540 #endif

```

## 18.201 ViennaRNA/plotting/probabilities.h File Reference

Various functions for plotting RNA secondary structures, dot-plots and other visualizations.

Include dependency graph for probabilities.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_dotplot\\_auxdata\\_t](#)

### Functions

- int [PS\\_dot\\_plot\\_list](#) (char \*seq, char \*filename, [vrna\\_ep\\_t](#) \*pl, [vrna\\_ep\\_t](#) \*mf, char \*comment)  
*Produce a postscript dot-plot from two pair lists.*
- int [PS\\_dot\\_plot](#) (char \*string, char \*file)  
*Produce postscript dot-plot.*

#### 18.201.1 Detailed Description

Various functions for plotting RNA secondary structures, dot-plots and other visualizations.

## 18.202 probabilities.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PLOT_PROBABILITIES_H
2 #define VIENNA_RNA_PACKAGE_PLOT_PROBABILITIES_H
3
4
5 #include <ViennaRNA/datastructures/basic.h>
6 #include <ViennaRNA/utils/structures.h>
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(__clang__)
10 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
11 # elif defined(__GNUC__)
12 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
13 # else
14 #  define DEPRECATED(func, msg) func
15 # endif
16 #else
17 # define DEPRECATED(func, msg) func
18 #endif
19
20 #define VRNA_PLOT_PROBABILITIES_BP 1U
21 #define VRNA_PLOT_PROBABILITIES_ACC 2U
22
23 #define VRNA_PLOT_PROBABILITIES_UD 4U
24 #define VRNA_PLOT_PROBABILITIES_UD_LIN 8U
25
26 #define VRNA_PLOT_PROBABILITIES_SD 16U
27
28 #define VRNA_PLOT_PROBABILITIES_SC_MOTIF 32U
29 #define VRNA_PLOT_PROBABILITIES_SC_UP 64U
30 #define VRNA_PLOT_PROBABILITIES_SC_BP 128U
31
32 #define VRNA_PLOT_PROBABILITIES_DEFAULT (VRNA_PLOT_PROBABILITIES_BP \
33 | VRNA_PLOT_PROBABILITIES_SD \
34 | VRNA_PLOT_PROBABILITIES_SC_MOTIF \
35 | VRNA_PLOT_PROBABILITIES_UD_LIN)
36
37 typedef struct {
38     char *comment;
39     char *title;
40
41     vrna_data_lin_t **top;
42     char **top_title;
43
44     vrna_data_lin_t **bottom;
45     char **bottom_title;
46
47     vrna_data_lin_t **left;
48     char **left_title;
49
50     vrna_data_lin_t **right;
51     char **right_title;
52 } vrna_dotplot_auxdata_t;
53
54 int
55 vrna_plot_dp_EPS(const char *filename,
56                  const char *sequence,
57                  vrna_ep_t *upper,
58                  vrna_ep_t *lower,
59                  vrna_dotplot_auxdata_t *auxdata,
60                  unsigned int options);
61
62 int
63 vrna_plot_dp_PS_list(char *seq,
64                      int cp,
65                      char *wastlfile,
66                      vrna_ep_t *pl,
67                      vrna_ep_t *mf,
68                      char *comment);
69
70 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
71
72 int
73 PS_color_dot_plot(char *string,
74                   vrna_cpair_t *pi,
75                   char *filename);
76
77 int
78 PS_color_dot_plot_turn(char *seq,
79                        vrna_cpair_t *pi,
80                        char *filename,
81                        int winSize);
82
83 int

```

```

100 PS_dot_plot_turn(char      *seq,
101                  vrna_ep_t *pl,
102                  char      *filename,
103                  int       winSize);
104
105
125 int PS_dot_plot_list(char      *seq,
126                     char      *filename,
127                     vrna_ep_t *pl,
128                     vrna_ep_t *mf,
129                     char      *comment);
130
131
147 DEPRECATED(int PS_dot_plot(char *string,
148                          char *file),
149             "Use vrna_plot_dp_EPS() instead");
150
151 #endif
152
157 #endif

```

## 18.203 ViennaRNA/plotting/RNApuzzler/RNApuzzler.h File Reference

Implementation of the RNApuzzler RNA secondary structure layout algorithm [24].

This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_plot\\_options\\_puzzler\\_t](#)

*Options data structure for RNApuzzler algorithm implementation. [More...](#)*

### Functions

- int [vrna\\_plot\\_coords\\_puzzler](#) (const char \*structure, float \*\*x, float \*\*y, double \*\*arc\_coords, [vrna\\_plot\\_options\\_puzzler\\_t](#) \*options)

*Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].*

- int [vrna\\_plot\\_coords\\_puzzler\\_pt](#) (short const \*const pair\_table, float \*\*x, float \*\*y, double \*\*arc\_coords, [vrna\\_plot\\_options\\_puzzler\\_t](#) \*puzzler)

*Compute nucleotide coordinates for secondary structure plot using the RNApuzzler algorithm [24].*

- [vrna\\_plot\\_options\\_puzzler\\_t](#) \* [vrna\\_plot\\_options\\_puzzler](#) (void)

*Create an RNApuzzler options data structure.*

- void [vrna\\_plot\\_options\\_puzzler\\_free](#) ([vrna\\_plot\\_options\\_puzzler\\_t](#) \*options)

*Free memory occupied by an RNApuzzler options data structure.*

### 18.203.1 Detailed Description

Implementation of the RNApuzzler RNA secondary structure layout algorithm [24].

## 18.204 RNApuzzler.h

[Go to the documentation of this file.](#)

```

1 #ifndef RNAPUZZLER_H
2 #define RNAPUZZLER_H
3
20 typedef struct {
21     /*
22      * variables fixed during operation
23      * drawing behavior
24      */
25     short    drawArcs;
26     double   paired;
27     double   unpaired;
28
29     /* intersection resolution behavior */
30     short    checkAncestorIntersections;
31     short    checkSiblingIntersections;
32     short    checkExteriorIntersections;

```



```

33  short      allowFlipping;
34  short      optimize;
35  int         maximumNumberOfConfigChangesAllowed;
36
37
38  /* import behavior - unused for now */
39  char        *config; /* file path */
40
41  /* other stuff */
42  const char  *filename;
43
44  /* variables changed during operation */
45  int         numberOfChangesAppliedToConfig;
46  int         psNumber;
47 } vrna_plot_options_puzzler_t;
48
49
87 int
88 vrna_plot_coords_puzzler(const char      *structure,
89                          float          **x,
90                          float          **y,
91                          double         **arc_coords,
92                          vrna_plot_options_puzzler_t *options);
93
94
115 int
116 vrna_plot_coords_puzzler_pt(short const *const pair_table,
117                             float       **x,
118                             float       **y,
119                             double      **arc_coords,
120                             vrna_plot_options_puzzler_t *puzzler);
121
122
131 vrna_plot_options_puzzler_t *
132 vrna_plot_options_puzzler(void);
133
134
143 void
144 vrna_plot_options_puzzler_free(vrna_plot_options_puzzler_t *options);
145
146
152 #endif

```

## 18.205 ViennaRNA/plotting/RNApuzzler/RNAturtle.h File Reference

Implementation of the RNAturtle RNA secondary structure layout algorithm [24].

This graph shows which files directly or indirectly include this file:

### Functions

- int [vrna\\_plot\\_coords\\_turtle](#) (const char \*structure, float \*\*x, float \*\*y, double \*\*arc\_coords)  
Compute nucleotide coordinates for secondary structure plot using the RNAturtle algorithm [24].
- int [vrna\\_plot\\_coords\\_turtle\\_pt](#) (short const \*const pair\_table, float \*\*x, float \*\*y, double \*\*arc\_coords)  
Compute nucleotide coordinates for secondary structure plot using the RNAturtle algorithm [24].

### 18.205.1 Detailed Description

Implementation of the RNAturtle RNA secondary structure layout algorithm [24].

## 18.206 RNAturtle.h

[Go to the documentation of this file.](#)

```

1  #ifndef RNATURTLE_H
2  #define RNATURTLE_H
3
52 int
53 vrna_plot_coords_turtle(const char  *structure,
54                         float       **x,
55                         float       **y,
56                         double      **arc_coords);
57
58
78 int
79 vrna_plot_coords_turtle_pt(short const *const pair_table,

```

```

80             float          **x,
81             float          **y,
82             double         **arc_coords);
83
84
89 #endif

```

## 18.207 ViennaRNA/plotting/structures.h File Reference

Various functions for plotting RNA secondary structures.

Include dependency graph for structures.h: This graph shows which files directly or indirectly include this file:

### Functions

- `int vrna_file_PS_rnaplot` (const char \*seq, const char \*structure, const char \*file, `vrna_md_t` \*md\_p)  
*Produce a secondary structure graph in PostScript and write it to 'filename'.*
- `int vrna_file_PS_rnaplot_a` (const char \*seq, const char \*structure, const char \*file, const char \*pre, const char \*post, `vrna_md_t` \*md\_p)  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.*
- `int gmlRNA` (char \*string, char \*structure, char \*ssfile, char option)  
*Produce a secondary structure graph in Graph Meta Language (gml) and write it to a file.*
- `int ssv_rna_plot` (char \*string, char \*structure, char \*ssfile)  
*Produce a secondary structure graph in SStructView format.*
- `int svg_rna_plot` (char \*string, char \*structure, char \*ssfile)  
*Produce a secondary structure plot in SVG format and write it to a file.*
- `int xrna_plot` (char \*string, char \*structure, char \*ssfile)  
*Produce a secondary structure plot for further editing in XRNA.*
- `int PS_rna_plot` (char \*string, char \*structure, char \*file)  
*Produce a secondary structure graph in PostScript and write it to 'filename'.*
- `int PS_rna_plot_a` (char \*string, char \*structure, char \*file, char \*pre, char \*post)  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename'.*
- `int PS_rna_plot_a_gquad` (char \*string, char \*structure, char \*ssfile, char \*pre, char \*post)  
*Produce a secondary structure graph in PostScript including additional annotation macros and write it to 'filename' (detect and draw g-quadruplexes)*

### 18.207.1 Detailed Description

Various functions for plotting RNA secondary structures.

## 18.208 structures.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PLOT_STRUCTURE_H
2 #define VIENNA_RNA_PACKAGE_PLOT_STRUCTURE_H
3
4 #include <ViennaRNA/model.h>
5 #include <ViennaRNA/plotting/layouts.h>
6 #include "ViennaRNA/plotting/RNApuzzler/RNApuzzler.h"
7
8 #ifdef VRNA_WARN_DEPRECATED
9 # if defined(__clang__)
10 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
11 # elif defined(__GNUC__)
12 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
13 # else
14 #  define DEPRECATED(func, msg) func
15 # endif
16 #else
17 # define DEPRECATED(func, msg) func
18 #endif
19
20 int
21 vrna_file_PS_rnaplot(const char *seq,

```

```

46         const char *structure,
47         const char *file,
48         vrna_md_t  *md_p);
49
50
51 int vrna_file_PS_rnaplot_a( const char      *seq,
52                             const char      *structure,
53                             const char      *file,
54                             const char      *pre,
55                             const char      *post,
56                             vrna_md_t      *md_p);
57
58
59 int
60 vrna_file_PS_rnaplot_layout(const char      *seq,
61                             const char      *structure,
62                             const char      *ssfile,
63                             const char      *pre,
64                             const char      *post,
65                             vrna_md_t      *md_p,
66                             vrna_plot_layout_t *layout);
67
68 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
69
70 /* write PostScript drawing of structure to file with annotation */
71 int
72 PS_rna_plot_snoop_a(const char *string,
73                     const char *structure,
74                     const char *ssfile,
75                     int         *relative_access,
76                     const char *seqs[]);
77
78
79 int
80 gmlRNA(char *string,
81         char *structure,
82         char *ssfile,
83         char option);
84
85
86 int
87 ssv_rna_plot(char *string,
88              char *structure,
89              char *ssfile);
90
91
92 int
93 svg_rna_plot(char *string,
94              char *structure,
95              char *ssfile);
96
97
98 int
99 xrna_plot(char *string,
100           char *structure,
101           char *ssfile);
102
103 DEPRECATED(int PS_rna_plot(char *string,
104                             char *structure,
105                             char *file),
106            "Use vrna_file_PS_rnaplot() instead");
107
108 DEPRECATED(int PS_rna_plot_a(char *string,
109                              char *structure,
110                              char *file,
111                              char *pre,
112                              char *post),
113            "Use vrna_file_PS_rnaplot_a() instead");
114
115 DEPRECATED(int PS_rna_plot_a_gquad(char *string,
116                                    char *structure,
117                                    char *ssfile,
118                                    char *pre,
119                                    char *post),
120            "Use vrna_file_PS_rnaplot_a() instead");
121
122 #endif
123 #endif

```

## 18.209 ViennaRNA/utils/structures.h File Reference

Various utility- and helper-functions for secondary structure parsing, converting, etc.

Include dependency graph for structures.h: This graph shows which files directly or indirectly include this file:

## Data Structures

- struct [vrna\\_elem\\_prob\\_s](#)  
Data structure representing a single entry of an element probability list (e.g. list of pair probabilities) [More...](#)
- struct [vrna\\_hx\\_s](#)  
Data structure representing an entry of a helix list. [More...](#)

## Macros

- **#define** [VRNA\\_BRACKETS\\_ALPHA](#) 4U  
Bitflag to indicate secondary structure notations using uppercase/lowercase letters from the latin alphabet.
- **#define** [VRNA\\_BRACKETS\\_RND](#) 8U  
Bitflag to indicate secondary structure notations using round brackets (parenthesis), ( )
- **#define** [VRNA\\_BRACKETS\\_CLY](#) 16U  
Bitflag to indicate secondary structure notations using curly brackets, { }
- **#define** [VRNA\\_BRACKETS\\_ANG](#) 32U  
Bitflag to indicate secondary structure notations using angular brackets, < >
- **#define** [VRNA\\_BRACKETS\\_SQR](#) 64U  
Bitflag to indicate secondary structure notations using square brackets, [ ]
- **#define** [VRNA\\_BRACKETS\\_DEFAULT](#)  
Default bitmask to indicate secondary structure notation using any pair of brackets.
- **#define** [VRNA\\_BRACKETS\\_ANY](#)  
Bitmask to indicate secondary structure notation using any pair of brackets or uppercase/lowercase alphabet letters.
- **#define** [VRNA\\_PLIST\\_TYPE\\_BASEPAIR](#) 0  
A Base Pair element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_GQUAD](#) 1  
A G-Quadruplex element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_H\\_MOTIF](#) 2  
A Hairpin loop motif element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_I\\_MOTIF](#) 3  
An Internal loop motif element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_UD\\_MOTIF](#) 4  
An Unstructured Domain motif element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_STACK](#) 5  
A Base Pair stack element.
- **#define** [VRNA\\_PLIST\\_TYPE\\_UNPAIRED](#) 6  
An unpaired base.
- **#define** [VRNA\\_PLIST\\_TYPE\\_TRIPLE](#) 7  
One pair of a base triplet.
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_HIT](#) 1U  
Homeomorphically Irreducible [Tree](#) (HIT) representation of a secondary structure.
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_SHORT](#) 2U  
(short) Coarse Grained representation of a secondary structure
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO](#) 3U  
(full) Coarse Grained representation of a secondary structure
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_EXT](#) 4U  
(extended) Coarse Grained representation of a secondary structure
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_SHAPIRO\\_WEIGHT](#) 5U  
(weighted) Coarse Grained representation of a secondary structure
- **#define** [VRNA\\_STRUCTURE\\_TREE\\_EXPANDED](#) 6U  
Expanded [Tree](#) representation of a secondary structure.

## Typedefs

- typedef struct [vrna\\_hx\\_s](#) [vrna\\_hx\\_t](#)  
*Convenience typedef for data structure [vrna\\_hx\\_s](#).*
- typedef struct [vrna\\_elem\\_prob\\_s](#) [vrna\\_ep\\_t](#)  
*Convenience typedef for data structure [vrna\\_elem\\_prob\\_s](#).*

## Functions

- char \* [vrna\\_db\\_pack](#) (const char \*struc)  
*Pack secondary structure, 5:1 compression using base 3 encoding.*
- char \* [vrna\\_db\\_unpack](#) (const char \*packed)  
*Unpack secondary structure previously packed with [vrna\\_db\\_pack\(\)](#)*
- void [vrna\\_db\\_flatten](#) (char \*structure, unsigned int options)  
*Substitute pairs of brackets in a string with parenthesis.*
- void [vrna\\_db\\_flatten\\_to](#) (char \*string, const char target[3], unsigned int options)  
*Substitute pairs of brackets in a string with another type of pair characters.*
- char \* [vrna\\_db\\_from\\_ptable](#) (const short \*pt)  
*Convert a pair table into dot-parenthesis notation.*
- char \* [vrna\\_db\\_from\\_plist](#) ([vrna\\_ep\\_t](#) \*pairs, unsigned int n)  
*Convert a list of base pairs into dot-bracket notation.*
- char \* [vrna\\_db\\_to\\_element\\_string](#) (const char \*structure)  
*Convert a secondary structure in dot-bracket notation to a nucleotide annotation of loop contexts.*
- char \* [vrna\\_db\\_pk\\_remove](#) (const char \*structure, unsigned int options)  
*Remove pseudo-knots from an input structure.*
- short \* [vrna\\_ptable](#) (const char \*structure)  
*Create a pair table from a dot-bracket notation of a secondary structure.*
- short \* [vrna\\_ptable\\_from\\_string](#) (const char \*structure, unsigned int options)  
*Create a pair table for a secondary structure string.*
- short \* [vrna\\_pt\\_pk\\_get](#) (const char \*structure)  
*Create a pair table of a secondary structure (pseudo-knot version)*
- short \* [vrna\\_ptable\\_copy](#) (const short \*pt)  
*Get an exact copy of a pair table.*
- short \* [vrna\\_pt\\_ali\\_get](#) (const char \*structure)  
*Create a pair table of a secondary structure (snoop align version)*
- short \* [vrna\\_pt\\_snoop\\_get](#) (const char \*structure)  
*Create a pair table of a secondary structure (snoop version)*
- short \* [vrna\\_pt\\_pk\\_remove](#) (const short \*ptable, unsigned int options)  
*Remove pseudo-knots from a pair table.*
- [vrna\\_ep\\_t](#) \* [vrna\\_plist](#) (const char \*struc, float pr)  
*Create a [vrna\\_ep\\_t](#) from a dot-bracket string.*
- [vrna\\_ep\\_t](#) \* [vrna\\_plist\\_from\\_probs](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, double cut\_off)  
*Create a [vrna\\_ep\\_t](#) from base pair probability matrix.*
- char \* [vrna\\_db\\_from\\_WUSS](#) (const char \*wuss)  
*Convert a WUSS annotation string to dot-bracket format.*
- char \* [vrna\\_abstract\\_shapes](#) (const char \*structure, unsigned int level)  
*Convert a secondary structure in dot-bracket notation to its abstract shapes representation.*
- char \* [vrna\\_abstract\\_shapes\\_pt](#) (const short \*pt, unsigned int level)  
*Convert a secondary structure to its abstract shapes representation.*
- [vrna\\_hx\\_t](#) \* [vrna\\_hx\\_from\\_ptable](#) (short \*pt)  
*Convert a pair table representation of a secondary structure into a helix list.*
- [vrna\\_hx\\_t](#) \* [vrna\\_hx\\_merge](#) (const [vrna\\_hx\\_t](#) \*list, int maxdist)

- Create a merged helix list from another helix list.*

  - `int * vrna_loopidx_from_ptable` (const short \*pt)
- Get a loop index representation of a structure.*

  - `int vrna_bp_distance_pt` (const short \*pt1, const short \*pt2)

*Compute the "base pair" distance between two pair tables pt1 and pt2 of secondary structures.*
- `int vrna_bp_distance` (const char \*str1, const char \*str2)

*Compute the "base pair" distance between two secondary structures s1 and s2.*
- `unsigned int * vrna_refBPcnt_matrix` (const short \*reference\_pt, unsigned int turn)

*Make a reference base pair count matrix.*
- `unsigned int * vrna_refBPdist_matrix` (const short \*pt1, const short \*pt2, unsigned int turn)

*Make a reference base pair distance matrix.*
- `char * vrna_db_from_probs` (const FLT\_OR\_DBL \*pr, unsigned int length)

*Create a dot-bracket like structure string from base pair probability matrix.*
- `char vrna_bpp_symbol` (const float \*x)

*Get a pseudo dot bracket notation for a given probability information.*
- `char * vrna_db_from_bp_stack` (vrna\_bp\_stack\_t \*bp, unsigned int length)

*Create a dot-bracket/parenthesis structure from backtracking stack.*
- `char * vrna_db_to_tree_string` (const char \*structure, unsigned int type)

*Convert a Dot-Bracket structure string into tree string representation.*
- `char * vrna_tree_string_unweight` (const char \*structure)

*Remove weights from a linear string tree representation of a secondary structure.*
- `char * vrna_tree_string_to_db` (const char \*tree)

*Convert a linear tree string representation of a secondary structure back to Dot-Bracket notation.*
- `void assign_plist_from_db` (vrna\_ep\_t \*\*pl, const char \*struc, float pr)

*Create a vrna\_ep\_t from a dot-bracket string.*
- `char * pack_structure` (const char \*struc)

*Pack secondary secondary structure, 5:1 compression using base 3 encoding.*
- `char * unpack_structure` (const char \*packed)

*Unpack secondary structure previously packed with pack\_structure()*
- `short * make_pair_table` (const char \*structure)

*Create a pair table of a secondary structure.*
- `short * copy_pair_table` (const short \*pt)

*Get an exact copy of a pair table.*
- `short * alimake_pair_table` (const char \*structure)
- `short * make_pair_table_snoop` (const char \*structure)
- `int bp_distance` (const char \*str1, const char \*str2)

*Compute the "base pair" distance between two secondary structures s1 and s2.*
- `unsigned int * make_referenceBP_array` (short \*reference\_pt, unsigned int turn)

*Make a reference base pair count matrix.*
- `unsigned int * compute_BPdifferences` (short \*pt1, short \*pt2, unsigned int turn)

*Make a reference base pair distance matrix.*
- `void assign_plist_from_pr` (vrna\_ep\_t \*\*pl, FLT\_OR\_DBL \*probs, int length, double cutoff)

*Create a vrna\_ep\_t from a probability matrix.*
- `void parenthesis_structure` (char \*structure, vrna\_bp\_stack\_t \*bp, int length)

*Create a dot-bracket/parenthesis structure from backtracking stack.*
- `void parenthesis_zuker` (char \*structure, vrna\_bp\_stack\_t \*bp, int length)

*Create a dot-bracket/parenthesis structure from backtracking stack obtained by Zuker suboptimal calculation in cofold.c.*
- `void bppm_to_structure` (char \*structure, FLT\_OR\_DBL \*pr, unsigned int length)

*Create a dot-bracket like structure string from base pair probability matrix.*
- `char bppm_symbol` (const float \*x)

*Get a pseudo dot bracket notation for a given probability information.*

### 18.209.1 Detailed Description

Various utility- and helper-functions for secondary structure parsing, converting, etc.

## 18.210 structures.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_STRUCT_UTILS_H
2 #define VIENNA_RNA_PACKAGE_STRUCT_UTILS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__ ((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16
17
18
19
20
21
22
23 typedef struct vrna_hx_s vrna_hx_t;
24
25
26
27
28 typedef struct vrna_elem_prob_s vrna_ep_t;
29
30
31
32
33
34
35
36
37 #define VRNA_BRACKETS_ALPHA      4U
38
39
40
41
42
43
44 #define VRNA_BRACKETS_RND        8U
45
46
47
48
49
50
51 #define VRNA_BRACKETS_CLY        16U
52
53
54
55
56
57
58 #define VRNA_BRACKETS_ANG        32U
59
60
61
62
63
64
65 #define VRNA_BRACKETS_SQR        64U
66
67
68
69
70
71
72 #define VRNA_BRACKETS_DEFAULT \
73     (VRNA_BRACKETS_RND | \
74      VRNA_BRACKETS_CLY | \
75      VRNA_BRACKETS_ANG | \
76      VRNA_BRACKETS_SQR)
77
78
79
80
81
82
83 #define VRNA_BRACKETS_ANY \
84     (VRNA_BRACKETS_RND | \
85      VRNA_BRACKETS_CLY | \
86      VRNA_BRACKETS_ANG | \
87      VRNA_BRACKETS_SQR | \
88      VRNA_BRACKETS_ALPHA)
89
90
91
92
93
94
95
96
97 #include <stdio.h>
98
99
100 #include <ViennaRNA/datastructures/basic.h>
101
102
103 char *
104 vrna_db_pack(const char *struc);
105
106
107
108
109 char *
110 vrna_db_unpack(const char *packed);
111
112
113
114
115 void
116 vrna_db_flatten(char          *structure,
117                unsigned int  options);
118
119
120
121
122 void
123 vrna_db_flatten_to(char          *string,
124                   const char  target[3],
125                   unsigned int  options);
126
127
128
129
130 char *
131 vrna_db_from_ptable(const short *pt);
132
133

```

```
239
240 char *
241 vrna_db_from_plist(vrna_ep_t *pairs,
242                  unsigned int n);
243
244 char *
245 vrna_db_to_element_string(const char *structure);
246
247 char *
248 vrna_db_pk_remove(const char *structure,
249                  unsigned int options);
250
251 /* End dot-bracket interface */
252 short *
253 vrna_ptable(const char *structure);
254
255 short *
256 vrna_ptable_from_string(const char *structure,
257                        unsigned int options);
258
259 short *
260 vrna_pt_pk_get(const char *structure);
261
262 short *
263 vrna_ptable_copy(const short *pt);
264
265 short *
266 vrna_pt_ali_get(const char *structure);
267
268 short *
269 vrna_pt_snoop_get(const char *structure);
270
271 short *
272 vrna_pt_pk_remove(const short *ptable,
273                  unsigned int options);
274
275 /* End pair table interface */
276 #define VRNA_PLIST_TYPE_BASEPAIR 0
277
278 #define VRNA_PLIST_TYPE_GQUAD 1
279
280 #define VRNA_PLIST_TYPE_H_MOTIF 2
281
282 #define VRNA_PLIST_TYPE_I_MOTIF 3
283
284 #define VRNA_PLIST_TYPE_UD_MOTIF 4
285
286 #define VRNA_PLIST_TYPE_STACK 5
287
288 #define VRNA_PLIST_TYPE_UNPAIRED 6
289
290 #define VRNA_PLIST_TYPE_TRIPLE 7
291
292 struct vrna_elem_prob_s {
293     int i;
294     int j;
295     float p;
296     int type;
297 };
298
299 vrna_ep_t *vrna_plist(const char *struc,
300                      float pr);
301
302 vrna_ep_t *vrna_plist_from_probs(vrna_fold_compound_t *vc,
303                                  double cut_off);
304
305 /* End pair list interface */
306 char *
```



```

597 vrna_db_from_WUSS(const char *wuss);
598
599
600 /* End WUSS notation interface */
601 char *
602 vrna_abstract_shapes(const char *structure,
603                     unsigned int level);
604
605
606 char *
607 vrna_abstract_shapes_pt(const short *pt,
608                       unsigned int level);
609
610
611 /* End abstract shapes interface */
612 struct vrna_hx_s {
613     unsigned int start;
614     unsigned int end;
615     unsigned int length;
616     unsigned int up5;
617     unsigned int up3;
618 };
619
620 vrna_hx_t *
621 vrna_hx_from_ptable(short *pt);
622
623
624 vrna_hx_t *
625 vrna_hx_merge(const vrna_hx_t *list,
626              int maxdist);
627
628
629 /* End helix list interface */
630 int *
631 vrna_loopidx_from_ptable(const short *pt);
632
633
634 int
635 vrna_bp_distance_pt(const short *pt1,
636                   const short *pt2);
637
638
639 int
640 vrna_bp_distance(const char *str1,
641                 const char *str2);
642
643
644 double
645 vrna_dist_mountain(const char *str1,
646                  const char *str2,
647                  unsigned int p);
648
649
650 /* End metrics interface */
651 unsigned int *
652 vrna_refBPcnt_matrix(const short *reference_pt,
653                    unsigned int turn);
654
655
656 unsigned int *
657 vrna_refBPdist_matrix(const short *pt1,
658                     const short *pt2,
659                     unsigned int turn);
660
661
662 char *
663 vrna_db_from_probs(const FLT_OR_DBL *pr,
664                  unsigned int length);
665
666
667 char
668 vrna_bpp_symbol(const float *x);
669
670
671 char *
672 vrna_db_from_bp_stack(vrna_bp_stack_t *bp,
673                     unsigned int length);
674
675
676 void
677 vrna_letter_structure(char *structure,
678                    vrna_bp_stack_t *bp,
679                    unsigned int length);
680
681
682 #define VRNA_STRUCTURE_TREE_HIT 1U
683
684

```

```

921
922 #define VRNA_STRUCTURE_TREE_SHAPIRO_SHORT 2U
923
924
925
926 #define VRNA_STRUCTURE_TREE_SHAPIRO 3U
927
928
929
930 #define VRNA_STRUCTURE_TREE_SHAPIRO_EXT 4U
931
932
933
934 #define VRNA_STRUCTURE_TREE_SHAPIRO_WEIGHT 5U
935
936
937
938 #define VRNA_STRUCTURE_TREE_EXPANDED 6U
939
940
941
942 char *
943 vrna_db_to_tree_string(const char *structure,
944                       unsigned int type);
945
946
947
948 char *
949 vrna_tree_string_unweight(const char *structure);
950
951
952
953 char *
954 vrna_tree_string_to_db(const char *tree);
955
956
957
958 /* End tree representations */
959 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
960
961 /*****
962  * deprecated functions below
963  *****/
964
965 DEPRECATED(void assign_plist_from_db(vrna_ep_t **pl,
966                                     const char *struc,
967                                     float pr),
968           "Use vrna_plist() instead");
969
970 DEPRECATED(char *pack_structure(const char *struc),
971           "Use vrna_db_pack() instead");
972
973 DEPRECATED(char *unpack_structure(const char *packed),
974           "Use vrna_db_unpack() instead");
975
976 DEPRECATED(short *make_pair_table(const char *structure),
977           "Use vrna_ptable() instead");
978
979 DEPRECATED(short *make_pair_table_pk(const char *structure),
980           "Use vrna_ptable_from_string() instead");
981
982 DEPRECATED(short *copy_pair_table(const short *pt),
983           "Use vrna_ptable_copy() instead");
984
985 DEPRECATED(short *alimake_pair_table(const char *structure),
986           "Use vrna_pt_ali_get() instead");
987
988 DEPRECATED(short *make_pair_table_snoop(const char *structure),
989           "Use vrna_pt_snoop_get() instead");
990
991 DEPRECATED(int *make_loop_index_pt(short *pt),
992           "Use vrna_loopidx_from_ptable() instead");
993
994 DEPRECATED(int bp_distance(const char *str1,
995                             const char *str2),
996           "Use vrna_bp_distance() instead");
997
998 DEPRECATED(unsigned int *make_referenceBP_array(short *reference_pt,
999  unsigned int turn),
1000           "Use vrna_refBPcnt_matrix() instead");
1001
1002 DEPRECATED(unsigned int *compute_BPdifferences(short *pt1,
1003  short *pt2,
1004  unsigned int turn),
1005           "Use vrna_refBPdist_matrix() instead");
1006
1007 DEPRECATED(void assign_plist_from_pr(vrna_ep_t **pl,
1008                                     FLT_OR_DBL *probs,
1009                                     int length,
1010                                     double cutoff),
1011           "Use vrna_plist_from_probs() instead");
1012
1013 DEPRECATED(void parenthesis_structure(char *structure,
1014                                       vrna_bp_stack_t *bp,
1015                                       int length),
1016           "Use vrna_parenthesis_structure() instead");

```

```

1217
1227 DEPRECATED(void parenthesis_zuker(char          *structure,
1228                                vrna_bp_stack_t *bp,
1229                                int             length),
1230    "Use vrna_parenthesis_zuker() instead");
1231
1232 DEPRECATED(void letter_structure(char          *structure,
1233                                vrna_bp_stack_t *bp,
1234                                int             length),
1235    "Use vrna_letter_structure() instead");
1236
1242 DEPRECATED(void bppm_to_structure(char          *structure,
1243                                FLT_OR_DBL      *pr,
1244                                unsigned int     length),
1245    "Use vrna_db_from_probs() instead");
1246
1252 DEPRECATED(char      bppm_symbol(const float *x),
1253    "Use vrna_bpp_symbol() instead");
1254
1255 #endif
1256
1261 #endif

```

## 18.211 ProfileAln.h

```

1 #ifndef VIENNA_RNA_PACKAGE_PROFILEALN_H
2 #define VIENNA_RNA_PACKAGE_PROFILEALN_H
3
4 float profile_aln(const float *T1,
5                  const char  *seq1,
6                  const float *T2,
7                  const char  *seq2);
8
9
10 int set_paln_params(double gap_open,
11                    double gap_ext,
12                    double seqweight,
13                    int free_ends);
14
15
16 #endif

```

## 18.212 ViennaRNA/profiledist.h File Reference

Include dependency graph for profiledist.h:

### Functions

- float [profile\\_edit\\_distance](#) (const float \*T1, const float \*T2)  
*Align the 2 probability profiles T1, T2*
- float \* [Make\\_bp\\_profile\\_bppm](#) (FLT\_OR\_DBL \*bppm, int length)  
*condense pair probability matrix into a vector containing probabilities for unpaired, upstream paired and downstream paired.*
- void [print\\_bppm](#) (const float \*T)  
*print string representation of probability profile*
- void [free\\_profile](#) (float \*T)  
*free space allocated in Make\_bp\_profile*
- float \* [Make\\_bp\\_profile](#) (int length)

### 18.212.1 Detailed Description

### 18.212.2 Function Documentation

**18.212.2.1 profile\_edit\_distance()**

```
float profile_edit_distance (
    const float * T1,
    const float * T2 )
```

Align the 2 probability profiles T1, T2

.

This is like a Needleman-Wunsch alignment, we should really use affine gap-costs ala Gotoh

**18.212.2.2 Make\_bp\_profile\_bppm()**

```
float * Make_bp_profile_bppm (
    FLT_OR_DBL * bppm,
    int length )
```

condense pair probability matrix into a vector containing probabilities for unpaired, upstream paired and downstream paired.

This resulting probability profile is used as input for profile\_edit\_distance

**Parameters**

|               |                                               |
|---------------|-----------------------------------------------|
| <i>bppm</i>   | A pointer to the base pair probability matrix |
| <i>length</i> | The length of the sequence                    |

**Returns**

The bp profile

**18.212.2.3 free\_profile()**

```
void free_profile (
    float * T )
```

free space allocated in Make\_bp\_profile

Backward compatibility only. You can just use plain free()

**18.212.2.4 Make\_bp\_profile()**

```
float * Make_bp_profile (
    int length )
```

**Note**

This function is NOT threadsafe

**See also**

[Make\\_bp\\_profile\\_bppm\(\)](#)

**Deprecated** This function is deprecated and will be removed soon! See [Make\\_bp\\_profile\\_bppm\(\)](#) for a replacement

**18.213 profiledist.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PROFILEDIST_H
2 #define VIENNA_RNA_PACKAGE_PROFILEDIST_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
```

```

10 # define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <ViennaRNA/datastructures/basic.h>
17
20 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
21
28 float profile_edit_distance(const float *T1,
29                             const float *T2);
30
31
42 float *Make_bp_profile_bppm(FLT_OR_DBL *bppm,
43                             int length);
44
45
49 void print_bppm(const float *T);
50
51
57 void free_profile(float *T);
58
59
68 DEPRECATED(float *Make_bp_profile(int length),
69 "Use Make_bp_profile_bppm() instead");
70
71 #endif
72
73 #endif

```

## 18.214 ViennaRNA/PS\_dot.h File Reference

Use [ViennaRNA/plotting/probabilities.h](#) instead.

Include dependency graph for PS\_dot.h:

### 18.214.1 Detailed Description

Use [ViennaRNA/plotting/probabilities.h](#) instead.

**Deprecated** Use [ViennaRNA/plotting/probabilities.h](#) instead

## 18.215 PS\_dot.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_PLOT_PROBABILITIES_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PLOT_PROBABILITIES_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/PS_dot.h>! Use <ViennaRNA/plotting/probabilities.h>
    instead!"
13 # endif
14 #include <ViennaRNA/plotting/probabilities.h>
15 #include <ViennaRNA/plotting/layouts.h>
16 #include <ViennaRNA/plotting/structures.h>
17 #endif
18
19 #endif

```

## 18.216 ViennaRNA/read\_epars.h File Reference

Use [ViennaRNA/params/io.h](#) instead.

Include dependency graph for read\_epars.h:

### 18.216.1 Detailed Description

Use [ViennaRNA/params/io.h](#) instead.

**Deprecated** Use [ViennaRNA/params/io.h](#) instead

## 18.217 read\_epars.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_PARAMS_IO_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_PARAMS_IO_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/read_epars.h>! Use <ViennaRNA/params/io.h>
    instead!"
13 #   endif
14 #include <ViennaRNA/params/io.h>
15 #endif
16
17 #endif
```

## 18.218 ViennaRNA/ribo.h File Reference

Parse RiboSum Scoring Matrices for Covariance Scoring of Alignments.

This graph shows which files directly or indirectly include this file:

### Functions

- float \*\* **get\_ribosum** (const char \*\*Aseq, int n\_seq, int length)  
*Retrieve a RiboSum Scoring Matrix for a given Alignment.*
- float \*\* **readribosum** (char \*name)  
*Read a RiboSum or other user-defined Scoring Matrix and Store into global Memory.*

### 18.218.1 Detailed Description

Parse RiboSum Scoring Matrices for Covariance Scoring of Alignments.

## 18.219 ribo.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_RIBOSUM_H
2 #define VIENNA_RNA_PACKAGE_RIBOSUM_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11
22 float **get_ribosum(const char **Aseq,
23                    int n_seq,
24                    int length);
25
26
31 float **readribosum(char *name);
32
33
37 #endif
38
39 #endif
```

## 18.220 ViennaRNA/RNAstruct.h File Reference

Parsing and Coarse Graining of Structures.

### Functions

- char \* **b2HIT** (const char \*structure)  
*Converts the full structure from bracket notation to the HIT notation including root.*
- char \* **b2C** (const char \*structure)  
*Converts the full structure from bracket notation to the a coarse grained notation using the 'H' 'B' 'I' 'M' and 'R' identifiers.*
- char \* **b2Shapiro** (const char \*structure)

*Converts the full structure from bracket notation to the weighted coarse grained notation using the 'H' 'B' 'I' 'M' 'S' 'E' and 'R' identifiers.*

- char \* [add\\_root](#) (const char \*structure)

*Adds a root to an un-rooted tree in any except bracket notation.*

- char \* [expand\\_Shapiro](#) (const char \*coarse)

*Inserts missing 'S' identifiers in unweighted coarse grained structures as obtained from [b2C\(\)](#).*

- char \* [expand\\_Full](#) (const char \*structure)

*Convert the full structure from bracket notation to the expanded notation including root.*

- char \* [unexpand\\_Full](#) (const char \*ffull)

*Restores the bracket notation from an expanded full or HIT tree, that is any tree using only identifiers 'U' 'P' and 'R'.*

- char \* [unweight](#) (const char \*wcoarse)

*Strip weights from any weighted tree.*

- void [unexpand\\_aligned\\_F](#) (char \*align[2])

*Converts two aligned structures in expanded notation.*

- void [parse\\_structure](#) (const char \*structure)

*Collects a statistic of structure elements of the full structure in bracket notation.*

## Variables

- int **loop\_size** [2000]

*contains a list of all loop sizes. loop\_size[0] contains the number of external bases.*

- int **helix\_size** [2000]

*contains a list of all stack sizes.*

- int **loop\_degree** [2000]

*contains the corresponding list of loop degrees.*

- int **loops**

*contains the number of loops ( and therefore of stacks ).*

- int **unpaired**

*contains the number of unpaired bases.*

- int **pairs**

*contains the number of base pairs in the last parsed structure.*

## 18.220.1 Detailed Description

Parsing and Coarse Graining of Structures.

Example:

```
*  .((..(((...)))..((...))).  is the bracket or full tree
*  becomes expanded:  - expand_Full() -
*  ((U)((U)(U)((U)(U)(U)P)P)P)(U)((U)(U)P)P)P)(U)R)
*  HIT:  - b2HIT() -
*  ((U1)((U2)((U3)P3)(U2)((U2)P2)P2)(U1)R)
*  Coarse:  - b2C() -
*  ((H)((H)M)R)
*  becomes expanded:  - expand_Shapiro() -
*  (((((H)S)((H)S)M)S)R)
*  weighted Shapiro:  - b2Shapiro() -
*  (((((H3)S3)((H2)S2)M4)S2)E2)R)
*
```

## 18.221 RNAstruct.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_RNASTRUCT_H
2 #define VIENNA_RNA_PACKAGE_RNASTRUCT_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
```

```

7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 #   define DEPRECATED(func, msg) func
14 #endif
15
40 #define STRUC      2000
41
52 DEPRECATED(char *b2HIT(const char *structure),
53             "Use vrna_db_to_tree_string() instead!");           /* Full   -> HIT    [incl. root] */
54
55
66 DEPRECATED(char *b2C(const char *structure),
67             "Use vrna_db_to_tree_string() instead!");           /* Full   -> Coarse [incl. root] */
68
69
81 DEPRECATED(char *b2Shapiro(const char *structure),
82             "Use vrna_db_to_tree_string() instead!");           /* Full -> weighted Shapiro [i.r.] */
83
84
91 DEPRECATED(char *add_root(const char *structure),
92             "");           /* {Tree} -> ({Tree}R) */
93
94
102 DEPRECATED(char *expand_Shapiro(const char *coarse),
103            "Use vrna_db_to_tree_string() instead!");
104
105
106 /* add S for stacks to coarse struct */
114 DEPRECATED(char *expand_Full(const char *structure),
115            "Use vrna_db_to_tree_string() instead!");           /* Full   -> FFull */
116
117
125 DEPRECATED(char *unexpand_Full(const char *ffull),
126            "Use vrna_tree_string_to_db() instead!");           /* FFull  -> Full */
127
128
135 DEPRECATED(char *unweight(const char *wcoarse),
136            "Use vrna_tree_string_unweight() instead!");           /* remove weights from coarse struct */
137
138
148 DEPRECATED(void unexpand_aligned_F(char *align[2]),
149            "");
150
151
161 DEPRECATED(void parse_structure(const char *structure),
162            ""); /* make structure statistics */
163
164
169 DEPRECATED(extern int loop_size[STRUC],
170            ""); /* loop sizes of a structure */
171
175 DEPRECATED(extern int helix_size[STRUC],
176            ""); /* helix sizes of a structure */
177
181 DEPRECATED(extern int loop_degree[STRUC],
182            ""); /* loop degrees of a structure */
183
187 DEPRECATED(extern int loops,
188            ""); /* n of loops and stacks */
189
193 DEPRECATED(extern int unpaired,
194            "");
195
199 DEPRECATED(extern int pairs,
200            ""); /* n of unpaired digits and pairs */
201
206 #endif

```

## 18.222 ViennaRNA/search/BoyerMoore.h File Reference

Variants of the Boyer-Moore string search algorithm.

### Functions

- `const unsigned int *vrna_search_BMH_num` (`const unsigned int *needle`, `size_t needle_size`, `const unsigned int *haystack`, `size_t haystack_size`, `size_t start`, `size_t *badchars`, `unsigned char cyclic`)



*Search for a string of elements in a larger string of elements using the Boyer-Moore-Horspool algorithm.*

- `const char * vrna_search_BMH` (`const char *needle`, `size_t needle_size`, `const char *haystack`, `size_t haystack_size`, `size_t start`, `size_t *badchars`, `unsigned char cyclic`)

*Search for an ASCII pattern within a larger ASCII string using the Boyer-Moore-Horspool algorithm.*

- `size_t * vrna_search_BM_BCT_num` (`const unsigned int *pattern`, `size_t pattern_size`, `unsigned int num_max`)

*Retrieve a Boyer-Moore Bad Character Table for a pattern of elements represented by natural numbers.*

- `size_t * vrna_search_BM_BCT` (`const char *pattern`)

*Retrieve a Boyer-Moore Bad Character Table for a NULL-terminated pattern of ASCII characters.*

### 18.222.1 Detailed Description

Variants of the Boyer-Moore string search algorithm.

,

## 18.223 BoyerMoore.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_SEARCH_BOYER_MOORE_H
2 #define VIENNA_RNA_PACKAGE_SEARCH_BOYER_MOORE_H
3
36 const unsigned int *
37 vrna_search_BMH_num(const unsigned int *needle,
38                    size_t needle_size,
39                    const unsigned int *haystack,
40                    size_t haystack_size,
41                    size_t start,
42                    size_t *badchars,
43                    unsigned char cyclic);
44
45
67 const char *
68 vrna_search_BMH(const char *needle,
69                size_t needle_size,
70                const char *haystack,
71                size_t haystack_size,
72                size_t start,
73                size_t *badchars,
74                unsigned char cyclic);
75
76
92 size_t *
93 vrna_search_BM_BCT_num(const unsigned int *pattern,
94                      size_t pattern_size,
95                      unsigned int num_max);
96
97
110 size_t *
111 vrna_search_BM_BCT(const char *pattern);
112
113
117 #endif
```

## 18.224 ViennaRNA/sequence.h File Reference

Functions and data structures related to sequence representations ,.

Include dependency graph for sequence.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct `vrna_sequence_s`  
*Data structure representing a nucleotide sequence. [More...](#)*
- struct `vrna_alignment_s`

## Typedefs

- typedef struct [vrna\\_sequence\\_s](#) [vrna\\_seq\\_t](#)

*Typename for nucleotide sequence representation data structure [vrna\\_sequence\\_s](#).*

## Enumerations

- enum [vrna\\_seq\\_type\\_e](#) { [VRNA\\_SEQ\\_UNKNOWN](#) , [VRNA\\_SEQ\\_RNA](#) , [VRNA\\_SEQ\\_DNA](#) }

*A enumerator used in [vrna\\_sequence\\_s](#) to distinguish different nucleotide sequences.*

### 18.224.1 Detailed Description

Functions and data structures related to sequence representations ,.

## 18.225 [sequence.h](#)

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_SEQUENCE_H
2 #define VIENNA_RNA_PACKAGE_SEQUENCE_H
3
17 typedef struct vrna_sequence_s vrna_seq_t;
18
19 typedef struct vrna_alignment_s vrna_msa_t;
20
21 #include <ViennaRNA/fold_compound.h>
22
23
24 #define VRNA_SEQUENCE_RNA      1U
25
26 #define VRNA_SEQUENCE_DNA      2U
27
31 typedef enum {
32     VRNA_SEQ_UNKNOWN,
33     VRNA_SEQ_RNA,
34     VRNA_SEQ_DNA
35 } vrna_seq_type_e;
36
37
41 struct vrna_sequence_s {
42     vrna_seq_type_e type;
43     char            *name;
44     char            *string;
45     short           *encoding;
46     short           *encoding5;
47     short           *encoding3;
48     unsigned int    length;
49 };
50
51
52 struct vrna_alignment_s {
53     unsigned int    n_seq;
54     vrna_seq_t      *sequences;
55     char            **gapfree_seq;
56     unsigned int     gapfree_size; /* for MAF alignment coordinates */
57     unsigned long long genome_size; /* for MAF alignment coordinates */
58     unsigned long long start;       /* for MAF alignment coordinates */
59     unsigned char     *orientation; /* for MAF alignment coordinates */
60     unsigned int      **a2s;
61 };
62
63
64 vrna_seq_t *
65 vrna_sequence(const char    *string,
66              unsigned int   options);
67
68
69 int
70 vrna_sequence_add(vrna_fold_compound_t *fc,
71                  const char            *string,
72                  unsigned int           options);
73
74
75 int
76 vrna_sequence_remove(vrna_fold_compound_t *fc,
77                     unsigned int           i);
78
79
80 void
```

```

81 vrna_sequence_remove_all(vrna_fold_compound_t *fc);
82
83
84 void
85 vrna_sequence_prepare(vrna_fold_compound_t *fc);
86
87
88 int
89 vrna_sequence_order_update(vrna_fold_compound_t *fc,
90                             const unsigned int *order);
91
92
93 int
94 vrna_msa_add(vrna_fold_compound_t *fc,
95              const char **alignment,
96              const char **names,
97              const unsigned char *orientation,
98              const unsigned long long *start,
99              const unsigned long long *genome_size,
100              unsigned int options);
101
102
107 #endif

```

## 18.226 snofold.h

```

1  /* function from fold.c */
2  #ifndef VIENNA_RNA_PACKAGE_SNOFOLD_H
3  #define VIENNA_RNA_PACKAGE_SNOFOLD_H
4
5  #include <ViennaRNA/datastructures/basic.h>
6
7  #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
8
9  /* Normal fold */
10
11 int snofold(const char *sequence,
12             char *structure,
13             const int max_assym,
14             const int threshold,
15             const int min_s2,
16             const int max_s2,
17             const int half_stem,
18             const int max_half_stem);
19
20
21 void snofree_arrays(const int length); /* free arrays for mfe folding */
22
23
24 void snoinitialize_fold(int length); /* allocate arrays for folding */
25
26
27 void snoupdate_fold_params(void); /* recalculate parameters */
28
29
30 int snoloop_energy(short *ptable,
31                   short *s,
32                   short *sl,
33                   int i);
34
35
36 void snoexport_fold_arrays(int **indx_p,
37                            int **mLoop_p,
38                            int **cLoop_p,
39                            folden ***fold_p,
40                            folden ***fold_p_XS);
41
42
43 char *snobacktrack_fold_from_pair(const char *sequence,
44                                   int i,
45                                   int j);
46
47
48 /* alifold */
49 float alisnofold(const char **strings,
50                 const int max_assym,
51                 const int threshloop,
52                 const int min_s2,
53                 const int max_s2,
54                 const int half_stem,
55                 const int max_half_stem);
56
57 void alisnofree_arrays(const int length);
58
59

```

```

67
68 char *alishnbacktrack_fold_from_pair(const char **sequence,
69                                     int          i,
70                                     int          j,
71                                     int          *cov);
72
73
74 extern double cv_fact /* =1 */;
75 extern double nc_fact /* =1 */;
76
77 /* max number of mismatch >>>..(( ))>>> */
78 #define MISMATCH 3
79
80 #endif
81
82 #endif

```

## 18.227 snoop.h

```

1 #ifndef VIENNA_RNA_PACKAGE_SNOOP_H
2 #define VIENNA_RNA_PACKAGE_SNOOP_H
3
4 #include <ViennaRNA/datastructures/basic.h>
5
6 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
7
12 snoopT snoopfold(const char *s1,
13                  const char *s2,
14                  const int  penalty,
15                  const int  threshloop,
16                  const int  threshLE,
17                  const int  threshRE,
18                  const int  threshDE,
19                  const int  threshD,
20                  const int  half_stem,
21                  const int  max_half_stem,
22                  const int  min_s2,
23                  const int  max_s2,
24                  const int  min_s1,
25                  const int  max_s1,
26                  const int  min_d1,
27                  const int  min_d2,
28                  const int  fullStemEnergy);
29
30
36 snoopT *snoop_subopt(const char *s1,
37                      const char *s2,
38                      int          delta,
39                      int          w,
40                      const int  penalty,
41                      const int  threshloop,
42                      const int  threshLE,
43                      const int  threshRE,
44                      const int  threshDE,
45                      const int  threshTE,
46                      const int  threshSE,
47                      const int  threshD,
48                      const int  distance,
49                      const int  half_stem,
50                      const int  max_half_stem,
51                      const int  min_s2,
52                      const int  max_s2,
53                      const int  min_s1,
54                      const int  max_s1,
55                      const int  min_d1,
56                      const int  min_d2,
57                      const int  fullStemEnergy);
58
59
65 void Lsnoop_subopt(const char *s1,
66                   const char *s2,
67                   int          delta,
68                   int          w,
69                   const int  penalty,
70                   const int  threshloop,
71                   const int  threshLE,
72                   const int  threshRE,
73                   const int  threshDE,
74                   const int  threshTE,
75                   const int  threshSE,
76                   const int  threshD,
77                   const int  distance,
78                   const int  half_stem,
79                   const int  max_half_stem,
80                   const int  min_s2,

```

```
81         const int    max_s2,
82         const int    min_s1,
83         const int    max_s1,
84         const int    min_d1,
85         const int    min_d2,
86         const int    alignment_length,
87         const char    *name,
88         const int     fullStemEnergy);
89
90
91 void Lsnoop_subopt_list(const char *s1,
92                        const char *s2,
93                        int         delta,
94                        int         w,
95                        const int   penalty,
96                        const int   threshloop,
97                        const int   threshLE,
98                        const int   threshRE,
99                        const int   threshDE,
100                       const int   threshTE,
101                       const int   threshSE,
102                       const int   threshD,
103                       const int   distance,
104                       const int   half_stem,
105                       const int   max_half_stem,
106                       const int   min_s2,
107                       const int   max_s2,
108                       const int   min_s1,
109                       const int   max_s1,
110                       const int   min_d1,
111                       const int   min_d2,
112                       const int   alignment_length,
113                       const char *name,
114                       const int   fullStemEnergy);
115
116 void Lsnoop_subopt_list_XS(const char *s1,
117                           const char *s2,
118                           const int   **access_s1,
119                           int         delta,
120                           int         w,
121                           const int   penalty,
122                           const int   threshloop,
123                           const int   threshLE,
124                           const int   threshRE,
125                           const int   threshDE,
126                           const int   threshTE,
127                           const int   threshSE,
128                           const int   threshD,
129                           const int   distance,
130                           const int   half_stem,
131                           const int   max_half_stem,
132                           const int   min_s2,
133                           const int   max_s2,
134                           const int   min_s1,
135                           const int   max_s1,
136                           const int   min_d1,
137                           const int   min_d2,
138                           const int   alignment_length,
139                           const char *name,
140                           const int   fullStemEnergy);
141
142 void snoop_subopt_XS(const char *s1,
143                     const char *s2,
144                     const int   **access_s1,
145                     int         delta,
146                     int         w,
147                     const int   penalty,
148                     const int   threshloop,
149                     const int   threshLE,
150                     const int   threshRE,
151                     const int   threshDE,
152                     const int   threshTE,
153                     const int   threshSE,
154                     const int   threshD,
155                     const int   distance,
156                     const int   half_stem,
157                     const int   max_half_stem,
158                     const int   min_s2,
159                     const int   max_s2,
160                     const int   min_s1,
161                     const int   max_s1,
162                     const int   min_d1,
163                     const int   min_d2,
164                     const int   alignment_length,
165                     const char *name,
```

```

183         const int fullStemEnergy);
184
185
186
187
188
189
190 snoopT *alisnoop_subopt(const char **s1,
191                        const char **s2,
192                        int delta,
193                        int w,
194                        const int penalty,
195                        const int threshloop,
196                        const int threshLE,
197                        const int threshRE,
198                        const int threshDE,
199                        const int threshTE,
200                        const int threshSE,
201                        const int threshD,
202                        const int distance,
203                        const int half_stem,
204                        const int max_half_stem,
205                        const int min_s2,
206                        const int max_s2,
207                        const int min_s1,
208                        const int max_s1,
209                        const int min_d1,
210                        const int min_d2);
211
212
213
214
215
216
217
218 snoopT *aliIsnoop_subopt_list(const char **s1,
219                              const char **s2,
220                              int delta,
221                              int w,
222                              const int penalty,
223                              const int threshloop,
224                              const int threshLE,
225                              const int threshRE,
226                              const int threshDE,
227                              const int threshTE,
228                              const int threshSE,
229                              const int threshD,
230                              const int distance,
231                              const int half_stem,
232                              const int max_half_stem,
233                              const int min_s2,
234                              const int max_s2,
235                              const int min_s1,
236                              const int max_s1,
237                              const int min_d1,
238                              const int min_d2,
239                              const int alignment_length);
240
241
242
243
244
245
246
247 snoopT alisnoopfold(const char **s1,
248                    const char **s2,
249                    const int penalty,
250                    const int threshloop,
251                    const int threshLE,
252                    const int threshRE,
253                    const int threshDE,
254                    const int threshD,
255                    const int half_stem,
256                    const int max_half_stem,
257                    const int min_s2,
258                    const int max_s2,
259                    const int min_s1,
260                    const int max_s1,
261                    const int min_d1,
262                    const int min_d2);
263
264
265
266
267
268
269 snoopT snoopfold_XS(const char *s1,
270                   const char *s2,
271                   const int **access_s1,
272                   const int pos,
273                   const int max_pos_j,
274                   const int penalty,
275                   const int threshloop,
276                   const int threshLE,
277                   const int threshRE,
278                   const int threshDE,
279                   const int threshD,
280                   const int half_stem,
281                   const int max_half_stem,
282                   const int min_s2,
283                   const int max_s2,
284                   const int min_s1,
285                   const int max_s1,
286                   const int min_d1,
287                   const int min_d2,

```

```

288             const int    fullStemEnergy);
289
290
291 extern int snoop_subopt_sorted;
292 #endif
293
294 #endif

```

## 18.228 special\_const.h

```

1 extern const char    wall;
2 extern const char    bg;
3 extern const char    star;
4 extern const char    probe;
5 extern const char    start[];
6 extern const char    end[];
7 extern const char    success[];
8 extern const char    injector[];
9 extern unsigned int  injector_len;
10 extern const char    flash[];
11 extern const char    head1l[];
12 extern const char    head2l[];
13 extern const char    lvlstr[];
14 extern const char    inv[];

```

## 18.229 ViennaRNA/datastructures/stream\_output.h File Reference

An implementation of a buffered, ordered stream output data structure.

This graph shows which files directly or indirectly include this file:

### Typedefs

- typedef struct vrna\_ordered\_stream\_s \* **vrna\_ostream\_t**  
*An ordered output stream structure with unordered insert capabilities.*
- typedef void() **vrna\_callback\_stream\_output**(void \*auxdata, unsigned int i, void \*data)  
*Ordered stream processing callback.*

### Functions

- **vrna\_ostream\_t** **vrna\_ostream\_init** (**vrna\_callback\_stream\_output** \*output, void \*auxdata)  
*Get an initialized ordered output stream.*
- void **vrna\_ostream\_free** (**vrna\_ostream\_t** dat)  
*Free an initialized ordered output stream.*
- void **vrna\_ostream\_request** (**vrna\_ostream\_t** dat, unsigned int num)  
*Request index in ordered output stream.*
- void **vrna\_ostream\_provide** (**vrna\_ostream\_t** dat, unsigned int i, void \*data)  
*Provide output stream data for a particular index.*

### 18.229.1 Detailed Description

An implementation of a buffered, ordered stream output data structure.

,

## 18.230 stream\_output.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_STREAM_OUTPUT_H
2 #define VIENNA_RNA_PACKAGE_STREAM_OUTPUT_H
3
18 typedef struct vrna_ordered_stream_s *vrna_ostream_t;
19
34 typedef void (vrna_callback_stream_output) (void      *auxdata,
35   unsigned int i,
36   void      *data);

```

```

37
47 vrna_ostream_t
48 vrna_ostream_init(vrna_callback_stream_output *output,
49                  void *auxdata);
50
51
59 void
60 vrna_ostream_free(vrna_ostream_t dat);
61
62
63 int
64 vrna_ostream_threadsafe(void);
65
66
79 void
80 vrna_ostream_request(vrna_ostream_t dat,
81                     unsigned int num);
82
83
96 void
97 vrna_ostream_provide(vrna_ostream_t dat,
98                     unsigned int i,
99                     void *data);
100
101
107 #endif

```

## 18.231 ViennaRNA/stream\_output.h File Reference

Use [ViennaRNA/datastructures/stream\\_output.h](#) instead.

Include dependency graph for stream\_output.h:

### 18.231.1 Detailed Description

Use [ViennaRNA/datastructures/stream\\_output.h](#) instead.

**Deprecated** Use [ViennaRNA/datastructures/stream\\_output.h](#) instead

## 18.232 stream\_output.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_DATA_STRUCTURES_STREAM_OUTPUT_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_DATA_STRUCTURES_STREAM_OUTPUT_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/stream_output.h>! Use
    <ViennaRNA/datastructures/stream_output.h> instead!"
13 #  endif
14 #include <ViennaRNA/datastructures/stream_output.h>
15 #endif
16
17 #endif

```

## 18.233 ViennaRNA/string\_utils.h File Reference

Use [ViennaRNA/utis/strings.h](#) instead.

Include dependency graph for string\_utils.h:

### 18.233.1 Detailed Description

Use [ViennaRNA/utis/strings.h](#) instead.

**Deprecated** Use [ViennaRNA/utis/strings.h](#) instead

## 18.234 string\_utils.h

[Go to the documentation of this file.](#)



```

1 #ifndef VIENNA_RNA_PACKAGE_STRING_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_STRING_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #  ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/string_utils.h>! Use <ViennaRNA/Utils/strings.h>
    instead!"
13 #  endif
14 #include <ViennaRNA/Utils/strings.h>
15 #endif
16
17 #endif

```

## 18.235 ViennaRNA/stringdist.h File Reference

Functions for String Alignment.

Include dependency graph for stringdist.h:

### Functions

- [swString](#) \* [Make\\_swString](#) (char \*string)  
Convert a structure into a format suitable for [string\\_edit\\_distance\(\)](#).
- float [string\\_edit\\_distance](#) ([swString](#) \*T1, [swString](#) \*T2)  
Calculate the string edit distance of T1 and T2.

### 18.235.1 Detailed Description

Functions for String Alignment.

### 18.235.2 Function Documentation

#### 18.235.2.1 Make\_swString()

```

swString * Make_swString (
    char * string )

```

Convert a structure into a format suitable for [string\\_edit\\_distance\(\)](#).

##### Parameters

|               |  |
|---------------|--|
| <i>string</i> |  |
|---------------|--|

##### Returns

#### 18.235.2.2 string\_edit\_distance()

```

float string_edit_distance (
    swString * T1,
    swString * T2 )

```

Calculate the string edit distance of T1 and T2.

##### Parameters

|           |  |
|-----------|--|
| <i>T1</i> |  |
| <i>T2</i> |  |

## Returns

## 18.236 stringdist.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_STRING_DIST_H
2 #define VIENNA_RNA_PACKAGE_STRING_DIST_H
3
9 #include <ViennaRNA/dist_vars.h>
10
11
18 swString *Make_swString(char *string);
19
27 float      string_edit_distance( swString *T1,
28                                swString *T2);
29
30 #endif
```

## 18.237 ViennaRNA/structure\_utils.h File Reference

Use [ViennaRNA/utis/structures.h](#) instead.

Include dependency graph for structure\_utils.h:

### 18.237.1 Detailed Description

Use [ViennaRNA/utis/structures.h](#) instead.

**Deprecated** Use [ViennaRNA/utis/structures.h](#) instead

## 18.238 structure\_utils.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_STRUCTURE_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_STRUCTURE_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/structure_utils.h>! Use
    <ViennaRNA/utis/structures.h> instead!"
13 # endif
14 #include <ViennaRNA/utis/structures.h>
15 #endif
16
17 #endif
```

## 18.239 ViennaRNA/structured\_domains.h File Reference

This module provides interfaces that deal with additional structured domains in the folding grammar.

This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_structured\\_domains\\_s](#)

### 18.239.1 Detailed Description

This module provides interfaces that deal with additional structured domains in the folding grammar.

## 18.240 structured\_domains.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_STRUCTURAL_DOMAINS_H
```

```

2 #define VIENNA_RNA_PACKAGE_STRUCTURAL_DOMAINS_H
3
23 typedef struct vrna_structured_domains_s vrna_sd_t;
24
25
26 struct vrna_structured_domains_s {
27     char __placeholder; /* dummy placeholder to not leave this struct empty */
28 };
29
30 #endif

```

## 18.241 ViennaRNA/subopt.h File Reference

RNAsubopt and density of states declarations.

Include dependency graph for subopt.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_subopt\\_sol\\_s](#)  
*Solution element from subopt.c.*

### Macros

- #define **MAXDOS** 1000  
*Maximum density of states discretization for subopt.*

### Typedefs

- typedef struct [vrna\\_subopt\\_sol\\_s](#) **vrna\_subopt\_solution\_t**  
*Typename for the subopt solution list representing data structure [vrna\\_subopt\\_sol\\_s](#).*
- typedef void() [vrna\\_subopt\\_callback](#)(const char \*structure, float energy, void \*data)  
*Callback for [vrna\\_subopt\\_cb\(\)](#)*
- typedef struct [vrna\\_subopt\\_sol\\_s](#) **SOLUTION**  
*Backward compatibility typedef for [vrna\\_subopt\\_sol\\_s](#).*

### Functions

- [vrna\\_subopt\\_solution\\_t](#) \* [vrna\\_subopt](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int delta, int sorted, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- void [vrna\\_subopt\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, int delta, [vrna\\_subopt\\_callback](#) \*cb, void \*data)  
*Generate suboptimal structures within an energy band around the MFE.*
- **SOLUTION** \* [subopt](#) (char \*seq, char \*structure, int delta, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- **SOLUTION** \* **subopt\_par** (char \*seq, char \*structure, [vrna\\_param\\_t](#) \*parameters, int delta, int is\_↔ constrained, int is\_circular, FILE \*fp)  
*Returns list of subopt structures or writes to fp.*
- **SOLUTION** \* [subopt\\_circ](#) (char \*seq, char \*sequence, int delta, FILE \*fp)  
*Returns list of circular subopt structures or writes to fp.*
- **SOLUTION** \* [zukersubopt](#) (const char \*string)  
*Compute Zuker type suboptimal structures.*
- **SOLUTION** \* [zukersubopt\\_par](#) (const char \*string, [vrna\\_param\\_t](#) \*parameters)  
*Compute Zuker type suboptimal structures.*

## Variables

- double **print\_energy**  
*printing threshold for use with logML*
- int **subopt\_sorted**  
*Sort output by energy.*
- int **density\_of\_states** [MAXDOS+1]  
*The Density of States.*

### 18.241.1 Detailed Description

RNAsubopt and density of states declarations.

### 18.241.2 Typedef Documentation

#### 18.241.2.1 SOLUTION

typedef struct [vrna\\_subopt\\_sol\\_s](#) SOLUTION  
Backward compatibility typedef for [vrna\\_subopt\\_sol\\_s](#).

**Deprecated** Use [vrna\\_subopt\\_solution\\_t](#) instead!

## 18.242 subopt.h

[Go to the documentation of this file.](#)

```
1 /* subopt.h */
2 #ifndef VIENNA_RNA_PACKAGE_SUBOPT_H
3 #define VIENNA_RNA_PACKAGE_SUBOPT_H
4
5 #ifdef VRNA_WARN_DEPRECATED
6 # if defined(__clang__)
7 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
8 # elif defined(__GNUC__)
9 #  define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
10 # else
11 #  define DEPRECATED(func, msg) func
12 # endif
13 #else
14 # define DEPRECATED(func, msg) func
15 #endif
16
31 typedef struct vrna_subopt_sol_s vrna_subopt_solution_t;
32
48 typedef void (vrna_subopt_callback)(const char *structure,
49                                     float energy,
50                                     void *data);
51
52 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
53
58 typedef struct vrna_subopt_sol_s SOLUTION;
59
60 #endif
61
62 #include <stdio.h>
63
64 #include <ViennaRNA/datastructures/basic.h>
65 #include <ViennaRNA/fold_compound.h>
66 #include <ViennaRNA/params/basic.h>
67
68
72 struct vrna_subopt_sol_s {
73     float energy;
74     char *structure;
75 };
76
80 #define MAXDOS 1000
81
89 #define VRNA_UNSORTED 0
90 #define VRNA_SORT_BY_ENERGY_LEXICOGRAPHIC_ASC 1
91 #define VRNA_SORT_BY_ENERGY_ASC 2
92
```

```

123 vrna_subopt_solution_t *
124 vrna_subopt(vrna_fold_compound_t *fc,
125             int delta,
126             int sorted,
127             FILE *fp);
128
129
130 void
131 vrna_subopt_cb(vrna_fold_compound_t *fc,
132               int delta,
133               vrna_subopt_callback *cb,
134               void *data);
135
136 extern double print_energy;
137
138 extern int subopt_sorted;
139
140 extern int density_of_states[MAXDOS + 1];
141 /* End of group dos */
142
143 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
144
145 DEPRECATED(SOLUTION * subopt(char *seq, char *structure, int delta, FILE * fp),
146           "Use vrna_subopt() or vrna_subopt_cb() instead");
147
148 DEPRECATED(SOLUTION *
149           subopt_par(char *seq, char *structure, vrna_param_t * parameters, int delta,
150                    int is_constrained,
151                    int is_circular, FILE * fp),
152           "Use vrna_subopt() or vrna_subopt_cb() instead");
153
154 DEPRECATED(SOLUTION * subopt_circ(char *seq, char *sequence, int delta, FILE * fp),
155           "Use vrna_subopt() or vrna_subopt_cb() instead");
156
157 DEPRECATED(SOLUTION * zukersubopt(const char *string),
158           "Use vrna_subopt_zuker() instead");
159
160 DEPRECATED(SOLUTION * zukersubopt_par(const char *string, vrna_param_t * parameters),
161           "Use vrna_subopt_zuker() instead");
162
163 #endif
164 #endif

```

## 18.243 subopt\_zuker.h

```

1 /* subopt_zuker.h */
2 #ifndef VIENNA_RNA_PACKAGE_SUBOPT_ZUKER_H
3 #define VIENNA_RNA_PACKAGE_SUBOPT_ZUKER_H
4
5 #include <ViennaRNA/fold_compound.h>
6 #include <ViennaRNA/subopt.h>
7
8 vrna_subopt_solution_t *
9 vrna_subopt_zuker(vrna_fold_compound_t *fc);
10
11 #endif

```

## 18.244 ViennaRNA/svm\_utils.h File Reference

Use [ViennaRNA/utis/svm.h](#) instead.

Include dependency graph for svm\_utils.h:

### 18.244.1 Detailed Description

Use [ViennaRNA/utis/svm.h](#) instead.

**Deprecated** Use [ViennaRNA/utis/svm.h](#) instead

## 18.245 svm\_utils.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_UTILS_SVM_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_UTILS_SVM_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/svm_utils.h>! Use <ViennaRNA/Utils/svm.h> instead!"
13 #   endif
14 #include <ViennaRNA/Utils/svm.h>
15 #endif
16
17 #endif

```

## 18.246 ViennaRNA/treedist.h File Reference

Functions for [Tree](#) Edit Distances.

Include dependency graph for treedist.h:

### Functions

- [Tree](#) \* [make\\_tree](#) (char \*struc)  
*Constructs a [Tree](#) ( essentially the postorder list ) of the structure 'struc', for use in [tree\\_edit\\_distance\(\)](#).*
- float [tree\\_edit\\_distance](#) ([Tree](#) \*T1, [Tree](#) \*T2)  
*Calculates the edit distance of the two trees.*
- void [print\\_tree](#) ([Tree](#) \*t)  
*Print a tree (mainly for debugging)*
- void [free\\_tree](#) ([Tree](#) \*t)  
*Free the memory allocated for [Tree](#) t.*

### 18.246.1 Detailed Description

Functions for [Tree](#) Edit Distances.

### 18.246.2 Function Documentation

#### 18.246.2.1 [make\\_tree\(\)](#)

```

Tree * make\_tree (
    char * struc )

```

Constructs a [Tree](#) ( essentially the postorder list ) of the structure 'struc', for use in [tree\\_edit\\_distance\(\)](#).

#### Parameters

|              |                                             |
|--------------|---------------------------------------------|
| <i>struc</i> | may be any rooted structure representation. |
|--------------|---------------------------------------------|

#### Returns

#### 18.246.2.2 [tree\\_edit\\_distance\(\)](#)

```

float tree\_edit\_distance (
    Tree * T1,
    Tree * T2 )

```

Calculates the edit distance of the two trees.

## Parameters

|           |  |
|-----------|--|
| <i>T1</i> |  |
| <i>T2</i> |  |

## Returns

**18.246.2.3 free\_tree()**

```
void free_tree (
    Tree * t )
```

Free the memory allocated for [Tree](#) t.

## Parameters

|          |  |
|----------|--|
| <i>t</i> |  |
|----------|--|

**18.247 treedist.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_TREE_DIST_H
2 #define VIENNA_RNA_PACKAGE_TREE_DIST_H
3
9 #include <ViennaRNA/dist_vars.h>
10
18 Tree *make_tree(char *struc);
19
20
28 float tree_edit_distance(Tree *T1,
29                          Tree *T2);
30
31
35 void print_tree(Tree *t);
36
37
43 void free_tree(Tree *t);
44
45
46 #endif
```

**18.248 ViennaRNA/units.h File Reference**

Use [ViennaRNA/units/units.h](#) instead.

Include dependency graph for units.h:

**18.248.1 Detailed Description**

Use [ViennaRNA/units/units.h](#) instead.

**Deprecated** Use [ViennaRNA/units/units.h](#) instead

**18.249 units.h**

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_UNITS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_UNITS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
```

```

12 #warning "Including deprecated header file <ViennaRNA/units.h>! Use <ViennaRNA/utls/units.h> instead!"
13 # endif
14 #include <ViennaRNA/utls/units.h>
15 #endif
16
17 #endif

```

## 18.250 ViennaRNA/utls/units.h File Reference

Physical Units and Functions to convert them into each other.

This graph shows which files directly or indirectly include this file:

### Enumerations

- enum [vrna\\_unit\\_energy\\_e](#) {  
[VRNA\\_UNIT\\_J](#) , [VRNA\\_UNIT\\_KJ](#) , [VRNA\\_UNIT\\_CAL\\_IT](#) , [VRNA\\_UNIT\\_DACAL\\_IT](#) ,  
[VRNA\\_UNIT\\_KCAL\\_IT](#) , [VRNA\\_UNIT\\_CAL](#) , [VRNA\\_UNIT\\_DACAL](#) , [VRNA\\_UNIT\\_KCAL](#) ,  
[VRNA\\_UNIT\\_G\\_TNT](#) , [VRNA\\_UNIT\\_KG\\_TNT](#) , [VRNA\\_UNIT\\_T\\_TNT](#) , [VRNA\\_UNIT\\_EV](#) ,  
[VRNA\\_UNIT\\_WH](#) , [VRNA\\_UNIT\\_KWH](#) }  
*Energy / Work Units.*
- enum [vrna\\_unit\\_temperature\\_e](#) {  
[VRNA\\_UNIT\\_K](#) , [VRNA\\_UNIT\\_DEG\\_C](#) , [VRNA\\_UNIT\\_DEG\\_F](#) , [VRNA\\_UNIT\\_DEG\\_R](#) ,  
[VRNA\\_UNIT\\_DEG\\_N](#) , [VRNA\\_UNIT\\_DEG\\_DE](#) , [VRNA\\_UNIT\\_DEG\\_RE](#) , [VRNA\\_UNIT\\_DEG\\_RO](#) }  
*Temperature Units.*

### Functions

- double [vrna\\_convert\\_energy](#) (double energy, [vrna\\_unit\\_energy\\_e](#) from, [vrna\\_unit\\_energy\\_e](#) to)  
*Convert between energy / work units.*
- double [vrna\\_convert\\_temperature](#) (double temp, [vrna\\_unit\\_temperature\\_e](#) from, [vrna\\_unit\\_temperature\\_e](#) to)  
*Convert between temperature units.*
- int [vrna\\_convert\\_kcal\\_to\\_dcal](#) (double energy)  
*Convert floating point energy value into integer representation.*
- double [vrna\\_convert\\_dcal\\_to\\_kcal](#) (int energy)  
*Convert an integer representation of free energy in deka-cal/mol to kcal/mol.*

### 18.250.1 Detailed Description

Physical Units and Functions to convert them into each other.

,

## 18.251 units.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_UNITS_H
2 #define VIENNA_RNA_PACKAGE_UNITS_H
3
21 typedef enum {
22     VRNA_UNIT_J,
23     VRNA_UNIT_KJ,
24     VRNA_UNIT_CAL_IT,
25     VRNA_UNIT_DACAL_IT,
26     VRNA_UNIT_KCAL_IT,
27     VRNA_UNIT_CAL,
28     VRNA_UNIT_DACAL,
29     VRNA_UNIT_KCAL,
30     VRNA_UNIT_G_TNT,
31     VRNA_UNIT_KG_TNT,
32     VRNA_UNIT_T_TNT,
33     VRNA_UNIT_EV,
34     VRNA_UNIT_WH,
35     VRNA_UNIT_KWH,

```



```

36 } vrna_unit_energy_e;
37
38
44 typedef enum {
45     VRNA_UNIT_K,
46     VRNA_UNIT_DEG_C,
47     VRNA_UNIT_DEG_F,
48     VRNA_UNIT_DEG_R,
49     VRNA_UNIT_DEG_N,
50     VRNA_UNIT_DEG_DE,
51     VRNA_UNIT_DEG_RE,
52     VRNA_UNIT_DEG_RO,
53 } vrna_unit_temperature_e;
54
55
65 double
66 vrna_convert_energy(double energy,
67                    vrna_unit_energy_e from,
68                    vrna_unit_energy_e to);
69
70
80 double
81 vrna_convert_temperature(double temp,
82                        vrna_unit_temperature_e from,
83                        vrna_unit_temperature_e to);
84
85
97 int
98 vrna_convert_kcal_to_dcal(double energy);
99
100
111 double
112 vrna_convert_dcal_to_kcal(int energy);
113
114
119 #endif

```

## 18.252 ViennaRNA/unstructured\_domains.h File Reference

Functions to modify unstructured domains, e.g. to incorporate ligands binding to unpaired stretches.

Include dependency graph for unstructured\_domains.h: This graph shows which files directly or indirectly include this file:

### Data Structures

- struct [vrna\\_unstructured\\_domain\\_s](#)  
*Data structure to store all functionality for ligand binding. [More...](#)*
- struct [vrna\\_unstructured\\_domain\\_motif\\_s](#)

### Macros

- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_EXT\_LOOP 1U**  
*Flag to indicate ligand bound to unpaired stretch in the exterior loop.*
- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_HP\_LOOP 2U**  
*Flag to indicate ligand bound to unpaired stretch in a hairpin loop.*
- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_INT\_LOOP 4U**  
*Flag to indicate ligand bound to unpaired stretch in an interior loop.*
- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_MB\_LOOP 8U**  
*Flag to indicate ligand bound to unpaired stretch in a multibranch loop.*
- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_MOTIF 16U**  
*Flag to indicate ligand binding without additional unbound nucleotides (motif-only)*
- **#define VRNA\_UNSTRUCTURED\_DOMAIN\_ALL\_LOOPS**  
*Flag to indicate ligand bound to unpaired stretch in any loop (convenience macro)*

## Typedefs

- typedef struct [vrna\\_unstructured\\_domain\\_s](#) [vrna\\_ud\\_t](#)  
*Typename for the ligand binding extension data structure [vrna\\_unstructured\\_domain\\_s](#).*
- typedef int() [vrna\\_callback\\_ud\\_energy](#)([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, unsigned int loop\_type, void \*data)  
*Callback to retrieve binding free energy of a ligand bound to an unpaired sequence segment.*
- typedef [FLT\\_OR\\_DBL](#)() [vrna\\_callback\\_ud\\_exp\\_energy](#)([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, unsigned int loop\_type, void \*data)  
*Callback to retrieve Boltzmann factor of the binding free energy of a ligand bound to an unpaired sequence segment.*
- typedef void() [vrna\\_callback\\_ud\\_production](#)([vrna\\_fold\\_compound\\_t](#) \*vc, void \*data)  
*Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature.*
- typedef void() [vrna\\_callback\\_ud\\_exp\\_production](#)([vrna\\_fold\\_compound\\_t](#) \*vc, void \*data)  
*Callback for pre-processing the production rule of the ligand binding to unpaired stretches feature (partition function variant)*
- typedef void() [vrna\\_callback\\_ud\\_probs\\_add](#)([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, unsigned int loop\_type, [FLT\\_OR\\_DBL](#) exp\_energy, void \*data)  
*Callback to store/add equilibrium probability for a ligand bound to an unpaired sequence segment.*
- typedef [FLT\\_OR\\_DBL](#)() [vrna\\_callback\\_ud\\_probs\\_get](#)([vrna\\_fold\\_compound\\_t](#) \*vc, int i, int j, unsigned int loop\_type, int motif, void \*data)  
*Callback to retrieve equilibrium probability for a ligand bound to an unpaired sequence segment.*

## Functions

- [vrna\\_ud\\_motif\\_t](#) \* [vrna\\_ud\\_motifs\\_centroid](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Detect unstructured domains in centroid structure.*
- [vrna\\_ud\\_motif\\_t](#) \* [vrna\\_ud\\_motifs\\_MEA](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure, [vrna\\_ep\\_t](#) \*probability\_list)  
*Detect unstructured domains in MEA structure.*
- [vrna\\_ud\\_motif\\_t](#) \* [vrna\\_ud\\_motifs\\_MFE](#) ([vrna\\_fold\\_compound\\_t](#) \*fc, const char \*structure)  
*Detect unstructured domains in MFE structure.*
- void [vrna\\_ud\\_add\\_motif](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, const char \*motif, double motif\_en, const char \*motif↔\_name, unsigned int loop\_type)  
*Add an unstructured domain motif, e.g. for ligand binding.*
- int \* [vrna\\_ud\\_get\\_motif\\_size\\_at](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, int i, unsigned int loop\_type)  
*Get a list of unique motif sizes that start at a certain position within the sequence.*
- void [vrna\\_ud\\_remove](#) ([vrna\\_fold\\_compound\\_t](#) \*vc)  
*Remove ligand binding to unpaired stretches.*
- void [vrna\\_ud\\_set\\_data](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, void \*data, [vrna\\_callback\\_free\\_auxdata](#) \*free\_cb)  
*Attach an auxiliary data structure.*
- void [vrna\\_ud\\_set\\_prod\\_rule\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_ud\\_production](#) \*pre\_cb, [vrna\\_callback\\_ud\\_energy](#) \*e\_cb)  
*Attach production rule callbacks for free energies computations.*
- void [vrna\\_ud\\_set\\_exp\\_prod\\_rule\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_ud\\_exp\\_production](#) \*pre↔\_cb, [vrna\\_callback\\_ud\\_exp\\_energy](#) \*exp\_e\_cb)  
*Attach production rule for partition function.*
- void [vrna\\_ud\\_set\\_prob\\_cb](#) ([vrna\\_fold\\_compound\\_t](#) \*vc, [vrna\\_callback\\_ud\\_probs\\_add](#) \*setter, [vrna\\_callback\\_ud\\_probs\\_get](#) \*getter)

### 18.252.1 Detailed Description

Functions to modify unstructured domains, e.g. to incorporate ligands binding to unpaired stretches.

## 18.252.2 Function Documentation

### 18.252.2.1 vrna\_ud\_set\_prob\_cb()

```
void vrna_ud_set_prob_cb (
    vrna_fold_compound_t * vc,
    vrna_callback_ud_probs_add * setter,
    vrna_callback_ud_probs_get * getter )
```

**SWIG Wrapper Notes** This function is attached as method `ud_set_prob_cb()` to objects of type `fold_compound`

## 18.253 unstructured\_domains.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_UNSTRUCTURED_DOMAIN_H
2 #define VIENNA_RNA_PACKAGE_UNSTRUCTURED_DOMAIN_H
3
69 typedef struct vrna_unstructured_domain_s vrna_ud_t;
70
71 typedef struct vrna_unstructured_domain_motif_s vrna_ud_motif_t;
72
73 #include <ViennaRNA/datastructures/basic.h>
74 #include <ViennaRNA/fold_compound.h>
75 #include <ViennaRNA/utils/structures.h>
76
95 typedef int (vrna_callback_ud_energy) (vrna_fold_compound_t *vc,
96   int i,
97   int j,
98   unsigned int loop_type,
99   void *data);
100
119 typedef FLT_OR_DBL (vrna_callback_ud_exp_energy) (vrna_fold_compound_t *vc,
120  int i,
121  int j,
122  unsigned int loop_type,
123  void *data);
124
135 typedef void (vrna_callback_ud_production) (vrna_fold_compound_t *vc,
136   void *data);
137
148 typedef void (vrna_callback_ud_exp_production) (vrna_fold_compound_t *vc,
149  void *data);
150
151
161 typedef void (vrna_callback_ud_probs_add) (vrna_fold_compound_t *vc,
162   int i,
163   int j,
164   unsigned int loop_type,
165   FLT_OR_DBL exp_energy,
166   void *data);
167
177 typedef FLT_OR_DBL (vrna_callback_ud_probs_get) (vrna_fold_compound_t *vc,
178  int i,
179  int j,
180  unsigned int loop_type,
181  int motif,
182  void *data);
183
184
189 #define VRNA_UNSTRUCTURED_DOMAIN_EXT_LOOP 1U
190
195 #define VRNA_UNSTRUCTURED_DOMAIN_HP_LOOP 2U
196
201 #define VRNA_UNSTRUCTURED_DOMAIN_INT_LOOP 4U
202
207 #define VRNA_UNSTRUCTURED_DOMAIN_MB_LOOP 8U
208
213 #define VRNA_UNSTRUCTURED_DOMAIN_MOTIF 16U
214
219 #define VRNA_UNSTRUCTURED_DOMAIN_ALL_LOOPS (VRNA_UNSTRUCTURED_DOMAIN_EXT_LOOP | \
220  VRNA_UNSTRUCTURED_DOMAIN_HP_LOOP | \
221  VRNA_UNSTRUCTURED_DOMAIN_INT_LOOP | \
222  VRNA_UNSTRUCTURED_DOMAIN_MB_LOOP)
223
228 struct vrna_unstructured_domain_s {
229     /*
230     *****
231     * Keep track of all motifs added
```

```

232  *****
233  */
234  int          uniq_motif_count;
235  unsigned int *uniq_motif_size;
237  int          motif_count;
238  char         **motif;
239  char         **motif_name;
240  unsigned int *motif_size;
241  double       *motif_en;
242  unsigned int *motif_type;
244  /*
245  *****
246  * Grammar extension for ligand
247  * binding
248  *****
249  */
250  vrna_callback_ud_production *prod_cb;
254  vrna_callback_ud_exp_production *exp_prod_cb;
255  vrna_callback_ud_energy *energy_cb;
256  vrna_callback_ud_exp_energy *exp_energy_cb;
257  void *data;
258  vrna_callback_free_auxdata *free_data;
259  vrna_callback_ud_probs_add *probs_add;
260  vrna_callback_ud_probs_get *probs_get;
261 };
262
263
264 struct vrna_unstructured_domain_motif_s {
265     int start;
266     int number;
267 };
268
269
289 vrna_ud_motif_t *
290 vrna_ud_motifs_centroid(vrna_fold_compound_t *fc,
291                        const char *structure);
292
293
314 vrna_ud_motif_t *
315 vrna_ud_motifs_MEA(vrna_fold_compound_t *fc,
316                  const char *structure,
317                  vrna_ep_t *probability_list);
318
319
338 vrna_ud_motif_t *
339 vrna_ud_motifs_MFE(vrna_fold_compound_t *fc,
340                  const char *structure);
341
342
368 void vrna_ud_add_motif(vrna_fold_compound_t *vc,
369                       const char *motif,
370                       double motif_en,
371                       const char *motif_name,
372                       unsigned int loop_type);
373
374
379 int *vrna_ud_get_motif_size_at(vrna_fold_compound_t *vc,
380                               int i,
381                               unsigned int loop_type);
382
383
384 int *
385 vrna_ud_get_motifs_at(vrna_fold_compound_t *vc,
386                     int i,
387                     unsigned int loop_type);
388
389
390 vrna_ud_motif_t *
391 vrna_ud_detect_motifs(vrna_fold_compound_t *vc,
392                     const char *structure);
393
394
405 void vrna_ud_remove(vrna_fold_compound_t *vc);
406
407
424 void vrna_ud_set_data(vrna_fold_compound_t *vc,
425                      void *data,
426                      vrna_callback_free_auxdata *free_cb);
427
428
463 void vrna_ud_set_prod_rule_cb(vrna_fold_compound_t *vc,
464                              vrna_callback_ud_production *pre_cb,
465                              vrna_callback_ud_energy *e_cb);
466
467
492 void vrna_ud_set_exp_prod_rule_cb(vrna_fold_compound_t *vc,
493                                   vrna_callback_ud_exp_production *pre_cb,

```

```

494                                     vrna_callback_ud_exp_energy      *exp_e_cb);
495
496
497 void  vrna_ud_set_prob_cb(vrna_fold_compound_t      *vc,
498                          vrna_callback_ud_probs_add *setter,
499                          vrna_callback_ud_probs_get  *getter);
500
501
502 #endif

```

## 18.254 ViennaRNA/io/utils.h File Reference

Several utilities for file handling.

Include dependency graph for utils.h: This graph shows which files directly or indirectly include this file:

### Functions

- void **vrna\_file\_copy** (FILE \*from, FILE \*to)  
*Inefficient 'cp'.*
- char \* **vrna\_read\_line** (FILE \*fp)  
*Read a line of arbitrary length from a stream.*
- int **vrna\_mkdir\_p** (const char \*path)  
*Recursively create a directory tree.*
- char \* **vrna\_basename** (const char \*path)  
*Extract the filename from a file path.*
- char \* **vrna\_dirname** (const char \*path)  
*Extract the directory part of a file path.*
- char \* **vrna\_filename\_sanitize** (const char \*name, const char \*replacement)  
*Sanitize a file name.*
- int **vrna\_file\_exists** (const char \*filename)  
*Check if a file already exists in the file system.*

### 18.254.1 Detailed Description

Several utilities for file handling.

,

## 18.255 utils.h

[Go to the documentation of this file.](#)

```

1  #ifndef VIENNA_RNA_PACKAGE_FILE_UTILS_H
2  #define VIENNA_RNA_PACKAGE_FILE_UTILS_H
3
10 #include <stdio.h>
11
21 void vrna_file_copy(FILE *from,
22                    FILE *to);
23
24
35 char *vrna_read_line(FILE *fp);
36
37
41 int vrna_mkdir_p(const char *path);
42
43
47 char *vrna_basename(const char *path);
48
49
53 char *vrna_dirname(const char *path);
54
55
97 char *vrna_filename_sanitize(const char *name,
98                             const char *replacement);
99
100
107 int

```

```

108 vrna_file_exists(const char *filename);
109
110
115 #endif

```

## 18.256 ViennaRNA/plotting/utils.h File Reference

Various utilities to assist in plotting secondary structures and consensus structures.

Include dependency graph for utils.h: This graph shows which files directly or indirectly include this file:

### Functions

- char \*\* **vrna\_annotate\_covar\_db** (const char \*\*alignment, const char \*structure, [vrna\\_md\\_t](#) \*md\_p)  
*Produce covariance annotation for an alignment given a secondary structure.*
- [vrna\\_cpair\\_t](#) \* **vrna\_annotate\_covar\_pairs** (const char \*\*alignment, [vrna\\_ep\\_t](#) \*pl, [vrna\\_ep\\_t](#) \*mfel, double threshold, [vrna\\_md\\_t](#) \*md)  
*Produce covariance annotation for an alignment given a set of base pairs.*

### 18.256.1 Detailed Description

Various utilities to assist in plotting secondary structures and consensus structures.

,

## 18.257 utils.h

[Go to the documentation of this file.](#)

```

1  #ifndef VIENNA_RNA_PACKAGE_PLOT_UTILS_H
2  #define VIENNA_RNA_PACKAGE_PLOT_UTILS_H
3
10 #include <ViennaRNA/datastructures/basic.h>
11 #include <ViennaRNA/model.h>
12 #include <ViennaRNA/utils/structures.h>
13
32 char **
33 vrna_annotate_covar_db(const char  **alignment,
34                      const char  *structure,
35                      vrna\_md\_t    *md_p);
36
37
38 char **
39 vrna_annotate_covar_db_extended(const char  **alignment,
40                               const char  *structure,
41                               vrna\_md\_t    *md_p,
42                               unsigned int  options);
43
44
49 vrna\_cpair\_t *
50 vrna_annotate_covar_pairs(const char  **alignment,
51                          vrna\_ep\_t    *pl,
52                          vrna\_ep\_t    *mfel,
53                          double      threshold,
54                          vrna\_md\_t    *md);
55
56
61 #endif

```

## 18.258 ViennaRNA/utils.h File Reference

Use [ViennaRNA/utils/basic.h](#) instead.

Include dependency graph for utils.h:

### 18.258.1 Detailed Description

Use [ViennaRNA/utils/basic.h](#) instead.

**Deprecated** Use [ViennaRNA/utils/basic.h](#) instead

**Deprecated** Use [ViennaRNA/utils/basic.h](#) instead

## 18.259 utils.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_UTILS_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_UTILS_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 #   ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/Utils.h>! Use <ViennaRNA/Utils/Basic.h> instead!"
13 #   endif
14 #include <ViennaRNA/Utils/Basic.h>
15 #include <ViennaRNA/Utils/Strings.h>
16 #include <ViennaRNA/Utils/Structures.h>
17 #include <ViennaRNA/IO/Utils.h>
18 #include <ViennaRNA/Alphabet.h>
19 #endif
20
21 #endif
```

## 18.260 cpu.h

```
1 #ifndef VIENNA_RNA_PACKAGE_UTILS_CPU_H
2 #define VIENNA_RNA_PACKAGE_UTILS_CPU_H
3
4 #define VRNA_CPU_SIMD_NONE      0U
5 #define VRNA_CPU_SIMD_SSE2     1U
6 #define VRNA_CPU_SIMD_SSE3     2U
7 #define VRNA_CPU_SIMD_SSE41    4U
8 #define VRNA_CPU_SIMD_SSE42    8U
9 #define VRNA_CPU_SIMD_AVX      16U
10 #define VRNA_CPU_SIMD_AVX2     32U
11 #define VRNA_CPU_SIMD_AVX512F  64U
12
13
14 char *
15 vrna_cpu_vendor_string(void);
16
17
18 unsigned int
19 vrna_cpu_simd_capabilities(void);
20
21
22 #endif
```

## 18.261 higher\_order\_functions.h

```
1 #ifndef VIENNA_RNA_PACKAGE_UTILS_FUN_H
2 #define VIENNA_RNA_PACKAGE_UTILS_FUN_H
3
4 void
5 vrna_fun_dispatch_disable(void);
6
7
8 void
9 vrna_fun_dispatch_enable(void);
10
11
12 int
13 vrna_fun_zip_add_min(const int *e1,
14                     const int *e2,
15                     int count);
16
17
18 #endif
```

## 18.262 ViennaRNA/Utils/Strings.h File Reference

General utility- and helper-functions for RNA sequence and structure strings used throughout the ViennaRNA Package.

Include dependency graph for strings.h: This graph shows which files directly or indirectly include this file:

### Macros

- #define XSTR(s) STR(s)

- *Stringify a macro after expansion.*
- `#define STR(s) #s`  
*Stringify a macro argument.*
- `#define FILENAME_MAX_LENGTH 80`  
*Maximum length of filenames that are generated by our programs.*
- `#define FILENAME_ID_LENGTH 42`  
*Maximum length of id taken from fasta header for filename generation.*
- `#define VRNA_TRIM_LEADING 1U`  
*Trim only characters leading the string.*
- `#define VRNA_TRIM_TRAILING 2U`  
*Trim only characters trailing the string.*
- `#define VRNA_TRIM_IN_BETWEEN 4U`  
*Trim only characters within the string.*
- `#define VRNA_TRIM_SUBST_BY_FIRST 8U`  
*Replace remaining characters after trimming with the first delimiter in list.*
- `#define VRNA_TRIM_DEFAULT ( VRNA_TRIM_LEADING | VRNA_TRIM_TRAILING )`  
*Default settings for trimming, i.e. trim leading and trailing.*
- `#define VRNA_TRIM_ALL ( VRNA_TRIM_DEFAULT | VRNA_TRIM_IN_BETWEEN )`  
*Trim characters anywhere in the string.*

## Functions

- `char * vrna_strdup_printf (const char *format,...)`  
*Safely create a formatted string.*
- `char * vrna_strdup_vprintf (const char *format, va_list argp)`  
*Safely create a formatted string.*
- `int vrna_strcat_printf (char **dest, const char *format,...)`  
*Safely append a formatted string to another string.*
- `int vrna_strcat_vprintf (char **dest, const char *format, va_list args)`  
*Safely append a formatted string to another string.*
- `unsigned int vrna_strtrim (char *string, const char *delimiters, unsigned int keep, unsigned int options)`  
*Trim a string by removing (multiple) occurrences of a particular character.*
- `char ** vrna_strsplit (const char *string, const char *delimiter)`  
*Split a string into tokens using a delimiting character.*
- `char * vrna_random_string (int l, const char symbols[])`  
*Create a random string using characters from a specified symbol set.*
- `int vrna_hamming_distance (const char *s1, const char *s2)`  
*Calculate hamming distance between two sequences.*
- `int vrna_hamming_distance_bound (const char *s1, const char *s2, int n)`  
*Calculate hamming distance between two sequences up to a specified length.*
- `void vrna_seq_toRNA (char *sequence)`  
*Convert an input sequence (possibly containing DNA alphabet characters) to RNA alphabet.*
- `void vrna_seq_toupper (char *sequence)`  
*Convert an input sequence to uppercase.*
- `void vrna_seq_reverse (char *sequence)`  
*Reverse a string in-place.*
- `char * vrna_DNA_complement (const char *sequence)`  
*Retrieve a DNA sequence which resembles the complement of the input sequence.*
- `char * vrna_seq_ungapped (const char *sequence)`  
*Remove gap characters from a nucleotide sequence.*
- `char * vrna_cut_point_insert (const char *string, int cp)`



- Add a separating '&' character into a string according to cut-point position.*
- char \* [vrna\\_cut\\_point\\_remove](#) (const char \*string, int \*cp)
- Remove a separating '&' character from a string.*
- void [str\\_uppercase](#) (char \*sequence)
- Convert an input sequence to uppercase.*
- void [str\\_DNA2RNA](#) (char \*sequence)
- Convert a DNA input sequence to RNA alphabet.*
- char \* [random\\_string](#) (int l, const char symbols[])
- Create a random string using characters from a specified symbol set.*
- int [hamming](#) (const char \*s1, const char \*s2)
- Calculate hamming distance between two sequences.*
- int [hamming\\_bound](#) (const char \*s1, const char \*s2, int n)
- Calculate hamming distance between two sequences up to a specified length.*

### 18.262.1 Detailed Description

General utility- and helper-functions for RNA sequence and structure strings used throughout the ViennaRNA Package.

,

### 18.262.2 Function Documentation

#### 18.262.2.1 str\_uppercase()

```
void str_uppercase (
    char * sequence )
```

Convert an input sequence to uppercase.

**Deprecated** Use [vrna\\_seq\\_toupper\(\)](#) instead!

#### 18.262.2.2 str\_DNA2RNA()

```
void str_DNA2RNA (
    char * sequence )
```

Convert a DNA input sequence to RNA alphabet.

**Deprecated** Use [vrna\\_seq\\_toRNA\(\)](#) instead!

#### 18.262.2.3 random\_string()

```
char * random_string (
    int l,
    const char symbols[] )
```

Create a random string using characters from a specified symbol set.

**Deprecated** Use [vrna\\_random\\_string\(\)](#) instead!

#### 18.262.2.4 hamming()

```
int hamming (
    const char * s1,
    const char * s2 )
```

Calculate hamming distance between two sequences.

**Deprecated** Use [vrna\\_hamming\\_distance\(\)](#) instead!

#### 18.262.2.5 hamming\_bound()

```
int hamming_bound (
    const char * s1,
    const char * s2,
    int n )
```

Calculate hamming distance between two sequences up to a specified length.

**Deprecated** Use [vrna\\_hamming\\_distance\\_bound\(\)](#) instead!

### 18.263 strings.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_STRING_UTILS_H
2 #define VIENNA_RNA_PACKAGE_STRING_UTILS_H
3
4 #ifdef VRNA_WARN_DEPRECATED
5 # if defined(__clang__)
6 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
7 # elif defined(__GNUC__)
8 #   define DEPRECATED(func, msg) func __attribute__((deprecated(msg)))
9 # else
10 #   define DEPRECATED(func, msg) func
11 # endif
12 #else
13 # define DEPRECATED(func, msg) func
14 #endif
15
16 #include <stdarg.h>
17 #include <ViennaRNA/datastructures/basic.h>
18
19 #define XSTR(s) STR(s)
20
21 #define STR(s) #s
22
23 #ifndef FILENAME_MAX_LENGTH
24 #define FILENAME_MAX_LENGTH 80
25
26 #define FILENAME_ID_LENGTH 42
27
28 #endif
29
30 #ifdef HAVE_CONFIG_H
31 #include <config.h>
32 #endif
33
34 #ifdef HAVE_STRDUP
35 char *
36 strdup(const char *s);
37
38 #endif
39
40 #endif
41
42 char *
43 vrna_strdup_printf(const char *format,
44                   ...);
45
46
47 char *
48 vrna_strdup_vprintf(const char *format,
49                    va_list argp);
50
51
52 int
53 vrna_strcat_printf(char **dest,
54                   const char *format,
```

```
134         ...);
135
136
149 int
150 vrna_strcat_vprintf(char      **dest,
151                    const char *format,
152                    va_list    args);
153
154
159 #define VRNA_TRIM_LEADING      1U
160
165 #define VRNA_TRIM_TRAILING    2U
166
171 #define VRNA_TRIM_IN_BETWEEN   4U
172
177 #define VRNA_TRIM_SUBST_BY_FIRST 8U
178
183 #define VRNA_TRIM_DEFAULT      ( VRNA_TRIM_LEADING | VRNA_TRIM_TRAILING )
184
189 #define VRNA_TRIM_ALL          ( VRNA_TRIM_DEFAULT | VRNA_TRIM_IN_BETWEEN )
190
237 unsigned int
238 vrna_strtrim(char      *string,
239              const char *delimiters,
240              unsigned int keep,
241              unsigned int options);
242
243
290 char **
291 vrna_strsplit(const char *string,
292              const char *delimiter);
293
294
295 char *
296 vrna_strjoin(const char **strings,
297             const char *delimiter);
298
299
307 char *
308 vrna_random_string(int      l,
309                   const char symbols[]);
310
311
319 int
320 vrna_hamming_distance(const char *s1,
321                     const char *s2);
322
323
334 int
335 vrna_hamming_distance_bound(const char *s1,
336                           const char *s2,
337                           int      n);
338
339
347 void
348 vrna_seq_toRNA(char *sequence);
349
350
356 void
357 vrna_seq_toupper(char *sequence);
358
359
374 void
375 vrna_seq_reverse(char *sequence);
376
377
396 char *
397 vrna_DNA_complement(const char *sequence);
398
399
406 char *
407 vrna_seq_ungapped(const char *sequence);
408
409
421 char *
422 vrna_cut_point_insert(const char *string,
423                     int      cp);
424
425
438 char *
439 vrna_cut_point_remove(const char *string,
440                     int      *cp);
441
442
447 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
448
453 DEPRECATED(void
```

```

454         str_uppercase(char *sequence),
455         "Use vrna_seq_toupper() instead");
456
462 DEPRECATED(void
463         str_DNA2RNA(char *sequence),
464         "Use vrna_seq_toRNA() instead");
465
471 DEPRECATED(char *random_string(int l,
472                                const char symbols[]),
473         "Use vrna_random_string() instead");
474
480 DEPRECATED(int
481         hamming(const char *s1,
482                const char *s2),
483         "Use vrna_hamming_distance() instead");
484
490 DEPRECATED(int
491         hamming_bound(const char *s1,
492                       const char *s2,
493                       int n),
494         "Use vrna_hamming_distance_bound() instead");
495
496 #endif
497
498 #endif

```

## 18.264 svm.h

```

1 #ifndef VIENNA_RNA_PACKAGE_UTILS_SVM_H
2 #define VIENNA_RNA_PACKAGE_UTILS_SVM_H
3
4 extern char *avg_model_string;
5 extern char *sd_model_string;
6
7 float      get_z(char *sequence,
8                 double energy);
9 double     avg_regression (int N,
10                           int A,
11                           int C,
12                           int G,
13                           int T,
14                           struct svm_model *avg_model,
15                           int *info );
16 double     sd_regression  (int N,
17                           int A,
18                           int C,
19                           int G,
20                           int T,
21                           struct svm_model *sd_model);
22 double     minimal_sd    (int N,
23                           int A,
24                           int C,
25                           int G,
26                           int T);
27 struct svm_model *svm_load_model_string(char *modelString);
28 int         *get_seq_composition( short *S,
29                                   unsigned int start,
30                                   unsigned int stop,
31                                   unsigned int length);
32
33 #endif

```

## 18.265 vrna\_config.h

```

1 #ifndef VIENNA_RNA_PACKAGE_CONFIG_H
2 #define VIENNA_RNA_PACKAGE_CONFIG_H
3
4 /* version number */
5 #define VRNA_VERSION "2.5.1"
6
7 #define VRNA_VERSION_MAJOR 2
8 #define VRNA_VERSION_MINOR 5
9 #define VRNA_VERSION_PATCH 1
10
11 /*
12  * The following pre-processor definitions specify whether
13  * or not certain features were activated upon build-time
14  */
15
16 /*
17  * Build with deactivated C11 Features
18  */

```

```

19  * It this feature is missing, the next line defines
20  * 'VRNA_DISABLE_C11_FEATURES'
21  */
22
23
24 /*
25  * Build with OpenMP support
26  *
27  * If this feature is present, the next line defines
28  * 'VRNA_WITH_OPENMP'
29  */
30 #define VRNA_WITH_OPENMP
31
32 /*
33  * Build with single precision partition function
34  *
35  * If this feature is present, the next line defines
36  * 'USE_FLOAT_PF'
37  */
38
39
40 /*
41  * Build with JSON input/output support
42  *
43  * If this feature is present, the next line defines
44  * 'VRNA_WITH_JSON_SUPPORT'
45  */
46 #define VRNA_WITH_JSON_SUPPORT
47
48 /*
49  * Build with Support Vector Machine (SVM) Z-score feature in RNALfold
50  *
51  * If this feature is present, the next line defines
52  * 'VRNA_WITH_SVM'
53  */
54 #define VRNA_WITH_SVM
55
56 /*
57  * Build with GSL minimizers
58  *
59  * If this feature is present, the next line defines
60  * 'VRNA_WITH_GSL'
61  */
62 #define VRNA_WITH_GSL
63
64 /*
65  * Build with colored TTY output
66  *
67  * If this feature is missing, the next line defines
68  * 'VRNA_WITHOUT_TTY_COLORS'
69  */
70
71
72 /*
73  * Build with Link Time Optimization support
74  *
75  * If this feature is enabled, the next line defines
76  * 'VRNA_WITH_LTO'
77  */
78
79
80 /*
81  * Build with Naview Layout algorithm of Brucoleri 1988
82  *
83  * If this feature is enabled, the next line defines
84  * 'VRNA_WITH_NAVIEW_LAYOUT'
85  */
86 #define VRNA_WITH_NAVIEW_LAYOUT
87
88
89
90 #endif

```

## 18.266 ViennaRNA/landscape/walk.h File Reference

Methods to generate particular paths such as gradient or random walks through the energy landscape of an RNA sequence.

Include dependency graph for walk.h: This graph shows which files directly or indirectly include this file:

## Macros

- `#define VRNA_PATH_STEEPEST_DESCENT 128`  
*Option flag to request a steepest descent / gradient path.*
- `#define VRNA_PATH_RANDOM 256`  
*Option flag to request a random walk path.*
- `#define VRNA_PATH_NO_TRANSITION_OUTPUT 512`  
*Option flag to omit returning the transition path.*
- `#define VRNA_PATH_DEFAULT (VRNA_PATH_STEEPEST_DESCENT | VRNA_MOVESET_DEFAULT)`  
*Option flag to request defaults (steepest descent / default move set)*

## Functions

- `vrna_move_t * vrna_path (vrna_fold_compound_t *vc, short *pt, unsigned int steps, unsigned int options)`  
*Compute a path, store the final structure, and return a list of transition moves from the start to the final structure.*
- `vrna_move_t * vrna_path_gradient (vrna_fold_compound_t *vc, short *pt, unsigned int options)`  
*Compute a steepest descent / gradient path, store the final structure, and return a list of transition moves from the start to the final structure.*
- `vrna_move_t * vrna_path_random (vrna_fold_compound_t *vc, short *pt, unsigned int steps, unsigned int options)`  
*Generate a random walk / path of a given length, store the final structure, and return a list of transition moves from the start to the final structure.*

### 18.266.1 Detailed Description

Methods to generate particular paths such as gradient or random walks through the energy landscape of an RNA sequence.

## 18.267 walk.h

[Go to the documentation of this file.](#)

```

1 #ifndef VIENNA_RNA_PACKAGE_WALK_H
2 #define VIENNA_RNA_PACKAGE_WALK_H
3
11 #include <ViennaRNA/fold_compound.h>
12 #include <ViennaRNA/landscape/move.h>
13
24 #define VRNA_PATH_STEEPEST_DESCENT 128
25
30 #define VRNA_PATH_RANDOM 256
31
36 #define VRNA_PATH_NO_TRANSITION_OUTPUT 512
37
43 #define VRNA_PATH_DEFAULT (VRNA_PATH_STEEPEST_DESCENT | VRNA_MOVESET_DEFAULT)
44
73 vrna_move_t *
74 vrna_path(vrna_fold_compound_t *vc,
75           short *pt,
76           unsigned int steps,
77           unsigned int options);
78
79
101 vrna_move_t *
102 vrna_path_gradient(vrna_fold_compound_t *vc,
103                   short *pt,
104                   unsigned int options);
105
106
129 vrna_move_t *
130 vrna_path_random(vrna_fold_compound_t *vc,
131                 short *pt,
132                 unsigned int steps,
133                 unsigned int options);
134
135
140 #endif /* VIENNA_RNA_PACKAGE_WALK_H */

```

## 18.268 ViennaRNA/walk.h File Reference

Use [ViennaRNA/landscape/walk.h](#) instead.

Include dependency graph for walk.h:

### 18.268.1 Detailed Description

Use [ViennaRNA/landscape/walk.h](#) instead.

**Deprecated** Use [ViennaRNA/landscape/walk.h](#) instead

## 18.269 walk.h

[Go to the documentation of this file.](#)

```
1 #ifndef VIENNA_RNA_PACKAGE_WALK_DEPRECATED_H
2 #define VIENNA_RNA_PACKAGE_WALK_DEPRECATED_H
3
10 #ifndef VRNA_DISABLE_BACKWARD_COMPATIBILITY
11 # ifdef VRNA_WARN_DEPRECATED
12 #warning "Including deprecated header file <ViennaRNA/walk.h>! Use <ViennaRNA/landscape/walk.h> instead!"
13 # endif
14 #include <ViennaRNA/landscape/walk.h>
15 #include <ViennaRNA/landscape/neighbor.h>
16 #endif
17
18 #endif
```

## 18.270 wrap\_dlib.h

```
1 #ifndef VIENNARNA_DLIB_WRAPPER_H
2 #define VIENNARNA_DLIB_WRAPPER_H
3
4 #ifdef __cplusplus
5 extern "C" {
6 #endif
7
8 double *
9 vrna_equilibrium_conc(const double      *eq_constants,
10                      double            *concentration_strands,
11                      const unsigned int **A,
12                      size_t            num_strands,
13                      size_t            num_complexes);
14
15
16 #ifdef __cplusplus
17 }
18 #endif
19
20 #endif
```

## 18.271 zscore.h

```
1 #ifndef VIENNA_RNA_PACKAGE_ZSCORE_H
2 #define VIENNA_RNA_PACKAGE_ZSCORE_H
3
4 typedef struct vrna_zsc_dat_s *vrna_zsc_dat_t;
5
6 #define VRNA_ZSCORE_OPTIONS_NONE      1U
7 #define VRNA_ZSCORE_FILTER_ON        2U
8 #define VRNA_ZSCORE_PRE_FILTER        4U
9 #define VRNA_ZSCORE_REPORT_SUBSUMED   8U
10 #define VRNA_ZSCORE_MODEL_DEFAULT     16U
11 #define VRNA_ZSCORE_SETTINGS_DEFAULT (VRNA_ZSCORE_FILTER_ON | VRNA_ZSCORE_MODEL_DEFAULT)
12
13 int
14 vrna_zsc_filter_init(vrna_fold_compound_t *fc,
15                     double                min_z,
16                     unsigned int          options);
17
18
19 int
20 vrna_zsc_filter_update(vrna_fold_compound_t *fc,
21                       double                min_z,
22                       unsigned int          options);
23
```

```
24
25 void
26 vrna_zsc_filter_free(vrna_fold_compound_t *fc);
27
28
29 int
30 vrna_zsc_filter_on(vrna_fold_compound_t *fc);
31
32
33 double
34 vrna_zsc_filter_threshold(vrna_fold_compound_t *fc);
35
36
37 double
38 vrna_zsc_compute(vrna_fold_compound_t *fc,
39                 unsigned int      i,
40                 unsigned int      j,
41                 int               e);
42
43
44 double
45 vrna_zsc_compute_raw(vrna_fold_compound_t *fc,
46                     unsigned int      i,
47                     unsigned int      j,
48                     int               e,
49                     double            *avg,
50                     double            *sd);
51
52
53 #endif
```



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